
Antibody constructs for FLT3 and CD3

The present invention relates to a bispecific antibody construct comprising a first binding domain which binds to human FLT3 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.

INTRODUCTION:

Acute Myeloid Leukemia (AML) is a heterogenous hematological malignancy that is the most common type of acute leukemia diagnosed in adults. AML accounts for roughly a third of all leukemias with an estimated 14,500 new cases reported in 2013 in the United States alone and poor overall survival rates. There has been little improvement in the standard of care for AML patients over the past thirty years. However, recent advances in molecular and cell biology have revolutionized our understanding of human hematopoiesis, both in normal and diseased states. Several key players involved in disease pathogenesis have been identified and can be interrogated as actionable targets. One such activating “driver” gene that is most commonly mutated in approximately 30% of AML is *FLT3*.

Fms-like tyrosine kinase 3 (FLT3) also known as fetal liver kinase 2 (FLK-2), human stem cell kinase 1 (SCK-1) or Cluster of Differentiation antigen (CD135) is a hematopoietic receptor tyrosine kinase that was cloned by two independent groups in the 1990s. The *FLT3* gene, located on chromosome 13q12 in humans encodes a Class III receptor tyrosine kinase protein that shares homology with other Class III family members including stem cell factor receptor (c-KIT), macrophage colony-stimulating factor receptor (FMS) and platelet-derived growth factor receptor (PDGFR).

Upon binding with the FLT3 ligand, FLT3 receptor undergoes homodimerization thereby enabling autophosphorylation of specific tyrosine residues in the juxtamembrane domain and downstream activation via PI3K/Akt, MAPK and STAT5 pathways. FLT3 thus plays a crucial role in controlling proliferation, survival and differentiation of normal hematopoietic cells.

Human FLT3 is expressed in CD34+CD38- hematopoietic stem cells (HSC) as well as in a subset of dendritic precursor cells. FLT3 expression can also be detected in multipotent progenitor cells like the CD34+CD38+CD45RA-CD123^{low} Common Myeloid Progenitor (CMP), the CD34+CD38+CD45RA+CD123^{low} Granulocyte Monocyte Progenitors (GMP), and CD34+CD38+CD10+CD19- Common Lymphoid Progenitor cells (CLP). Interestingly, FLT3 expression is almost absent in the CD34+CD38-CD45RA-CD123- Megakaryocyte Erythrocyte Progenitor cells (MEP). FLT3 expression is thus confined mainly to the early myeloid and lymphoid progenitor cells with some expression in the more mature monocytic lineage cells. This limited expression pattern of FLT3 is in striking contrast to that of FLT3 ligand, which is expressed in most hematopoietic tissues and the prostate, kidney, lung, colon and heart. These varied expression patterns such that FLT3 expression is the rate limiting step in determining tissue specificity of FLT3 signaling pathways.

The most common *FLT3* mutation in AML is the FLT3 internal tandem duplication (FLT3-ITD) that is found in 20 to 38% of patients with cytogenetically normal AML. FLT3-ITDs are formed when a portion of the juxtamembrane domain coding sequence gets duplicated and inserted in a head to tail orientation. *FLT3* mutations have not been identified in patients with chronic lymphoid leukemia (CLL), non-Hodgkin's lymphoma and multiple myeloma suggesting strong disease specificity for AML. Mutant FLT3 activation is generally observed across all FAB subtypes, however, it is significantly increased in AML patients with FAB M5 (monocytic leukemia), while FAB subtypes M2 and M6 (granulocytic or erythroid leukemia) are significantly less frequently associated with FLT3 activation, in line with normal expression patterns of FLT3. A small percentage of AML patients (5-7%) present with single amino acid mutations in the FLT3 tyrosine kinase domain (FLT3 TKD), most commonly at D835 or in some cases at T842 or I836 while even fewer patients (~1%) harbor mutations in the FLT3 juxtamembrane domain involving residues 579, 590, 591 and 594. Patients with *FLT3-ITD* mutant AML have an aggressive form of disease characterized by early relapse and poor survival, while overall survival and event-free survival are not significantly influenced by presence of *FLT3-TKD* mutations. Furthermore, AML patients with *FLT3-ITD* mutation with concurrent *TET2* or *DNMT3A* mutations have an unfavorable overall risk profile compared to *FLT3-ITD* mutant AML patients with wild-type *TET2* or *DNMT3A* underscoring the clinical and biological heterogeneity of AML.

Both FLT3-ITD and FLT3 TKD mutations induce ligand independent activation of FLT3 leading to downstream activation of the Ras/MAPK pathway and the PI3K/Akt pathways. However, the downstream signaling pathways associated with either mutation differ primarily in the

preferential activation of STAT5 by FLT3-ITD, thereby leading to increased proliferation potential and aberrant regulation of DNA repair pathways.

Independent of *FLT3* mutation status, FLT3 phosphorylation is evident in over two-thirds of AML patients and FLT3 is expressed in >80% AML blasts and in ~90% of all AML patients making it an attractive therapeutic target associated with disease pathogenesis in a large sample size.

Several small molecule inhibitors have emerged as attractive therapeutic options for AML patients with *FLT3* mutations. The first generation of FLT3 tyrosine kinase inhibitors (TKI) was characterized by lack of selectivity, potency and unfavorable pharmacokinetic properties. Newer and more selective agents have been developed to combat this issue; however, their efficacy has been limited by emergence of secondary resistance.

Several early FLT3 TKIs included midostaurin (PKC412), lestaurtinib (CEP-701), sunitinib (SUI1248) and sorafenib (BAY 43-9006) amongst others. Response rates in Phase I and Phase II with these multikinase targeting agents in patients with relapsed or refractory AML is limited, presumably due to their inability to achieve effective FLT3 inhibition without dose limiting toxicities. Quizartinib (AC220) has been developed as a second generation FLT3 TKI with high selectivity for FLT3 wild type and FLT3-ITD and has demonstrated benefit especially in the peri-transplant setting in a younger cohort of patients. However, secondary mutations in *FLT3* identified in relapsed patients who received quizartinib accentuate the need to develop better therapeutic strategies for AML patients, while highlighting the validity of FLT3 as a therapeutic target.

Several targeted agents have been tested in AML patients with either *de novo*, relapsed/refractory or secondary disease. Epigenetic silencing of tumor suppressor genes plays an important role in AML disease pathogenesis, and DNA methyltransferase (DNMT) inhibitors like azacitadine and decitabine have achieved some clinical success. Further, the recent identification of mutations that affect histone posttranslational modifications (e.g. *EZH2* and *ASXL1* mutations) or DNA methylation (e.g. *DNMT3A*, *TET2*, *IDH1/2*) in a subset of AML patients has led to development of a variety of therapeutic options including *EZH2*, *DOT1L*, *IDH1/2* inhibitors along with HDAC and proteasome inhibitors. However, preclinical studies of many of these compounds in AML cells suggest that these inhibitors may be altering the phenotype and gene expression characteristic of hematopoietic differentiation rather than causing direct cytotoxicity of AML blasts. There therefore remains a strong unmet medical need to identify novel targets/modalities to combat AML and cause targeted lysis of AML blast cells. Other therapeutic candidates for AML include Aurora kinase inhibitors including AMG 900 and inhibitors to polo-like kinases that play an important role in cell cycle progression.

The standard of care for AML patients has remained chemotherapy with stem cell transplantation when feasible. However the emergence of relapsed/refractory cases in a large majority of treated patients warrants additional therapeutic modalities. The identification and description of several leukemia specific antigens along with a clearer understanding of immune mediated graft-versus-leukemia effects have paved the way to development of immunomodulatory strategies for combating hematological malignancies, reviewed in several articles.

Gemtuzumab ozogamicin (GO) is an antibody-drug conjugate directed against CD33, a ubiquitous myeloid cell surface marker. GO was withdrawn from the market after randomized trials that showed no improvements in outcomes with GO therapy. However, there is a need for reappraisal of GO in AML and several trials have been initiated to evaluate the efficacy and toxicity of GO in a thorough manner. Other biological agents against AML include lintuzumab (SGN-33), a humanized anti-CD33 monoclonal antibody either in an unconjugated form or conjugated with radioactive bismuth and SL-401, comprised of human IL-3 coupled with a diphtheria toxin payload against the IL-3 receptor that is overexpressed in a majority of AML blasts. Next-generation monoclonal antibodies that target both tumor associated antigen and effector cytolytic T-cells include AMG 330 (a bi-specific T-cell engager or BiTE molecule that targets CD33) and MGD006, a dual affinity retargeting molecule which binds to CD123 and CD3.

The recent success of chimeric antigen receptor T-cells in refractory CLL and acute lymphoblastic leukemia (ALL) has paved the way forward to development of myeloid specific CAR-T cells including CD123 CAR-T and CD33 CAR-T therapies. Several efforts have also been invested in generating dendritic cell vaccines as well as combination with checkpoint blockade inhibitors in order to improve outcomes.

Therapeutic antibodies against FLT3 have also been generated. Antibody therapy is presumed to be more efficacious with low probability of development of secondary resistance mechanisms since the antibody is directed against the extracellular domain of FLT3, which is less prone to mutations than the intracellular kinase domain. The Imclone antibody, IMC-EB10 was evaluated in relapsed AML patients in a Phase I study, however, the study was terminated due to lack of efficacy (ClinicalTrials.gov Identifier: NCT00887926). There thus remains a pressing need to evaluate second generation monoclonal antibodies including bispecific antibodies for treatment of AML.

As there is still a need for having available further options for the treatment of hematological diseases diseases related to the expression of FLT3, there are provided herewith means and

methods for the solution of this problem in the form of a bispecific antibody construct having a binding domain directed to FLT3 on the surface of tumor target cells and a second binding domain directed to CD3 on the surface of T cells.

Thus, in a first aspect, the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human FLT3 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 FLT3 which is comprised within the extracellular region of FLT3 as depicted in SEQ ID NOs: 801-804.

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.

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 Dübeler, 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 FLT3 or CD3 epsilon (Schier, *Human Antibodies Hybridomas* 7 (1996), 97-105; Malmberg, *J. Immunol. Methods* 183 (1995), 7-13).

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

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

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

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

A preferred type of an amino acid substitutional variation of the antibody constructs involves substituting one or more hypervariable region residues of a parent antibody (e. g. a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e. g. 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e. g. binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the binding domain and, e.g., human FLT3. 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: FLT3 and CD3, respectively. The structure and function of the first binding domain (recognizing FLT3), 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 FLT3 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 FLT3 and 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: FLT3 and CD3, respectively.

The term "epitope" refers to a site on an antigen to which a binding domain, such as 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 one of the binding domains is comprised within the FLT3 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 FLT3 protein is exchanged / replaced with its corresponding region of a non-human and non-primate FLT3 antigen (e.g., mouse FLT3, 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 FLT3 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 FLT3 protein, whereby binding to the respective region in the human FLT3 protein is set to be 100%. It is envisaged that the aforementioned human FLT3 / non-human FLT3 chimeras are expressed in CHO cells. It is also envisaged that the human FLT3 / non-human FLT3 chimeras are fused with a transmembrane domain and/or cytoplasmic domain of a different membrane-bound protein such as EpCAM, see Example 1 and 2.

In an alternative or additional method for epitope mapping, several truncated versions of the human FLT3 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 FLT3 domains / sub-domains or regions are stepwise deleted, starting from the N-terminus. The truncated FLT3 versions that were generated and used in the context of the present invention are depicted in is envisaged that the truncated FLT3 versions may be expressed in CHO cells. It is also envisaged that the truncated FLT3 versions may be 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 FLT3 versions may encompass a signal peptide domain at their N-terminus, for example a signal peptide derived from mouse IgG heavy chain signal peptide. It is furtherore envisaged that the truncated FLT3 versions may 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 FLT3 versions which do not encompass any more the FLT3 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 FLT3 protein (or its extracellular region or domain) is set to be 100%, see Example 3.

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: FLT3 and CD3, respectively) and, generally, does not exhibit significant reactivity with proteins or antigens other than FLT3 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 FLT3 or CD3. Preferably, a binding domain of the invention does not essentially or substantially bind to proteins or antigens other than FLT3 or CD3 (*i.e.*, the first binding domain is not capable of binding to proteins other than FLT3 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 FLT3 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 FLT3 or CD3, whereby binding to FLT3 or CD3, respectively, is set to be 100%.

Specific binding is believed to be effected by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of secondary modifications of said structures. The specific interaction of the antigen-interaction-site with its specific antigen may result in a simple binding of said site to the antigen. Moreover, the specific interaction of the antigen-interaction-site with its specific antigen may alternatively or additionally result in the initiation of a signal, *e.g.* due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

In another aspect, the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human FLT3 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 FLT3 which is comprised within the region of the human FLT3 having a sequence as depicted in SEQ ID NO: 814 (cluster 1) or SEQ ID NO: 816 (cluster 3).

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:

SEQ ID NOs: 151-156, SEQ ID NOs: 161-166, SEQ ID NOs: 171-176, SEQ ID NOs: 181-186, SEQ ID NOs: 191-196, SEQ ID NOs: 201-206, SEQ ID NOs: 211-216, SEQ ID NOs: 221-226, SEQ ID NOs: 231-236, SEQ ID NOs: 241-246, SEQ ID NOs: 251-256, SEQ ID NOs: 261-266, SEQ ID NOs: 271-276, SEQ ID NOs: 281-286, SEQ ID NOs: 291-296, SEQ ID NOs: 301-306, SEQ ID NOs: 311-316, SEQ ID NOs: 321-326, SEQ ID NOs: 331-336, SEQ ID NOs: 341-346, SEQ ID NOs: 351-356, SEQ ID NOs: 361-366, SEQ ID NOs: 371-376, SEQ ID NOs: 381-386, SEQ ID NOs: 391-396, SEQ ID NOs: 401-406, SEQ ID NOs: 411-416, SEQ ID NOs: 421-426, SEQ ID NOs: 431-436, SEQ ID NOs: 441-446, SEQ ID NOs: 451-456, SEQ ID NOs: 461-466, SEQ ID NOs: 471-476, SEQ ID NOs: 481-486, SEQ ID NOs: 491-496, SEQ ID NOs: 501-506, SEQ ID NOs: 511-516, SEQ ID NOs: 521-526, SEQ ID NOs: 531-536, SEQ ID NOs: 541-546, SEQ ID NOs: 551-556, SEQ ID NOs: 561-566, SEQ ID NOs: 571-576, SEQ ID NOs: 581-586, SEQ ID NOs: 591-596, SEQ ID NOs: 601-606, SEQ ID NOs: 611-616, SEQ ID NOs: 621-626, SEQ ID NOs: 631-636, SEQ ID NOs: 641-646, SEQ ID NOs: 651-656, SEQ ID NOs: 661-666, SEQ ID NOs: 671-676, SEQ ID NOs: 681-686, SEQ ID NOs: 691-696, SEQ ID NOs: 701-706, SEQ ID NOs: 711-716, SEQ ID NOs: 721-726, SEQ ID NOs: 731-736, SEQ ID NOs: 741-746, SEQ ID NOs: 751-756, SEQ ID NOs: 761-766, SEQ ID NOs: 771-776, SEQ ID NOs: 781-786, SEQ ID NOs: 791-796.

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 FLT3 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 FLT3 as an antibody selected from the group consisting of FL-1 to FL-65, *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:

SEQ ID NOs: 151-156, SEQ ID NOs: 161-166, SEQ ID NOs: 171-176, SEQ ID NOs: 181-186, SEQ ID NOs: 191-196, SEQ ID NOs: 201-206, SEQ ID NOs: 211-216, SEQ ID NOs: 221-226, SEQ ID NOs: 231-236, SEQ ID NOs: 241-246, SEQ ID NOs: 251-256, SEQ ID NOs: 261-266,

SEQ ID NOs: 271-276, SEQ ID NOs: 281-286, SEQ ID NOs: 291-296, SEQ ID NOs: 301-306, SEQ ID NOs: 311-316, SEQ ID NOs: 321-326, SEQ ID NOs: 331-336, SEQ ID NOs: 341-346, SEQ ID NOs: 351-356, SEQ ID NOs: 361-366, SEQ ID NOs: 371-376, SEQ ID NOs: 381-386, SEQ ID NOs: 391-396, SEQ ID NOs: 401-406, SEQ ID NOs: 411-416, SEQ ID NOs: 421-426, SEQ ID NOs: 431-436, SEQ ID NOs: 441-446, SEQ ID NOs: 451-456, SEQ ID NOs: 461-466, SEQ ID NOs: 471-476, SEQ ID NOs: 481-486, SEQ ID NOs: 491-496, SEQ ID NOs: 501-506, SEQ ID NOs: 511-516, SEQ ID NOs: 521-526, SEQ ID NOs: 531-536, SEQ ID NOs: 541-546, SEQ ID NOs: 551-556, SEQ ID NOs: 561-566, SEQ ID NOs: 571-576, SEQ ID NOs: 581-586, SEQ ID NOs: 591-596, SEQ ID NOs: 601-606, SEQ ID NOs: 611-616, SEQ ID NOs: 621-626, SEQ ID NOs: 631-636, SEQ ID NOs: 641-646, SEQ ID NOs: 651-656, SEQ ID NOs: 661-666, SEQ ID NOs: 671-676, SEQ ID NOs: 681-686, SEQ ID NOs: 691-696, SEQ ID NOs: 701-706, SEQ ID NOs: 711-716, SEQ ID NOs: 721-726, SEQ ID NOs: 731-736, SEQ ID NOs: 741-746, SEQ ID NOs: 751-756, SEQ ID NOs: 761-766, SEQ ID NOs: 771-776, SEQ ID NOs: 781-786, SEQ ID NOs: 791-796.

Whether or not an antibody construct binds to the same epitope of FLT3 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 in the appended Examples.

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 FLT3 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 FL-1 to FL-65, *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. Possible means for the read-out includes flow cytometry.

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: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, and SEQ ID NO: 797.

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: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788, and SEQ ID NO: 798.

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 NO: 157+158, SEQ ID NO: 167+168, SEQ ID

NO: 177+178, SEQ ID NO: 187+188, SEQ ID NO: 197+198, SEQ ID NO: 207+208, SEQ ID NO: 217+218, SEQ ID NO: 227+228, SEQ ID NO: 237+238, SEQ ID NO: 247+248, SEQ ID NO: 257+258, SEQ ID NO: 267+268, SEQ ID NO: 277+278, SEQ ID NO: 287+288, SEQ ID NO: 297+298, SEQ ID NO: 307+308, SEQ ID NO: 317+318, SEQ ID NO: 327+328, SEQ ID NO: 337+338, SEQ ID NO: 347+348, SEQ ID NO: 357+358, SEQ ID NO: 367+368, SEQ ID NO: 377+378, SEQ ID NO: 387+388, SEQ ID NO: 397+398. , SEQ ID NO: 407+408, SEQ ID NO: 417+418, SEQ ID NO: 427+428, SEQ ID NO: 437+438, SEQ ID NO: 447+448, SEQ ID NO: 457+458, SEQ ID NO: 467+468, SEQ ID NO: 477+478, SEQ ID NO: 487+488, SEQ ID NO: 497+498, SEQ ID NO: 507+508, SEQ ID NO: 517+518, SEQ ID NO: 527+528, SEQ ID NO: 537+538, SEQ ID NO: 547+548, SEQ ID NO: 557+558, SEQ ID NO: 567+568, SEQ ID NO: 577+578, SEQ ID NO: 587+588, SEQ ID NO: 597+598, SEQ ID NO: 607+608, SEQ ID NO: 617+618, SEQ ID NO: 627+628, SEQ ID NO: 637+638, SEQ ID NO: 647+648, SEQ ID NO: 657+658, SEQ ID NO: 667+668, SEQ ID NO: 677+678, SEQ ID NO: 687+688, SEQ ID NO: 697+698, SEQ ID NO: 707+708, SEQ ID NO: 717+718, SEQ ID NO: 727+728, SEQ ID NO: 737+738, SEQ ID NO: 747+748, SEQ ID NO: 757+758, SEQ ID NO: 767+768, SEQ ID NO: 777+778, SEQ ID NO: 787+788, and SEQ ID NO: 797+798.

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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799.

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 an epitope of FLT3 which is comprised within the region as depicted in SEQ ID NO: 819.

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: FLT3), 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: 1), 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: 1-9. 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 those formats.

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 an also preferred embodiment of the antibody construct of the invention the heavy chain (VH) and of the light chain (VL) of a binding domain binding either to the target antigen FLT3 or CD3 are not directly connected via an above described peptide linker but the binding domain is formed due to the formation of a bispecific molecule as described for the diabody. Thus, the VH chain of the CD3 binding domain may be fused to the VL of the FLT3 binding domain via such peptide linker, while the VH chain of the FLT3 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 FLT3 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 FLT3 which is comprised within the region as depicted in SEQ ID NO: 819 (cluster 1).

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:

SEQ ID NOs: 151-156, SEQ ID NOs: 161-166, SEQ ID NOs: 171-176, SEQ ID NOs: 181-186, SEQ ID NOs: 191-196, SEQ ID NOs: 201-206, SEQ ID NOs: 211-216, SEQ ID NOs: 221-226, SEQ ID NOs: 231-236, SEQ ID NOs: 241-246, SEQ ID NOs: 251-256, SEQ ID NOs: 261-266, SEQ ID NOs: 271-276, SEQ ID NOs: 281-286, SEQ ID NOs: 291-296, SEQ ID NOs: 301-306, SEQ ID NOs: 311-316, SEQ ID NOs: 321-326, SEQ ID NOs: 331-336, SEQ ID NOs: 341-346, SEQ ID NOs: 351-356, SEQ ID NOs: 361-366, SEQ ID NOs: 371-376, SEQ ID NOs: 381-386, SEQ ID NOs: 391-396, SEQ ID NOs: 401-406, SEQ ID NOs: 411-416, SEQ ID NOs: 421-426,

SEQ ID NOs: 431-436, SEQ ID NOs: 441-446, SEQ ID NOs: 451-456, SEQ ID NOs: 461-466, SEQ ID NOs: 471-476, SEQ ID NOs: 481-486, SEQ ID NOs: 491-496, SEQ ID NOs: 501-506, SEQ ID NOs: 511-516, SEQ ID NOs: 521-526, SEQ ID NOs: 531-536, SEQ ID NOs: 541-546, SEQ ID NOs: 551-556, SEQ ID NOs: 561-566, SEQ ID NOs: 571-576, SEQ ID NOs: 581-586, SEQ ID NOs: 591-596, SEQ ID NOs: 601-606, SEQ ID NOs: 611-616, SEQ ID NOs: 621-626, SEQ ID NOs: 631-636, SEQ ID NOs: 641-646, SEQ ID NOs: 651-656, SEQ ID NOs: 661-666, SEQ ID NOs: 671-676, SEQ ID NOs: 681-686, SEQ ID NOs: 691-696, SEQ ID NOs: 701-706, SEQ ID NOs: 711-716, SEQ ID NOs: 721-726, SEQ ID NOs: 731-736, SEQ ID NOs: 741-746, SEQ ID NOs: 791-796.

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: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, and SEQ ID NO: 797.

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: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558,

SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, and SEQ ID NO: 798.

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 NO: 157+158, SEQ ID NO: 167+168, SEQ ID NO: 177+178, SEQ ID NO: 187+188, SEQ ID NO: 197+198, SEQ ID NO: 207+208, SEQ ID NO: 217+218, SEQ ID NO: 227+228, SEQ ID NO: 237+238, SEQ ID NO: 247+248, SEQ ID NO: 257+258, SEQ ID NO: 267+268, SEQ ID NO: 277+278, SEQ ID NO: 287+288, SEQ ID NO: 297+298, SEQ ID NO: 307+308, SEQ ID NO: 317+318, SEQ ID NO: 327+328, SEQ ID NO: 337+338, SEQ ID NO: 347+348, SEQ ID NO: 357+358, SEQ ID NO: 367+368, SEQ ID NO: 377+378, SEQ ID NO: 387+388, SEQ ID NO: 397+398. , SEQ ID NO: 407+408, SEQ ID NO: 417+418, SEQ ID NO: 427+428, SEQ ID NO: 437+438, SEQ ID NO: 447+448, SEQ ID NO: 457+458, SEQ ID NO: 467+468, SEQ ID NO: 477+478, SEQ ID NO: 487+488, SEQ ID NO: 497+498, SEQ ID NO: 507+508, SEQ ID NO: 517+518, SEQ ID NO: 527+528, SEQ ID NO: 537+538, SEQ ID NO: 547+548, SEQ ID NO: 557+558, SEQ ID NO: 567+568, SEQ ID NO: 577+578, SEQ ID NO: 587+588, SEQ ID NO: 597+598, SEQ ID NO: 607+608, SEQ ID NO: 617+618, SEQ ID NO: 627+628, SEQ ID NO: 637+638, SEQ ID NO: 647+648, SEQ ID NO: 657+658, SEQ ID NO: 667+668, SEQ ID NO: 697+698, SEQ ID NO: 707+708, SEQ ID NO: 717+718, SEQ ID NO: 727+728, SEQ ID NO: 737+738, SEQ ID NO: 747+748, and SEQ ID NO: 797+798.

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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID

NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 799.

It is also envisaged that the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human FLT3 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 FLT3 which is comprised within the region as depicted in SEQ ID NO: 821 (cluster 3).

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 as follows:

SEQ ID NOs: 671-676, SEQ ID NOs: 681-686, SEQ ID NOs: 751-756, SEQ ID NOs: 761-766, SEQ ID NOs: 771-776, and SEQ ID NOs: 781-786.

In one embodiment, the first binding domain of the antibody construct of the invention comprises a VH region depicted in SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, and SEQ ID NO: 787.

In a further embodiment, the first binding domain of the antibody construct of the invention comprises a VL region depicted in SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, and SEQ ID NO: 788.

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 NO: 677+678, SEQ ID NO: 687+688, SEQ ID NO: 757+758, SEQ ID NO: 767+768, SEQ ID NO: 777+778, and SEQ ID NO: 787+788.

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: 679, and SEQ ID NO: 689, SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789.

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 FLT3 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 FL-1 to FL-53, FL-55 to FL-60 and FL-65, *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.

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 FLT3xCD3 bispecific antibody constructs can be measured in various ways. See Examples 10. 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 FLT3, 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) FLT3, e.g. human or macaque FLT3. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with FLT3, e.g. human or macaque FLT3. Alternatively, the target cells can be a FLT3 positive natural expresser cell line, such as the FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11. Usually EC₅₀ values are expected to be lower with target cell lines expressing higher levels of FLT3 on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of FLT3xCD3 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 FLT3xCD3 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 FLT3xCD3 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 FLT3 transfected cells such as CHO cells or FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11 are used as target cells), the EC₅₀ value of the FLT3 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 FLT3xCD3 bispecific antibody construct is preferably ≤ 5000 pM or ≤ 4000 pM (in particular when the target cells are FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11), more preferably ≤ 2000 pM (in particular when the target cells are FLT3 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 FLT3 transfected cell line such as CHO cells is used as target cell line, the EC₅₀ value of the FLT3 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 FLT3xCD3 bispecific antibody constructs of the present invention do not induce / mediate lysis or do not essentially induce / mediate lysis of FLT3 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 FLT3 negative cells, whereby lysis of a FLT3 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 FLT3 xCD3 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 17. Potency gaps of the FLT3xCD3 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 FLT3 and human CD3, respectively, will also bind to FLT3 / CD3 of primates including (but not limited to) new world primates (such as *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus*), old world primates (such 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 **FLT3** on the surface of a target cell also binds at least to macaque **FLT3**, 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.

In one aspect of the invention, the first binding domain binds to human FLT3 and further binds to macaque FLT3, such as FLT3 of *Macaca fascicularis*, and more preferably, to macaque FLT3 expressed on the surface macaque cells. A preferred *Macaca fascicularis* FLT3 is depicted in SEQ ID NO: 802. The affinity of the first binding domain for macaque FLT3 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 FLT3 versus human FLT3 [ma FLT3:hu FLT3] (as determined e.g. by BiaCore or by Scatchard analysis) is < 100 , preferably < 20 , more preferably < 15 , further preferably < 10 , even more preferably < 8 , more preferably < 6 and most preferably < 2 . Preferred ranges for the affinity gap of the antibody constructs according to the invention for binding macaque FLT3 versus human FLT3 are between 0.1 and 20, more preferably between 0.2 and 10, even more preferably between 0.3 and 6, 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 5.

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-H1, 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: 18, SEQ ID NO: 27, SEQ ID NO: 36, SEQ ID NO: 45, SEQ ID NO: 54, SEQ ID NO: 63, SEQ ID NO: 72, SEQ ID NO: 81, SEQ ID NO: 90, SEQ ID NO: 99, and SEQ ID NO: 102 (see also 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: 17, SEQ ID NO: 26, SEQ ID NO: 35, SEQ ID NO: 44, SEQ ID NO: 53, SEQ ID NO: 62, SEQ ID NO: 71, SEQ ID NO: 80, SEQ ID NO: 89, SEQ ID NO: 98, and SEQ ID NO: 101 (see also 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.

Also preferred in connection with the antibody construct of the present invention is a second binding domain which binds to human CD3 on the surface of a T cell comprising a VL region as depicted in SEQ ID NO: 102 and a VH region as depicted in SEQ ID NO: 101.

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 NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103 (see also 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).

It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target molecules FLT3 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 FLT3, 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 antibody construct of the invention is described as follows:

(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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 10;
- (b) a polypeptide comprising in following order starting from the N-terminus:
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599,

SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103;
 - optionally a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 104-134; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 10;
- (c) a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having the amino acid sequence QRFVTGHFGGLX₁PANG (SEQ ID NO: 135) whereas X₁ is Y or H; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103;
 - a polypeptide having the amino acid sequence QRFVTGHFGGLHPANG (SEQ ID NO: 137) or QRFCTGHFGGLHPCNG (SEQ ID NO: 139); and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 10;
- (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: 17, SEQ ID NO: 26, SEQ ID NO: 35, SEQ ID NO: 44, SEQ ID NO: 53, SEQ ID NO: 62, SEQ ID NO: 71, SEQ ID NO: 80, SEQ ID NO: 89, SEQ ID NO: 98, and SEQ ID NO: 101;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788, and SEQ ID NO: 798 and a serine residue at the C-terminus;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 140; 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: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID

NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, and SEQ ID NO: 797;

- a peptide linker having the amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 27, SEQ ID NO: 36, SEQ ID NO: 45, SEQ ID NO: 54, SEQ ID NO: 63, SEQ ID NO: 72, SEQ ID NO: 81, SEQ ID NO: 90, SEQ ID NO: 99, and SEQ ID NO: 102 and a serine residue at the C-terminus;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 141;
- (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: 17, SEQ ID NO: 26, SEQ ID NO: 35, SEQ ID NO: 44, SEQ ID NO: 53, SEQ ID NO: 62, SEQ ID NO: 71, SEQ ID NO: 80, SEQ ID NO: 89, SEQ ID NO: 98, and SEQ ID NO: 101;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508,

SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788, and SEQ ID NO: 798;

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 142; 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: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, and SEQ ID NO: 797;
 - a peptide linker having an amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 27, SEQ ID NO: 36, SEQ ID NO: 45, SEQ ID NO: 54, SEQ ID NO: 63, SEQ ID NO: 72, SEQ ID NO: 81, SEQ ID NO: 90, SEQ ID NO: 99, and SEQ ID NO: 102 and a serine residue at the C-terminus; [CD3 VL]
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 143;
- (f) [V5 Hetero-Fc] 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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239,

SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 144; and
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 145;

(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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID

NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 146; 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: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 147;
- (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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 148; 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: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 149; 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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 150.
- (j) 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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599,

SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103;
- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and; and
- the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 843-850.

In a preferred aspect of the invention the binding of the first binding domain to human **FLT3** is reduced by FLT3-ligand by $\leq 25\%$, preferably $\leq 20\%$, more preferably $\leq 15\%$, further preferably $\leq 10\%$, even more preferably $\leq 8\%$, more preferably $\leq 6\%$ and most preferably $\leq 2\%$.

AS described in detail in Example 18 it has been surprisingly found that constructs comprising FL-53, FL-54, FL-61, F-62, FL-63 and FL-64, which all bind to epitope cluster 3 of FLT3, still showed a binding signal above the threshold described in Example 18 although those binder have an epitope in the region described for FLT3-ligand interaction with FLT3.

Moreover, in view of the interaction of FLT3 ligand with the region of epitope cluster 3 it was further assumed that binder for more distant epitope cluster, such as cluster 1 of FLT3, would not be impacted by the FLT3 ligand competition. However, there were a significant number of binders, which did not qualify for the 75% threshold. The binder FL-1 to FL-53, FL-55 to FL-60 and FL-65 were in the group of binders not sensitive for the FLT3 ligand competition.

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, in particular 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 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 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: 843-850. Each of said two polypeptide monomers preferably has an amino acid sequence that is selected from the group consisting of SEQ ID NOs: 835-842, 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: 1, 2, 3, 4, 5, 6, 7, 8 and 9.

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: 1-9;
- (c) the second binding domain;
- (d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 4, 5, 6, 8 and 9;
- (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: 852, 853, 854 and 855; 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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;
- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;

- the second binding domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103 (see also 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);
- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 4, 5, 6, 8 and 9; and
- the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 843-850.

In a preferred embodiment, the antibody construct of the present invention comprises or consists of a polypeptide depicted in SEQ ID NOs: 856 to 871.

In one preferred embodiment of the antibody construct of the invention the antibody construct comprises or consists of a polypeptide as depicted in SEQ ID NO: 856, 858, 860, 862, 864, 866, 868, and 870.

In one alternatively preferred embodiment of the antibody construct of the invention the antibody construct comprises or consists of a polypeptide as depicted in SEQ ID NO: 857, 859, 861, 863, 865, 867, 869, and 871.

In a preferred embodiment of the invention the antibody construct of the invention the antibody construct comprises or consists of a polypeptide as depicted in SEQ ID NO: 858, 859, 862, 863, 864 and 865.

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.

Cysteinyll residues most commonly are reacted with α -haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyll 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 alpha-amino-containing residues include imidoesters such as methyl picolinimate; 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.

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

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

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

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

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

Another means of increasing the number of carbohydrate moieties on the antibody construct is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330, and in Aplin and Wriston, 1981, *CRC Crit. Rev. Biochem.*, pp. 259-306.

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

Other modifications of the antibody construct are also contemplated herein. For example, another type of covalent modification of the antibody construct comprises linking the antibody construct to various non-proteinaceous polymers, including, but not limited to, various polyols

such as polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody construct, e.g. in order to facilitate the addition of polymers such as PEG.

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

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

By “fluorescent label” is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633,

Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland.

Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5,292,658; 5,418,155; 5,683,888; 5,741,668; 5,777,079; 5,804,387; 5,874,304; 5,876,995; 5,925,558).

Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz *et al.*, 1988, *Science* 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe *et al.*, 1994, *FEBS Letters* 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow *et al.*, 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising a FLT3 antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric FLT3 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) (SEQ ID NO:10) 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 FLT3 on the surface of a target cell. The preferred amino acid sequence of human FLT3 is represented by NOs: 801, 803, 804, and 805. 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 FLT3 extracellular domain (FLT3 ECD see SEQ ID NO:813). The first binding domain according to the invention hence preferably binds to FLT3 when it is expressed by naturally expressing cells or cell lines, and/or by cells or cell lines transformed or (stably / transiently) transfected with FLT3. In a preferred embodiment the first binding domain also binds to FLT3 when FLT3 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 FLT3 on its surface; preferably the target cell is a cell that is part of the human or animal body, such as a ovarian cancer cell, pancreatic cancer cell, mesothelioma cell, lung cancer cell, gastric cancer cell and triple negative breast cancer cell.

The term "FLT3 ECD" refers to a form of FLT3 which is essentially free of transmembrane and cytoplasmic domains of FLT3. It will be understood by the skilled artisan that the transmembrane domain identified for the FLT3 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 FLT3 ECD is shown in SEQ ID NO: 813.

The affinity of the first binding domain for human FLT3 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.

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 FLT3 and to CD3) of the unmodified parental molecule.

The term “amino acid” or “amino acid residue” typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H); isoleucine (Ile or I); leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); proline (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. Generally, amino acids can be grouped as having a nonpolar side chain (e.g., Ala, Cys, Ile, Leu, Met, Phe, Pro, Val); a negatively charged side chain (e.g., Asp, Glu); a positively charged 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 FLT3 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 FLT3 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 8. 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 FLT3. 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 13.

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 11. 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 ≤5%, more preferably ≤4%, even more preferably ≤3%, even more preferably ≤2.5%, even more preferably ≤2%, even more preferably ≤1.5%, and most preferably ≤1% or ≤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 ≤5%, more preferably ≤4%, even more preferably ≤3%, even more preferably ≤2.5%, even more preferably ≤2%, even more preferably ≤1.5%, and most preferably ≤1% or even ≤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 ≥45°C or ≥50°C, more preferably ≥52°C or ≥54°C, even more preferably ≥56°C or ≥57°C, and most preferably ≥58°C or ≥59°C. The thermostability parameter can be determined in terms of antibody aggregation temperature as follows: Antibody solution at a concentration 250 µg/ml is transferred into a single use cuvette and placed in a Dynamic Light Scattering (DLS) device. The sample is heated from 40°C to 70°C at a heating rate of 0.5°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 12.

Alternatively, temperature melting curves can be determined by Differential Scanning Calorimetry (DSC) to determine intrinsic biophysical protein stabilities of the antibody

constructs. These experiments are performed using a MicroCal LLC (Northampton, MA, U.S.A) VP-DSC device. The energy uptake of a sample containing an antibody construct is recorded from 20°C to 90°C compared to a sample containing only the formulation buffer. The antibody constructs are adjusted to a final concentration of 250 µg/ml e.g. in SEC running buffer. For recording of the respective melting curve, the overall sample temperature is increased stepwise. At each temperature T energy uptake of the sample and the formulation buffer reference is recorded. The difference in energy uptake C_p (kcal/mole/°C) of the sample minus the reference is plotted against the respective temperature. The melting temperature is defined as the temperature at the first maximum of energy uptake.

It is furthermore envisaged that the FLT3xCD3 bispecific antibody constructs of the invention do not cross-react with (*i.e.*, do not essentially bind to) the human FLT3 paralogues KIT v1 (SEQ ID NO: 805), CSF1R v1 (SEQ ID NO: 806), PDGFRA (SEQ ID NO: 807), and/or NTM v3 (SEQ ID NO: 808). Furthermore, it is envisaged that the FLT3xCD3 bispecific antibody constructs of the invention do not cross-react with (*i.e.*, do not essentially bind to) the macaque / cyno FLT3 paralogues KIT v1, CSF1R v1, PDGFRA and/or NTM v3. See Example 7.

The FLT3 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 14.

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 15.

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 FLT3 positive cancer cell line (e.g. OVCAR-8) are subcutaneously injected in the right dorsal flank of female NOD/SCID mice. When the mean tumor volume reaches about 100 mm^3 , in vitro expanded human CD3 positive T cells are transplanted into the mice by injection of about 2×10^7 cells into the peritoneal cavity of the animals. Mice of vehicle control group 1 do not receive effector cells and are used as an untransplanted control for comparison with vehicle control group 2 (receiving effector cells) to monitor the impact of T cells alone on tumor growth. The antibody treatment starts when the mean tumor volume reaches about 200 mm^3 . The mean tumor size of each treatment group on the day of treatment start should not be statistically different from any other group (analysis of variance). Mice are treated with 0.5 mg/kg/day of a FLT3 xCD3 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 SEPHAROSE™, 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. It is preferred for the pharmaceutical composition of the invention that the homogeneity of the antibody construct is $\geq 80\%$, more preferably $\geq 81\%$, $\geq 82\%$, $\geq 83\%$, $\geq 84\%$, or $\geq 85\%$, further preferably $\geq 86\%$, $\geq 87\%$, $\geq 88\%$, $\geq 89\%$, or $\geq 90\%$, still further preferably, $\geq 91\%$, $\geq 92\%$, $\geq 93\%$, $\geq 94\%$, or $\geq 95\%$ and most preferably $\geq 96\%$, $\geq 97\%$, $\geq 98\%$ or $\geq 99\%$.

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, thiocetic 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, myoinisitol, 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 cytostatics, 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 *hematological cancer* disease or 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 hematological cancer disease is AML and the metastatic cancer disease can be derived from the foregoing.

Preferred tumor or cancer diseases in connection with this invention are selected from a group consisting of breast cancer, Carcinoid, cervical cancer, colorectal cancer, endometrial cancer, gastric cancer, head and neck cancer, mesothelioma, liver cancer, lung cancer, ovarian cancer, pancreatic cancer, prostate cancer, skin cancer, renal cancer and stomach cancer. More preferably, the tumor or cancer disease, which is preferably a solid tumor disease, can be selected from the group consisting of ovarian cancer, pancreatic cancer, mesothelioma, lung cancer, gastric cancer and triple negative breast cancer. The metastatic cancer disease can be derived from any of the foregoing.

The invention also provides a method for the treatment or amelioration a hematological 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 FLT3-expressing tumors, a therapeutically effective amount of the antibody construct of the invention, e.g. an anti-FLT3 /anti-CD3 antibody construct, preferably inhibits cell growth or tumor growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may be evaluated in an animal model predictive of efficacy in human tumors.

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

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

The term "toxicity" as used herein refers to the toxic effects of a drug manifested in adverse events or severe adverse events. These side events might refer to a lack of tolerability of the

drug in general and/or a lack of local tolerance after administration. Toxicity could also include teratogenic or carcinogenic effects caused by the drug.

The term “safety”, “*in vivo* safety” or “tolerability” as used herein defines the administration of a drug without inducing severe adverse events directly after administration (local tolerance) and during a longer period of application of the drug. “Safety”, “*in vivo* safety” or “tolerability” can be evaluated e.g. at regular intervals during the treatment and follow-up period. Measurements include clinical evaluation, e.g. organ manifestations, and screening of laboratory abnormalities. Clinical evaluation may be carried out and deviations to normal findings recorded/coded according to NCI-CTC and/or MedDRA standards. Organ manifestations may include criteria such as allergy/immunology, blood/bone marrow, cardiac arrhythmia, coagulation and the like, as set forth e.g. in the Common Terminology Criteria for adverse events v3.0 (CTCAE). Laboratory parameters which may be tested include for instance hematology, clinical chemistry, coagulation profile and urine analysis and examination of other body fluids such as serum, plasma, lymphoid or spinal fluid, liquor and the like. Safety can thus be assessed e.g. by physical examination, imaging techniques (i.e. ultrasound, x-ray, CT scans, Magnetic Resonance Imaging (MRI), other measures with technical devices (i.e. electrocardiogram), vital signs, by measuring laboratory parameters and recording adverse events. For example, adverse events in non-chimpanzee primates in the uses and methods according to the invention may be examined by histopathological and/or histochemical methods.

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

In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, an antibody construct produced according to the process of the invention, a polynucleotide 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:

(a) Schematic Structure of the monomeric FLT3 protein and (b) crystal structure of the FLT3 homodimer interacting with FLT3LG homodimer.

Figure 2:

Schematic Structure of chimeric Human/Mouse FLT3 molecules used for the epitope cluster binder characterization

Figure 3:

Schematic Structure of the truncated FLT3 constructs used for epitope cluster binder characterization

Figure 4:

Assay to analyze the competition of FLT3 binder of the invention with FLT3-ligand for FLT3 binding.

CHO-human FLT3 cells were incubated with or w/o 10 µg/ml FLT3 Ligand for 30 min (no washing step). scFv periplasmic preps were added and incubated for 30 min. The detection was performed using mouse anti-FLAG + PE-conjugated goat anti-mouse and the Fluorescence median detected by FACS (median (+ ligand) / median (w/o ligand) * 100%)

Figure 5:

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with the human FLT3, human CD3+ T cell line HPBaLL, CHO cells

transfected with cynomolgus FLT3 and a macaque CD3⁺ T cell line LnPx 4119. The red line represents cells incubated with 2 µg/ml purified monomeric protein that are subsequently incubated with the mouse anti-I2C antibody and the PE labelled goat anti mouse IgG detection antibody. The black histogram line reflects the negative control: cells only incubated with the anti-I2C antibody as well as the PE labelled detection antibody (see example 6).

Figure 6:

Cytotoxic activity induced by designated cross-species specific single chain constructs redirected to CD56 depleted unstimulated human PBMCs as effector cells and CHO cells transfected with human FLT3 as target cells. (Example 9)

Figure 7:

Cross-reactive binding to CD3, FLT3 and its isoforms). 5 µg/ml BiTE protein: 4°C 60 min; 2 µg/ml anti-I2C-Ab 3E5.A5: 4°C 30 min; goat anti-mouse-PE 1:100: 4°C 30 min

Figure 8:

Non-Binding to ParAlogs and Untransfected CHO. 5 µg/ml BiTE protein: 4°C 60 min; 2 µg/ml anti-I2C-Ab 3E5.A5: 4°C 30 min; goat anti-mouse-PE 1:100: 4°C 30 min

Figure 9:

Epitope clusters mapping – Cluster E1

Figure 10:

FLT3 scFc antibody constructs are active using unstimulated human PBMC against human FLT3-transfected CHO cells in absence and presence of FLT3LG (FLT3 ligand)

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 chimeric FLT3

The FLT3 antigen can be subdivided into six different sub-domains or regions that are defined, for the purposes of Examples 1 and 2. The aa sequence of those five sub-domains is depicted in SEQ ID NOs: 814-818.

The following molecules were generated; see also Figure 1:

- hu lsp V5xFlt3-E1muxEpC-pEFDHFR SEQ ID NO: 827
- hu lsp V5xFlt3-E2muxEpC-pEFDHFR SEQ ID NO: 828
- hu lsp V5xFlt3-E3muxEpC-pEFDHFR SEQ ID NO: 829

- hu lsp V5xFlt3-E3AmuxEpC-pEFDHFR SEQ ID NO: 830
- hu lsp V5xFlt3-E3BmuxEpC-pEFDHFR SEQ ID NO: 831
- hu lsp V5xFlt3-E4muxEpC-pEFDHFR SEQ ID NO: 832
- hu lsp V5xFlt3-E5muxEpC-pEFDHFR SEQ ID NO: 833
- hu lsp V5xFlt3-E6muxEpC-pEFDHFR SEQ ID NO: 834
- hu lsp FLT3- full murine EDC
- hu lsp FLT3- full human EDC
- full length human FLT3 SEQ ID NO: 801
- full length cyno FLT3 SEQ ID NO: 802

For the generation of CHO/HEK cells expressing human, murine and chimeric FLT3 ExtraCellulrDomain (ECD), the respective coding sequences for human FLT3, murine FLT3 and the eight cimeric human/murine FLT3 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 murine FLT3 the original signal peptide was used. 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, chimeric and murine FLT3 on CHO cells was verified in a FACS assay.

Example 2

Epitope mapping of anti-FLT3 antibody constructs

Cells transfected with human, murine FLT3 and with the chimeric human FLT3 molecules (see Example 1) were stained with crude, undiluted periplasmic extract containing bispecific FLT3xCD3 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 FLT3 binding domains are indicated in the sequence table (Table 2). Loss of the FACS signal in the respective chimeric FLT3 constructs comprising the murine epitope cluster was the read out for the relevance of the respective

cluster for the binding. The respective results in table 2 are in line with the results according to example 3.

Example 3

Generation of CHO cells expressing wild type and truncated FLT3

The extracellular domain of the FLT3 antigen can be subdivided into different sub-domains or regions, respectively epitope cluster E1 to E6 that are defined, by the following amino acid positions:

E1		aa 27-79	SEQ ID NO: 819
E2	D1	aa 79-167	SEQ ID NO: 820
E3	D2	aa 168-244	SEQ ID NO: 821
E3A	D2A	aa 168-206	SEQ ID NO: 822
E3B	D2B	aa 207-244	SEQ ID NO: 823
E4	D3	aa 245-345	SEQ ID NO: 824
E5	D4	aa 346-434	SEQ ID NO: 825
E6	D5	aa 435-543	SEQ ID NO: 826

For the construction of the truncated FLT3 molecules used for epitope mapping (see figure 3), the sequences of the respective seven human regions as well as the five combinations of two neighboring human regions (see above) were replaced with the corresponding regions from murine FLT3. Furthermore, a V5 tag (GKPIPNNLLGLDST) was fused via a "GGGGS" linker to the C-terminus of the chimeric molecules. The final chimeric molecule sequences are depicted in SEQ ID NOs: 827-834. In addition, full length human FLT3 (SEQ ID NO: 801) and full-length cyno FLT3 (SEQ ID NO: 802) were constructed, both having a V5 tag (GKPIPNNLLGLDST) fused via a "GGGGS" linker to their C-terminus.

For the generation of CHO dhfr- cells expressing the above constructs, the respective coding sequences were cloned into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum *et al.* Cancer Immunol Immunother 50 (2001) 141-150). CHO cells transfected with human FLT3, but without the V5 tag, were also generated. All cloning procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). For each construct, a corresponding plasmid was transfected into DHFR deficient CHO cells for eukaryotic expression, as described by Kaufman R.J. (1990) Methods Enzymol. 185, 537-566.

The expression of the constructs on the CHO cells was verified using a monoclonal mouse IgG2a anti-v5 tag antibody (1 µg/ml; AbD Serotec, # MCA 1360). Bound monoclonal antibody

was detected with an anti-mouse IgG Fc-gamma-PE. As negative control, cells were incubated with isotype control antibody instead of the first antibody. The samples were measured by flow cytometry.

The results of this analysis are shown for the disclosed FLT3 binder in Table 2. Those results are in line with the epitope mapping analysis according to example 2

Table 2: Mapping of the epitope

Epitope cluster	Binder		Epitope cluster	Binder		Epitope cluster	Binder
FL-1	E1		FL-23	E1		FL-45	E1
FL-2	E1		FL-24	E1		FL-46	E1
FL-3	E1		FL-25	E1		FL-47	E1
FL-4	E1		FL-26	E1		FL-48	E1
FL-5	E1		FL-27	E1		FL-49	E1
FL-6	E1		FL-28	E1		FL-50	E1
FL-7	E1		FL-29	E1		FL-51	E1
FL-8	E1		FL-30	E1		FL-52	E1
FL-9	E1		FL-31	E1		FL-53	E3
FL-10	E1		FL-32	E1		FL-54	E3
FL-11	E1		FL-33	E1		FL-55	E1
FL-12	E1		FL-34	E1		FL-56	E1
FL-13	E1		FL-35	E1		FL-57	E1
FL-14	E1		FL-36	E1		FL-58	E1
FL-15	E1		FL-37	E1		FL-59	E1
FL-16	E1		FL-38	E1		FL-60	E1
FL-17	E1		FL-39	E1		FL-61	E3
FL-18	E1		FL-40	E1		FL-62	E3
FL-19	E1		FL-41	E1		FL-63	E3
FL-20	E1		FL-42	E1		FL-64	E3
FL-21	E1		FL-43	E1		FL-65	E1
FL-22	E1		FL-44	E1			

Example 4

Biacore-based determination of antibody affinity to human and cynomolgus FLT3

Biacore analysis experiments were performed using recombinant human / cyno FLT3-ECD fusion proteins with albumin to determine target binding of the antibody constructs of the invention.

In detail, CM5 Sensor Chips (GE Healthcare) were immobilized with approximately 600-800 RU of the respective recombinant antigen using acetate buffer pH 4.5 according to the manufacturer's manual. The FLT3xCD3 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 μ l/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.

Furthermore, the binding of the bispecific antibody constructs to human CD3 and macaque CD3 was confirmed in a Biacore assay.

Example 5

Scatchard-based analysis of FLT3xCD3 bispecific antibody construct affinity to human and macaque FLT3 on target antigen positive cells and determination of the interspecies affinity gap

The affinities of FLT3xCD3 bispecific antibody constructs to CHO cells transfected with human or macaque FLT3 were also determined by Scatchard analysis as the most reliable method for measuring potential affinity gaps between human and macaque FLT3. For the Scatchard analysis, saturation binding experiments are performed using a monovalent detection system to precisely determine monovalent binding of the FLT3xCD3 bispecific antibody constructs to the respective cell line.

2×10^4 cells of the respective cell line (recombinantly human FLT3-expressing CHO cell line, recombinantly macaque FLT3-expressing CHO cell line) were incubated each with 50 μ l of a triplet dilution series (twelve dilutions at 1:2) of the respective FLT3xCD3 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 (B_{max}). The concentrations of FLT3xCD3 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.

Example 6

Bispecific binding and interspecies cross-reactivity

For confirmation of binding to human FLT3 and CD3 and to cyno FLT3 and CD3, bispecific antibody constructs of the invention were tested by flow cytometry using

- CHO cells transfected with human FLT3 (SEQ ID NO: 801), with human FLT3 isoforms (Human FLT3 (T227M) isoform see SEQ ID NO: 803 and Human FLT3-ITD isoform see SEQ ID NO:804), and with macaque FLT3 (SEQ ID NO: 802), respectively,
- the FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11 (but other FLT3 positive human cell lines are also conceivable)
- CD3-expressing human T cell leukemia cell line HPB-all (DSMZ, Braunschweig, ACC483), and
- the cynomolgus CD3-expressing T cell line LnPx 4119

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

Table 3a: Affinities of FLT3 binding domains:

<i>FLT3-HLE BiTE</i>	Epitope cluster	Octet based affinity hu FLT3* [nM]	Octet based affinity mac FLT3* [nM]	Affinity gap KD_{mac}/KD_{hu} FLT3
FL 39 x I2C-scFc^o	E1	0.52 ± 0.03	1.65 ± 0.10	3.2
FL 16 x I2C-scFc	E1	0.57**	1.38**	2.4
FL 42 x I2C-scFc	E1	0.36 ± 0.11	1.11 ± 0.13	3.1
FL 36 x I2C-scFc	E1	5.30 ± 0.08	4.44 ± 0.72	0.8

FL 52 x I2C-scFc	E1	4.80 ± 0.25	4.14 ± 0.08	0.9
FL 23 x I2C-scFc	E1	0.97 ± 0.19	0.68 ± 0.01	0.7
FL 46 x I2C-scFc	E1	1.67 ± 0.08	7.9 ± 1.81	4.7
FL 61 x I2C-scFc	E3	26.50 ± 0.57	3.77 ± 3.74	0.14

Table 3b: Affinities of CD3 binding domains:

<i>FLT3-HLE BiTE</i>	Epitope cluster	Biacore based affinity hu FLT3* [nM]	Biacore based affinity mac FLT3* [nM]	Affinity gap KDmac/KDhu FLT3
FL 39 x I2C-scFc^o	E1	8.24 ± 0.15	6.84 ± 0.09	0.8
FL 16 x I2C-scFc	E1	6.08 ± 0.12	4.91 ± 0.10	0.8
FL 42 x I2C-scFc	E1	9.13 ± 1.03	7.31 ± 1.13	0.8
FL 36 x I2C-scFc	E1	7.73 ± 0.14	6.06 ± 0.42	0.8
FL 52 x I2C-scFc	E1	7.40 ± 0.80	5.99 ± 0.78	0.8
FL 23 x I2C-scFc	E1	9.64 ± 0.11	7.87 ± 0.15	0.8
FL 46 x I2C-scFc	E1	6.06 ± 0.47	4.86 ± 0.35	0.8
FL 61 x I2C-scFc	E3	11.65 ± 1.48	9.37 ± 1.46	0.8

Example 7**Confirmation of the absence of binding to human paralogues**

Human FLT3 paralogues KIT v1 (SEQ ID NO: 805), CSF1R v1 (SEQ ID NO: 806), PDGFRA (SEQ ID NO: 807), and NTM v3 (SEQ ID NO: 808) were stably transfected into CHO cells. The sequence of the paralogue as used in the present example as identified in the sequence listing.

Table 4a: Identity of the paralogues with FLT3 over the full length of the protein sequence

Protein	% Identity	Query id (%)
c-KIT	29	28
CSF1R	29	28
PDGFRA	27	30

Table 4b: Identity of the paralogues with FLT3 over the ECD of the protein sequence

Protein	% Identity	Query id (%)
NTM	25	28

Protein expression was confirmed in FACS analyses with specific antibodies. The flow cytometry assay was carried out as described in Example 6.

Example 8:

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 FLT3 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.

Example 9

Cytotoxic activity

The potency of FLT3xCD3 bispecific antibody constructs of the invention in redirecting effector T cells against FLT3-expressing target cells was analyzed in five *in vitro* cytotoxicity assays:

- The potency of FLT3xCD3 bispecific antibody constructs in redirecting stimulated human CD8⁺ effector T cells against human FLT3-transfected CHO cells was measured in an 18 hour 51-chromium release assay.
- The potency of FLT3xCD3 bispecific antibody constructs in redirecting stimulated human CD8⁺ effector T cells against the the FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11 (but other FLT3 positive human cell lines are also conceivable) was measured in an 18 hour 51-chromium release assay.
- The potency of FLT3xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC against human FLT3-transfected CHO cells was measured in a 48 hour FACS-based cytotoxicity assay.

Effector cells: unstimulated human PBMC (CD14-/CD56-). Target cells: EOL-1. Effector to target cell (E:T)-ratio: 10:1. BiTE protein as indicated

FLT3xCD3 antibody constructs								
	FL 39	FL 16	FL 42	FL 36	FL 52	FL 23	FL 46	FL 61
EC50 [pM]	7.5	13	34	35	91	20	25	745

Effector cells: unstimulated human PBMC (CD14-/CD56-). Target cells: MV4-11. Effector to target cell (E:T)-ratio: 10:1. BiTE protein as indicated.

FLT3xCD3 antibody constructs								
	FL 39	FL 16	FL 42	FL 36	FL 52	FL 23	FL 46	FL 61
EC50 [pM]	4.8	8.1	13	15	14	13	12	270

- The potency of FLT3xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC against the the FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11 (but other FLT3 positive human cell lines are also conceivable) was measured in a 48 hour FACS-based cytotoxicity assay.
- For confirmation that the cross-reactive FLT3xCD3 bispecific antibody constructs are capable of redirecting macaque T cells against macaque FLT3-transfected CHO cells, a 48 hour FACS-based cytotoxicity assay was performed with a macaque T cell line as effector T cells.

Effector cells: unstimulated human PBMC (CD14-/CD56-). Target cells : mac FLT3 transfected CHO cells Effector to target cell (E:T)-ratio: 10:1. BiTE protein as indicated.

FLT3xCD3 antibody constructs								
	FL 39	FL 16	FL 42	FL 36	FL 52	FL 23	FL 46	FL 61
EC50 [pM]	0.2	0.5	1.0	2.5	0.7	1.9	11	0.9

- The potency of FLT3xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC human FLT3-transfected CHO cells in the absence and presence of FLT3 ligand was measured in 48-hour FACS-based cytotoxicity assay. Effector cells: unstimulated human PBMC (CD14-/CD56-). Target cells: hu FLT3 transfected CHO cells. Effector to target cell (E:T)-ratio: 10:1. BiTE protein as indicated.

FLT3xCD3 antibody constructs	EC50 [pM]		
	w/o FLT3 LG	w/ 10 ng/ml FLT3 LG	w/ 1 µg/ml FLT3 LG
FL 39 x I2C-scFc^o	0.7	13	29
FL 16 x I2C-scFc	0.5	11	23
FL 42 x I2C-scFc	1.0	19	e
FL 36 x I2C-scFc	1.9	24	73
FL 52 x I2C-scFc	2.4	24	71
FL 23 x I2C-scFc	0.9	15	49
FL 46 x I2C-scFc	1.2	18	43
FL 61 x I2C-scFc	32	662	608

Example 10.1

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 FLT3- or human FLT3-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 10.2**Potency of redirecting stimulated human effector T cells against human FLT3-transfected CHO cells**

The cytotoxic activity of FLT3xCD3 bispecific antibody constructs according to the invention was analyzed in a 51-chromium (⁵¹Cr) release cytotoxicity assay using CHO cells transfected with human FLT3 as target cells, and stimulated human CD8⁺ T cells as effector cells. The experiment was carried out as described in Example 10.1.

Example 10.3

Potency of redirecting stimulated human effector T cells against a FLT3 positive human cell line

The cytotoxic activity of FLT3xCD3 bispecific antibody constructs was analyzed in a 51-chromium (^{51}Cr) release cytotoxicity assay using the FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11 as source of target cells, and stimulated human CD8⁺ T cells as effector cells. The assay was carried out as described in Example 10.1.

Example 10.4**FACS-based cytotoxicity assay with unstimulated human PBMC****Isolation of effector cells**

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

Depletion of CD14⁺ and CD56⁺ cells

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

Target cell labeling

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC₁₈ (DiO) (Molecular Probes, #V22886) was used to label human FLT3- or macaque FLT3-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 FLT3-transfected CHO cells in the presence of serial dilutions of FLT3 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 FLT3xCD3 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 10.5

Potency of redirecting unstimulated human PBMC against human FLT3-transfected CHO cells

The cytotoxic activity of FLT3xCD3 bispecific antibody constructs was analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with human FLT3 as target cells, and unstimulated human PBMC as effector cells. The assay was carried out as described in Example 8.4 above.

Example 10.6**Potency of redirecting unstimulated human PBMC against a FLT3 positive human ovarian carcinoma cell line**

The cytotoxic activity of FLT3xCD3 bispecific antibody constructs was furthermore analyzed in a FACS-based cytotoxicity assay using the FLT3 positive human AML cell lines EOL-1, MOLM-13 and MV4-11 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.

Example 10.7**Potency of redirecting macaque T cells against macaque FLT3-expressing CHO cells**

Finally, the cytotoxic activity of FLT3xCD3 bispecific antibody constructs was analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with macaque (cyno) FLT3 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 FLT3-transfected CHO cells and flow cytometry based analysis of cytotoxic activity was performed as described above.

Example 11**Monomer to dimer conversion after (i) three freeze/thaw cycles and (ii) 7 days of incubation at 250 µg/ml**

Bispecific FLT3xCD3 antibody monomeric construct was subjected to different stress conditions followed by high performance SEC to determine the percentage of initially monomeric antibody construct, which had been converted into dimeric antibody construct.

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

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

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

Example 12

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.

Example 13

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 FLT3-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.

Example 14

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.

Example 15

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.

Example 16

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.

Example 17

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 FLT3xCD3 bispecific antibody constructs (referred to as potency gap), an 18 hour ⁵¹-chromium release cytotoxicity assay was carried out as described hereinabove (Example 10.1) with purified bispecific antibody construct monomer and dimer. Effector cells were stimulated enriched human CD8⁺ T cells. Target cells were hu FLT3 transfected CHO cells. Effector to target cell (E:T) ratio was 10:1. The potency gap was calculated as ratio between EC₅₀ values.

FLT3xCD3 antibody constructs	EC ₅₀ [pM]		Monomer to dimer ratio (EC ₅₀ Monomer/ EC ₅₀ Dimer)
	Monomer	Dimer	
FL 39 x I2C-scFc ^o	0.37	0.23	0.5
FL 16 x I2C-scFc	0.52	0.16	2.0
FL 42 x I2C-scFc	0.53	0.76	1.2
FL 36 x I2C-scFc	2.70	0.88	1.1
FL 52 x I2C-scFc	1.45	1.69	9.9
FL 23 x I2C-scFc	0.20	0.20	0.2
FL 46 x I2C-scFc	0.34	0.15	0.9
FL 61 x I2C-scFc	18	24	6.3

Example 18

FLT3 ligand competition of binding of the FLT3 binder to its target

This assay was carried out to test whether the soluble FLT3 ligand would impair binding of the anti-FLT3 binding domains according to the invention to FLT3.

To verify binding of human FLT3 ligand to CHO cells transfected with human FLT3, cells were incubated with human FLT3 ligand for 30 minutes at 4°C. Bound FLT3 ligand was detected with an anti-HIS antibody (5 µg/ml; AbD Serotec) followed by an anti-mouse IgG Fc-gamma-PE (1:100; Jackson Immunoresearch # 115-116-071). As negative control cells were incubated with PBS/2%FCS instead of CD27.

To test competition/replacement of FLT3 binder by FLT3 ligand, CHO cells transfected with human FLT3 were incubated with or without FLT3 ligand for 30 minutes at 4°C (10 µg/FLT3

ligand). Afterwards cells were not washed but directly stained with FLT3 binder (scFv's). Bound scFv were detected with mouse monoclonal anti-FLAG M2 antibody (1 µg/ml; Sigma F1804) followed by an anti-mouse IgG Fc-gamma-PE (1:100; Jackson ImmunoResearch # 115-116-071). As negative control, cells were incubated with an unspecific scFv instead of FLT3 scFv. FLT3 ligand and all antibodies were diluted in PBS with 2%FCS.

For the evaluation of the data, the fluorescence median was detected by FACS. A loss of more than 25% of the signal as a result of the competition with the FLT3 ligand was understood as significant impact on the binding. This can be understood as significant steric interaction for the same domain of FLT3. All binders above the 75% threshold

$$(\text{median [+ligand]} / \text{median [w/o ligand]} * 100 \geq 75\%)$$

(which is true for FL-1 to FL-65) are identified as non-sensitive for the FLT3 ligand competition.

The interaction of FLT3 ligand with its receptor is described in the literature to take place in the region corresponding to epitope cluster 3. Therefore, it was expected that all binders identified in our screening to be specific for the epitope cluster 3, as well as those for the neighbouring cluster 2 and 4, would be significantly impacted in the signal of the fluorescence median by the competition with the FLT3 ligand. This expectation was in general correct. Surprisingly, FL-53, FL-54, FL-61, F-62, FL-63 and FL-64, which all bind to epitope cluster 3, still showed a signal above the threshold.

Moreover, in view of the interaction of FLT3 ligand with the region of epitope cluster 3 it was further assumed that binder for more distant epitope cluster, such as cluster 1 of FLT3, would not be impacted by the FLT3 ligand competition. However, there were a significant number of binders, which did not qualify for the 75% threshold. The binder FL-1 to FL-53, FL-55 to FL-60 and FL-65 were in the group of binders not sensitive for the FLT3 ligand competition.

Table 5: Sequence Listing

SEQ ID NO:	Description	Source	Sequence
1.	Peptide linker	artificial	GGGG
2.	Peptide linker	artificial	GGGS
3.	Peptide linker	artificial	GGGQ
4.	Peptide linker	artificial	PGGGS
5.	Peptide linker	artificial	PGDGS
6.	Peptide linker	artificial	SGGGS
7.	Peptide linker	artificial	GGGGSGGS
8.	Peptide linker	artificial	GGGGSGGGS
9.	Peptide linker	artificial	GGGGSGGGSGGGS
10.	Hexa-histidine	artificial	HHHHH
11.	CDR-L1 of F6A	artificial	GSSTGAVTSGYYPN
12.	CDR-L2 of F6A	artificial	GTKFLAP
13.	CDR-L3 of F6A	artificial	ALWYSNRWV
14.	CDR-H1 of F6A	artificial	IYAMN

15.	CDR-H2 of F6A	artificial	RIRSKYNNYATYYADSVKS
16.	CDR-H3 of F6A	artificial	HGNFGNSYVSFFAY
17.	VH of F6A	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYVSFFAYWGQGLTVTVSS
18.	VL of F6A	artificial	QTVVTTQEPSLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGKLTIVL
19.	VH-VL of F6A	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYVSFFAYWGQGLTVTVSSGGGGGGGGGSGTQVTVTQEPSLTVSPGGTTL TCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWV GGGKLTIVL
20.	CDR-L1 of H2C	artificial	GSSTGAVTSGYYPN
21.	CDR-L2 of H2C	artificial	GTKFLAP
22.	CDR-L3 of H2C	artificial	ALWYSNRWV
23.	CDR-H1 of H2C	artificial	KYAMN
24.	CDR-H2 of H2C	artificial	RIRSKYNNYATYYADSVKD
25.	CDR-H3 of H2C	artificial	HGNFGNSYISYWAY
26.	VH of H2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSS
27.	VL of H2C	artificial	QTVVTTQEPSLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGKLTIVL
28.	VH-VL of H2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGGGGGGSGTQVTVTQEPSLTVSPGGTTL TCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWV GGGKLTIVL
29.	CDR-L1 of H1E	artificial	GSSTGAVTSGYYPN
30.	CDR-L2 of H1E	artificial	GTKFLAP

31.	CDR-L3 of H1E	artificial	ALWYSNRWV
32.	CDR-H1 of H1E	artificial	SYAMN
33.	CDR-H2 of H1E	artificial	RIRSKYNNYATYYADSVKKG
34.	CDR-H3 of H1E	artificial	HGNFGNSYLSFWAY
35.	VH of H1E	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNFSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGLTVTVSS
36.	VL of H1E	artificial	QTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGGLTLTVL
37.	VH-VL of H1E	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNFSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGLTVTVSSGGGGGGGGGSGTQVTVTQEPSLTVSPGGTIVTL TCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGLTLTVL
38.	CDR-L1 of G4H	artificial	GSSTGAVTSGYYPN
39.	CDR-L2 of G4H	artificial	GTKFLAP
40.	CDR-L3 of G4H	artificial	ALWYSNRWV
41.	CDR-H1 of G4H	artificial	RYAMN
42.	CDR-H2 of G4H	artificial	RIRSKYNNYATYYADSVKKG
43.	CDR-H3 of G4H	artificial	HGNFGNSYLSYFAY
44.	VH of G4H	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGLTVTVSS
45.	VL of G4H	artificial	QTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGGLTLTVL
46.	VH-VL of G4H	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGLTVTVSSGGGGGGGGGSGTQVTVTQEPSLTVSPGGTIVTL TCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGLTLTVL

47.	CDR-L1 of A2J	artificial	RSSTGAVTSGYYPN
48.	CDR-L2 of A2J	artificial	ATDMRPS
49.	CDR-L3 of A2J	artificial	ALWYSNRWV
50.	CDR-H1 of A2J	artificial	VYAMN
51.	CDR-H2 of A2J	artificial	RIRSKYNNYATYYADSVKK
52.	CDR-H3 of A2J	artificial	HGNFGNSYLSWWAY
53.	VH of A2J	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNGNSYLSWWAYWGQGLTVTVSS
54.	VL of A2J	artificial	QTVVTQEPESLTVSPGGTIVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGKLTIVL
55.	VH-VL of A2J	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNGNSYLSWWAYWGQGLTVTVSSGGGGGGGGSGTQVVTQEPESLTVSPGGTIVL TCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWV GGGKLTIVL
56.	CDR-L1 of E1L	artificial	GSSTGAVTSGYYPN
57.	CDR-L2 of E1L	artificial	GTKFLAP
58.	CDR-L3 of E1L	artificial	ALWYSNRWV
59.	CDR-H1 of E1L	artificial	KYAMN
60.	CDR-H2 of E1L	artificial	RIRSKYNNYATYYADSVKS
61.	CDR-H3 of E1L	artificial	HGNFGNSYTSYYAY
62.	VH of E1L	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNLLKTEDTAVYYCVRHGNGNSYTSYYAYWGQGLTVTVSS
63.	VL of E1L	artificial	QTVVTQEPESLTVSPGGTIVLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV

64.	VH-VL of E1L	artificial	QPEDEAEYYCALWYSNRWVFGGTKLTVL EVQLVESGGGLVQPGGSLKLSCAASGFTTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYTSYAYWGQGLTVTVSSGGGGSGGGSGGGSQTIVVTQEPSTLTVSPGGTVTL TCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWV GGGTKLTVL
65.	CDR-L1 of E2M	artificial	RSSTGAVTSGYYPN
66.	CDR-L2 of E2M	artificial	ATDMRPS
67.	CDR-L3 of E2M	artificial	ALWYSNRWV
68.	CDR-H1 of E2M	artificial	GYAMN
69.	CDR-H2 of E2M	artificial	RIRSKYNNYATYYADSVKE
70.	CDR-H3 of E2M	artificial	HRNFGNSYLSWFAY
71.	VH of E2M	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKERFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYLSWFAYWGQGLTVTVSS
72.	VL of E2M	artificial	QTVVTQEPSTLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGTKLTVL
73.	VH-VL of E2M	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKERFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNGNSYLSWFAYWGQGLTVTVSSGGGGSGGGSGGGSQTIVVTQEPSTLTVSPGGTVTL TCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWV GGGTKLTVL
74.	CDR-L1 of F7O	artificial	GSSTGAVTSGYYPN
75.	CDR-L2 of F7O	artificial	GTKFLAP
76.	CDR-L3 of F7O	artificial	ALWYSNRWV
77.	CDR-H1 of F7O	artificial	VYAMN
78.	CDR-H2 of F7O	artificial	RIRSKYNNYATYYADSVKK

79.	CDR-H3 of F70	artificial	HGNFGNSYISWWAY
80.	VH of F70	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGLVTVSS
81.	VL of F70	artificial	QTVVTTQEPSLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCALWYSNRWVFGGKLTIVL
82.	VH-VL of F70	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGLVTVSSGGGGGGGGGSGTIVTTQEPSLTVSPGGTIVTL TCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWV GGGKLTIVL
83.	CDR-L1 of F12Q	artificial	GSSTGAVTSGNYPN
84.	CDR-L2 of F12Q	artificial	GTKFLAP
85.	CDR-L3 of F12Q	artificial	VLWYSNRWV
86.	CDR-H1 of F12Q	artificial	SYAMN
87.	CDR-H2 of F12Q	artificial	RIRSKYNNYATYYADSVKG
88.	CDR-H3 of F12Q	artificial	HGNFGNSYVSWWAY
89.	VH of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGLVTVSS
90.	VL of F12Q	artificial	QTVVTTQEPSLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGKLTIVL
91.	VH-VL of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGLVTVSSGGGGGGGGGSGTIVTTQEPSLTVSPGGTIVTL TCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWV GGGKLTIVL
92.	CDR-L1 of I2C	artificial	GSSTGAVTSGNYPN
93.	CDR-L2 of I2C	artificial	GTKFLAP
94.	CDR-L3 of I2C	artificial	VLWYSNRWV

	I2C			
95.	CDR-H1 of I2C	artificial	KYAMN	RIRSKYNNYATYYADSVKD
96.	CDR-H2 of I2C	artificial		HGNFGNSYISYWAY
97.	CDR-H3 of I2C	artificial		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS
98.	VH of I2C	artificial		AYLQMNLSKTTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS
99.	VL of I2C	artificial		QTVVTTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTL
100.	VH-VL of I2C	artificial		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS
101.	VH of F12q	artificial		AYLQMNLSKTTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS
102.	VL of F12q	artificial		QTVVTTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTL
103.	F12q	scFv		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS
104.	HALB	human		DAHKSEVAHRFKDLEGENFKALVLI
105.	HALB7	artificial		DAHKSEVAHRFKDLEGENFKALVLI

106.	HALB098	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQOCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
107.	HALB114	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQOCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
108.	HALB254	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQOCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
109.	HALB253	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQOCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
110.	HALB131	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQOCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL

111.	HALB135	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL LPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKLVAAASKAALGL
112.	HALB133	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL LPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKLVAAASKAALGL
113.	HALB234	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL LPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKLVAAASKAALGL
114.	HALB C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL LPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKLVAAASKAALGL
115.	HALB7 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL LPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKLVAAASKAALGL

116.	HALB098 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL L PKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAEEGPKLVAAASQAALGL
117.	HALB114 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL L PKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAEEGPKLVAAASQAALGL
118.	HALB254 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL L PKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAEEGPKLVAAASQAALGL
119.	HALB253 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL L PKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAEEGPKLVAAASQAALGL
120.	HALB131 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACL L PKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAEEGPKLVAAASQAALGL

121.	HALB135 C34S	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKPLVAA SQAALGL</p>
122.	HALB133 C34S	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKPLVAA SQAALGL</p>
123.	HALB234 C34S	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKPLVAA SQAALGL</p>
124.	HALB C34A	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKPLVAA SQAALGL</p>
125.	HALB7 C34A	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNP NL PRLVRPEVDVMCTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLRAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGKPLVAA SQAALGL</p>

126.	HALB098 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
127.	HALB114 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
128.	HALB254 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
129.	HALB253 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL
130.	HALB131 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKLNVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQE PERNECFLOHKDDNPNL PRLVRPEVDVMTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQJLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVEDETYVPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKKPKATKEQLKAVMDKFAAFVEKCKK ADDKETCFAEEGPKLVAAASQAALGL

131.	HALB135 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAFFEDHVKL VNEVTEFAKTCVADESAENCDSKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLOHKDDNPRLPRLVRPEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQELGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAAEEGPKLVAASKAALGL
132.	HALB133 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAFFEDHVKL VNEVTEFAKTCVADESAENCDSKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLOHKDDNPRLPRLVRPEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQELGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAAEEGPKLVAASKAALGL
133.	HALB234 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAFFEDHVKL VNEVTEFAKTCVADESAENCDSKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLOHKDDNPRLPRLVRPEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELDRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTK VHTECCHGDLLECADDDRADLAKY ICENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFKPLVEEPQNL IKQNCSELFQELGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKKPKATKEQLKAVMDKFAAFVEKCKCK ADDKETCFAAEEGPKLVAASKAALGL
134.	Ab156	artificial	RDWDFDVFGGGTPVGG
135.	linear FcRn binding peptide	artificial	QRFVTGHFGGLXPANG
136.	linear FcRn binding peptide Y	artificial	QRFVTGHFGGLYPANG
137.	linear FcRn binding peptide H	artificial	QRFVTGHFGGLHPANG
138.	core FcRn binding peptide H	artificial	TGHFGGLHP

139.	cyclic FeRn binding peptide H	artificial	QRFC TGHFGGLHPCNG
140.	Cross body 1 HC		ASTKGPSVFFLAPSSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQT YICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYDTTPVLDSDGSFFLYSDLITVDKSRWQQGNVFCSCVMHEALHNHYT QKSLSLSPGK
141.	Cross body 1 LC		GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITTPSKQSNKNKYAASSYLSTLTPEQWK SHRSYSCQVTHEGSTVEKTVAPTECSEPKSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPS RKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLITVDKSRWQQGNVFCSCVMHEALHN HYTKQKSLSLSPGK
142.	Cross body 2 HC		ASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQT YTCNVDHKPSNTKVDKTVPEKSSDKTHTCPPCPAEEAAGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYDTTPVLDSDGSFFLYSDLITVDKSRWQQGNVFCSCVMHEALHNHYT QKSLSLSPGK
143.	Cross body 2 LC		GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITTPSKQSNKNKYAASSYLSTLTPEQWK SHRSYSCQVTHEGSTVEKTVAPTECSEPKSDKTHTCPPCPAEEAAGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVY ITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLITVDKSRWQQGNVFCSCVMH EALHNHYTKQKSLSLSPGK
144.	Hetero-Fc binder Fc		DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLITVDKSRWQQGNVFCSCVMHEALHNHYTKQKSLSLSPGK
145.	Hetero-Fc partner Fc		DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYDTTPVLDSDGSFFLYSDLITVDKSRWQQGNVFCSCVMHEALHNHYTKQKSLSLSPGK
146.	Maxibody 1 target Fc		EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSRKEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLITVDKSRWQQGNVFCSCVMHEALHNHYTKQKSLSLSPGK
147.	Maxibody 1 CD3 Fc		EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSRKEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYDTTPVLDSDGSFFLYSDLITVDKSRWQQGNVFCSCVMHEALHNHYTKQKSLSLSPGK
148.	Maxibody 2 target Fc		EPKSSDKTHTCPPCPAEEAAGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSRKEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLITVDKSRWQQGNVFCSCVMHEALHNHYTKQKSLSLSPGK
149.	Maxibody 2		EPKSSDKTHTCPPCPAEEAAGGPSVFLFPPKPKDITLMI SRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT I SKAKGQPREPQVYITLPPSRKEMTKNQVSLTCLVKGFYPS

	CD3 Fc		
150.	Mono Fc		<p>DI AVEWESNGQPENNYDTTPVLDSDGSFFLYSDLTVDKSRWQQGNVFSCSVMEALHNHYTKQSLSLSPGK</p> <p>APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTTTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENN YDTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFSCSVMEALHNHYTKQSLSLSPGK</p>
151.	FL_1	VH CDR1	NARMGVS
152.	FL_1	VH CDR2	HIFSNAEKSYRTSLKS
153.	FL_1	VH CDR3	IPGYGGNGDYHYGMDV
154.	FL_1	VL CDR1	RASQGIRNDLG
155.	FL_1	VL CDR2	ASSTLQS
156.	FL_1	VL CDR3	LQHNFPWT
157.	FL_1	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLINARMGVSWIRQPPGKALEWLAHIFSNAEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARI PGYGGNGDYHYGMDVWGQGT'TVTVSS
158.	FL_1	VL	DIQMTQSPSSLSASLGDRVTITCRASQGI RNDLGWYQQKPKGAPKRLIYASSTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNFPWTFGGTKVEIK
159.	FL_1	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLINARMGVSWIRQPPGKALEWLAHIFSNAEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARI PGYGGNGDYHYGMDVWGQGT'TVTVSSGGGGGGGGGGSDIQMTQSPSSLSASLGDR VTITCRASQGI RNDLGWYQQKPKGAPKRLIYASSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNFPWTF GGTKVEIK
160.	FL_1	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLINARMGVSWIRQPPGKALEWLAHIFSNAEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARI PGYGGNGDYHYGMDVWGQGT'TVTVSSGGGGGGGGGGSDIQMTQSPSSLSASLGDR VTITCRASQGI RNDLGWYQQKPKGAPKRLIYASSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNFPWTF GGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNGNSYISYWAYWGQGT'TVTVSSGGGGGGGGGGSGTQTVVT QEPSTVSPGGT'TLTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT'PARFSGSLGGKAALTL SGVQPEDE AEYYCVLWYSNRWVFGGTKLTVL
161.	FL_2	VH CDR1	NARMGVS
162.	FL_2	VH CDR2	HIFSNDEKTYSTSLKS
163.	FL_2	VH	IPYGGSGSHNYGMDV

		CDR3	
164.	FL_2	VL CDR1	RASQDIRNDFG
165.	FL_2	VL CDR2	AASTLQS
166.	FL_2	VL CDR3	LQNTYPTWT
167.	FL_2	VH	QVTLKESGPVLVKPTETLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNDEKTYSTSLKSRLTISRDTSGQV VLTMTKMDPVDATYYCARIPIYGGSHNYGMDVWGQTTVTVSS
168.	FL_2	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRNDFGWYQQKPKAPQRLLYAASTLQSGVPSRFSGSGSGTEFTLTISLQ EDFATYYCLQNTYPTWTFGQTKVEIK
169.	FL_2	scFv	QVTLKESGPVLVKPTETLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNDEKTYSTSLKSRLTISRDTSGQV VLTMTKMDPVDATYYCARIPIYGGSHNYGMDVWGQTTVTVSSGGGGSGSGTEFTLTISLQPEDFATYYCLQNTYPTWTFGQ ITCRASQDIRNDFGWYQQKPKAPQRLLYAASTLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQNTYPTWTFGQ GTKVEIK
170.	FL_2	bispecific molecule	QVTLKESGPVLVKPTETLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNDEKTYSTSLKSRLTISRDTSGQV VLTMTKMDPVDATYYCARIPIYGGSHNYGMDVWGQTTVTVSSGGGGSGSGTEFTLTISLQPEDFATYYCLQNTYPTWTFGQ ITCRASQDIRNDFGWYQQKPKAPQRLLYAASTLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQNTYPTWTFGQ GTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNGNSYISYWAYWGQTLVTVSSGGGGSGGGSGQTVVTQE PSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAE YYCVLWYSNRWVFGGTKLTVL
171.	FL_3	VH CDR1	NARMAVS
172.	FL_3	VH CDR2	HIFSNGEKSYSTSLKS
173.	FL_3	VH CDR3	IVGYSDWLLPFDH
174.	FL_3	VL CDR1	RASQINRFLN
175.	FL_3	VL CDR2	AASLQS
176.	FL_3	VL CDR3	LQHNSYPTWT
177.	FL_3	VH	QVTLKESGPALVKPTETLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNGEKSYSTSLKSRLTISRDTSGQV VLTMTNTDPVDATYFCARIVGYSDWLLPFDHWGQIMVTVSS

178.	FL_3	VL	DIQMTQSPSSLSASVGDRTITCRASQININRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSSLQPEDFATYYCLQHNSYPWTFGGTKVDIK
179.	FL_3	scFv	QVTLKESGPALVKPTETLTITCTVSGFSLNARMVSWIRQPPGKALEWLAHIFSNGEKSYSTSLKSRLTISKDTSKTQV VLTMTNTPDVTATYFCARIVGYSDDLPPFDHWGQIMVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTIT CRASQININRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSSLQPEDFATYYCLQHNSYPWTFGGT KVDIK
180.	FL_3	bispecific molecule	QVTLKESGPALVKPTETLTITCTVSGFSLNARMVSWIRQPPGKALEWLAHIFSNGEKSYSTSLKSRLTISKDTSKTQV VLTMTNTPDVTATYFCARIVGYSDDLPPFDHWGQIMVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTIT CRASQININRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSSLQPEDFATYYCLQHNSYPWTFGGT KVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGGGGGGGSGTQTVVTVQEPS LTVSPGGTITLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
181.	FL_4	VH CDR1	NAKMGVS
182.	FL_4	VH CDR2	HIFSNDEKSYSTSLKS
183.	FL_4	VH CDR3	IVGYGSGWYGFDY
184.	FL_4	VL CDR1	RASQDIRDDL
185.	FL_4	VL CDR2	GASTLQS
186.	FL_4	VL CDR3	LQHNSYPLT
187.	FL_4	VH	QVTLKESGPALVKPTETLTITCTVSGFSLNARMVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDATYFCARIVGYSGWYGYFDYWGQGLTVTVSS
188.	FL_4	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRDDLQGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTDFTLTISSSLQ EDFATYYCLQHNSYPLTFGGGTKVDIK
189.	FL_4	scFv	QVTLKESGPALVKPTETLTITCTVSGFSLNARMVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDATYFCARIVGYSGWYGYFDYWGQGLTVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLQGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTDFTLTISSSLQPEDFATYYCLQHNSYPLTFGGG TKVDIK
190.	FL_4	bispecific molecule	QVTLKESGPALVKPTETLTITCTVSGFSLNARMVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDATYFCARIVGYSGWYGYFDYWGQGLTVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLQGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTDFTLTISSSLQPEDFATYYCLQHNSYPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDR RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGGGGGGGSGTQTVVTVQEP

			SLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
191.	FL_5	VH CDR1	NARMGV
192.	FL_5	VH CDR2	HIFWNDEKSYSTSLKS
193.	FL_5	VH CDR3	IPYYGSGSYNYGMDV
194.	FL_5	VL CDR1	RASQGIRNDLG
195.	FL_5	VL CDR2	AASSLQS
196.	FL_5	VL CDR3	LQHNTYPLT
197.	FL_5	VH	QVTLKESGPMVLVKPTETLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARIPIYGGSGSYNYGMDVWGQTTVTVSS
198.	FL_5	VL	DIQMTQSPSSLSASVGDRTITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPE EDFATYYCLQHNTYPLTFGGGKVDIK
199.	FL_5	scFv	QVTLKESGPMVLVKPTETLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARIPIYGGSGSYNYGMDVWGQTTVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRT ITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNTYPLTFGG GKVDIK
200.	FL_5	bispecific molecule	QVTLKESGPMVLVKPTETLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARIPIYGGSGSYNYGMDVWGQTTVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRT ITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNTYPLTFGG GKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGTFGNSYISYWAYWGQTTVTVSSGGGSGGGGGSGTQVVTQE PSLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAE YCVLWYSNRWVFGGKLTVL
201.	FL_6	VH CDR1	NARMAVS
202.	FL_6	VH CDR2	HIFSNDEKSYSPSLKS
203.	FL_6	VH CDR3	IVGYGTGWYGGFFDY
204.	FL_6	VL	RASQGIRNDLG

			CDR1	
205.	FL_6	VL	CDR2	AASVLQS
206.	FL_6	VL	CDR3	LQHNSYPLT
207.	FL_6	VH		QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMASVSWIRQPPGKTTLEWLAHIFSNDEKSYSPSLKSRLTISKDDTSSKQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFQYDYGQILVTVSS
208.	FL_6	VL		DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLQVQKPGKAPKRLIYAASVLQSGVPSRFSGSGSGTEFTLTITSSSLQ EDFATYYCLOHNSYPLTFGGGTKVDIK
209.	FL_6	scFv		QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMASVSWIRQPPGKTTLEWLAHIFSNDEKSYSPSLKSRLTISKDDTSSKQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFQYDYGQILVTVSSGGGGGGGGGGDIQMTQSPSSLSASVGDRTVIT TCRASQGIKNDLQVQKPGKAPKRLIYAASVLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLOHNSYPLTFGGG TKVDIK
210.	FL_6	bispecific molecule		QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMASVSWIRQPPGKTTLEWLAHIFSNDEKSYSPSLKSRLTISKDDTSSKQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFQYDYGQILVTVSSGGGGGGGGGGDIQMTQSPSSLSASVGDRTVIT TCRASQGIKNDLQVQKPGKAPKRLIYAASVLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLOHNSYPLTFGGG TKVDIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVK D RFTISRDDSKNTAYLQMNLIKTEDTAVYYCVRHGFNSYISYWAYWGQGLVTVSSGGGGGGGGGGSGTQVTVQEP SLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLQSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
211.	FL_7	VH	CDR1	NARMGVS
212.	FL_7	VH	CDR2	HIFSNDEKSYSTSLKN
213.	FL_7	VH	CDR3	IVGYGTGWFGYFDY
214.	FL_7	VL	CDR1	RASQDIRTDIA
215.	FL_7	VL	CDR2	AASSLQS
216.	FL_7	VL	CDR3	LQHNRYPIT
217.	FL_7	VH		QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMASVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDDSKTQV VLTMTNVDVDTATYYCARIVGYGTGWFGYDYGQGTQVTVSS
218.	FL_7	VL		DIQMTQSPSSLSASVGDRTVITCRASQDIRTDIAWYQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTITSSSLQ EDFATYYCLOHNRYPITFGGGTKVDIK

219.	FL_7	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSTQV VLTMTNVDPVDATYYCARIVGYGTFWGFYFDYWGQGTQVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTVI TCRASQDIRTDLAWYQQKPKGAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNRYPLTFFGG TKVDIK
220.	FL_7	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSTQV VLTMTNVDPVDATYYCARIVGYGTFWGFYFDYWGQGTQVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTVI TCRASQDIRTDLAWYQQKPKGAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNRYPLTFFGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGTFGNSYISYWAYWGQGTQVTVSSGGGGGGGGGGGGQTVVTQEP SLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
221.	FL_8	VH CDR1	YARMGV'S
222.	FL_8	VH CDR2	QIFSNDEKSYSTSLKS
223.	FL_8	VH CDR3	IVGYGTGWYGFDDY
224.	FL_8	VL CDR1	RASQGIKNDLG
225.	FL_8	VL CDR2	AASSLQS
226.	FL_8	VL CDR3	LQHNSYPLT
227.	FL_8	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKGTNSQV VLTMTNMDPEDATYYCARIVGYGTFWGFYFDYWGQGTQVTVSS
228.	FL_8	VL	DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGWYQQKPKGAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFFGGTKVDIK
229.	FL_8	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKGTNSQV VLTMTNMDPEDATYYCARIVGYGTFWGFYFDYWGQGTQVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTVI TCRASQGIKNDLGWYQQKPKGAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNRYPLTFFGG TKVDIK
230.	FL_8	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKGTNSQV VLTMTNMDPEDATYYCARIVGYGTFWGFYFDYWGQGTQVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTVI TCRASQGIKNDLGWYQQKPKGAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNRYPLTFFGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGTFGNSYISYWAYWGQGTQVTVSSGGGGGGGGGGGGQTVVTQEP SLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL

231.	FL_9	VH CDR1	NARMGVS
232.	FL_9	VH CDR2	HIFSNDEKSYSTSLKS
233.	FL_9	VH CDR3	IPGYGGNFYHYHYGMDV
234.	FL_9	VL CDR1	RASQGIRNDLA
235.	FL_9	VL CDR2	AASTVQS
236.	FL_9	VL CDR3	LQHNSFPWT
237.	FL_9	VH	QVTLKESGPTLVKPTETLTTLTCTVSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATATYYCARI PGYGGNFYHYHYGMDVWGQTTVTVSS
238.	FL_9	VL	DIQMTQSPSSLSASVGDRTVITCRASQGIRNDLAWYQQKPKGAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISLQ EDFATYYCLQHNSFPWTFGQGTKVDIK
239.	FL_9	scFv	QVTLKESGPTLVKPTETLTTLTCTVSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATATYYCARI PGYGGNFYHYHYGMDVWGQTTVTVSSGGGGSGSGTEFALTISLQPEDFATYYCLQHNSFPWTF VTITCRASQGIRNDLAWYQQKPKGAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISLQPEDFATYYCLQHNSFPWTF GQGTKVDIK
240.	FL_9	bispecific molecule	QVTLKESGPTLVKPTETLTTLTCTVSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATATYYCARI PGYGGNFYHYHYGMDVWGQTTVTVSSGGGGSGSGTEFALTISLQPEDFATYYCLQHNSFPWTF VTITCRASQGIRNDLAWYQQKPKGAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISLQPEDFATYYCLQHNSFPWTF GQGTKVDIKKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNFGNSYISYWAYWGQTTLVTVSSGGGGSGSGSGSGTQVTVT QEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAALTLGSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
241.	FL_10	VH CDR1	NARMGVS
242.	FL_10	VH CDR2	HIFSNDEKSYSTSLKS
243.	FL_10	VH CDR3	MPEYSSGWSGAFDI
244.	FL_10	VL CDR1	RASQDIRDDL
245.	FL_10	VL	GASTLQS

			CDR2	
246.	FL_10		VL CDR3	LQHNSYPLT
247.	FL_10		VH	QVTLKESGPVLVKPTEITLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSS
248.	FL_10		VL	DIQMTQSPSSLSASVGDRTITCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK
249.	FL_10		scFv	QVTLKESGPVLVKPTEITLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVDIK
250.	FL_10	bispecific molecule		QVTLKESGPVLVKPTEITLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGGSGDIQMTQSPSSLSASVGDRTITI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVDIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLTITVSSGGGGSGGGSGQTVVTTQEP SLTVSPGGTITLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
251.	FL_11	VH CDR1		NAKMGS
252.	FL_11	VH CDR2		QIFSNGEKSYSTSLKS
253.	FL_11	VH CDR3		IVGYSGWYGYFDY
254.	FL_11	VL CDR1		RASQGIRNDLG
255.	FL_11	VL CDR2		GASTLQS
256.	FL_11	VL CDR3		LQHNSYPLT
257.	FL_11	VH		QVTLKESGPVLVKPTEITLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAQIFSNGEKSYSTSLKSRLTISKDTSKGQV VLTMNMDPVDATATYCSRIVGYSGWYGYFDYWQGTLTIVSS
258.	FL_11	VL		DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
259.	FL_11	scFv		QVTLKESGPVLVKPTEITLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAQIFSNGEKSYSTSLKSRLTISKDTSKGQV VLTMNMDPVDATATYCSRIVGYSGWYGYFDYWQGTLTIVSSGGGGSGGGSGDIQMTQSPSSLSASVGDRTITI TCRASQGIRNDLGWYQQKPGKAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG

260.	FL_11		bispecific molecule	TKVEIK QVTLKESGPVLVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAQIFSNGEKSYSTSLKSRLTISKDTSKQV VLTMTNMDPVDATYYCSRIVGYSGWYGYFDYWGQGLTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
261.	FL_12	VH CDR1		NARMGV
262.	FL_12	VH CDR2		NIFSNDEKSYSTSLKS
263.	FL_12	VH CDR3		IVGYSGWYGYFDY
264.	FL_12	VL CDR1		RASQGI RNDLG
265.	FL_12	VL CDR2		AASSLQS
266.	FL_12	VL CDR3		LQHNSYPLT
267.	FL_12	VH		QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNMDPEDATYYCARI VGYSGWYGYFDYWGQGLTVTVSS
268.	FL_12	VL		DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQQKPGKAPQRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPE EDFATYYCLQHNSYPLTFGGTKVEIK
269.	FL_12	scFv		QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNMDPEDATYYCARI VGYSGWYGYFDYWGQGLTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPQRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
270.	FL_12	bispecific molecule		QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNMDPEDATYYCARI VGYSGWYGYFDYWGQGLTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPQRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
271.	FL_13	VH CDR1		NARMGV

272.	FL_13	VH CDR2	HIFSNDEKSYSTSLKN	
273.	FL_13	VH CDR3	IVGYGSGWYGFFDY	
274.	FL_13	VL CDR1	RASQDIRNDLG	
275.	FL_13	VL CDR2	AASTLQS	
276.	FL_13	VL CDR3	LQHNSYPLT	
277.	FL_13	VH	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDATATYICARIVGYGSGWYGFFDYWGQGTLLVTVSS	
278.	FL_13	VL	DIQMTQSPSSLSASVGDRTITCRASQGIKNDLWYQQKPKGKAPKRLIYAASLTQSGVPSRFSGSGTEFTLTISLQPE EDFATYYCLQHNSYPLTFGGGKVEIK	
279.	FL_13	scFv	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDATATYICARIVGYGSGWYGFFDYWGQGTLLVTVSSGGGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGSGSGGSGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL	
280.	FL_13	bispecific molecule	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDATATYICARIVGYGSGWYGFFDYWGQGTLLVTVSSGGGSGSGGSGDIQMTQSPSSLSASVGDRTIT TCRASQGIKNDLWYQQKPKGKAPKRLIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGSGSGGSGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL	
281.	FL_14	VH CDR1	NARMAVS	
282.	FL_14	VH CDR2	HIFSNDEKSYSTSLKS	
283.	FL_14	VH CDR3	IVGYGSGWYGFDY	
284.	FL_14	VL CDR1	RASQDIRNDLG	
285.	FL_14	VL CDR2	AASTLQS	
286.	FL_14	VL	LQHNSYPLT	

		CDR3	
287.	FL_14	VH	QVTLKESGPALVKPTETLTTLCTLSGFSLNARMVSVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSGQV VLTMTNMDPVDATYYCARIVGYSGWYGYFDYWGQGTLLVTVSS
288.	FL_14	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRNDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGGTKVEIK
289.	FL_14	scFv	QVTLKESGPALVKPTETLTTLCTLSGFSLNARMVSVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSGQV VLTMTNMDPVDATYYCARIVGYSGWYGYFDYWGQGTLLVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTI TCRASQDIRNDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
290.	FL_14	bispecific molecule	QVTLKESGPALVKPTETLTTLCTLSGFSLNARMVSVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSGQV VLTMTNMDPVDATYYCARIVGYSGWYGYFDYWGQGTLLVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTI TCRASQDIRNDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGGGGGGGGGGQTVVTQEP SLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWFVGGGTKLTVL
291.	FL_15	VH CDR1	NARMVS
292.	FL_15	VH CDR2	HIFSNDEKSYSTSLKS
293.	FL_15	VH CDR3	IVGYSGWYGYFDY
294.	FL_15	VL CDR1	RASQDIGNDLG
295.	FL_15	VL CDR2	AASSLQS
296.	FL_15	VL CDR3	LQHNSYPLT
297.	FL_15	VH	QVTLKESGPALVKPTETLTTLCTLSGFSLNARMVSVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSGQV VLTMTNMDPVDATYYCARIVGYSGWYGYFDYWGQGTLLVTVSS
298.	FL_15	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRNDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGGTKVEIK
299.	FL_15	scFv	QVTLKESGPALVKPTETLTTLCTLSGFSLNARMVSVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSGQV VLTMTNMDPVDATYYCARIVGYSGWYGYFDYWGQGTLLVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTI TCRASQDIGNDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
300.	FL_15	bispecific	QVTLKESGPALVKPTETLTTLCTLSGFSLNARMVSVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSGQV

		c molecule	VLTMNMDPVDATYYCARIVGYSGWYGYFDYWGQGLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDIGNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLVTVSSGGGGGGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
301.	FL_16	VH CDR1	NARMAVS
302.	FL_16	VH CDR2	HIFSNDEKSYSTSLKS
303.	FL_16	VH CDR3	IVGYGSGWYGYFDY
304.	FL_16	VL CDR1	RASQDIRYDLA
305.	FL_16	VL CDR2	AASSLQS
306.	FL_16	VL CDR3	LQHNFYPLT
307.	FL_16	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMAVSWIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYGYFDYWGQGLVTVSS
308.	FL_16	VL	DIQMTQSPSSVSASVGDRVTITCRASQDIRYDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNFYPLTFGGTKVEIK
309.	FL_16	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMAVSWIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYGYFDYWGQGLVTVSSGGGGGGGGGGSDIQMTQSPSSVSASVGDRVTITCRASQDIRYDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNFYPLTFGGG TKVEIK
310.	FL_16	bispecific c molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMAVSWIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYGYFDYWGQGLVTVSSGGGGGGGGGGSDIQMTQSPSSVSASVGDRVTITCRASQDIRYDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNFYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLVTVSSGGGGGGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
311.	FL_17	VH CDR1	NARMGVS
312.	FL_17	VH CDR2	NIFSNDEKSYSTSLKS

313.	FL_17	VH CDR3	IVGYGSGWYGFDY
314.	FL_17	VL CDR1	RASQDIRNDLG
315.	FL_17	VL CDR2	ATSIRQS
316.	FL_17	VL CDR3	LQHNSFPLT
317.	FL_17	VH	QVTLKESGPTLVKPTETLTCTVSGFSLNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNPNPVDGTYYCARIVGYSWYGFDYWGQGLVTVSS
318.	FL_17	VL	DIQMTQSPSSLSASVGDRTVITCRASQDIRNDLGWYQQKPKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQP EDFATYFCLQHNSFPLTFGGGKVEIK
319.	FL_17	scFv	QVTLKESGPTLVKPTETLTCTVSGFSLNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNPNPVDGTYYCARIVGYSWYGFDYWGQGLVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTVIT TCRASQDIRNDLGWYQQKPKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGGG TKVEIK
320.	FL_17	bispecific molecule	QVTLKESGPTLVKPTETLTCTVSGFSLNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNPNPVDGTYYCARIVGYSWYGFDYWGQGLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVIT TCRASQDIRNDLGWYQQKPKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLVTVSSGGGGGGGGGGSGQTVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSNYPNWVQQKPGQAPRGLIGGTFKFLAPGTTPARFSGSLLGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
321.	FL_18	VH CDR1	NARMGVS
322.	FL_18	VH CDR2	HIFSNDEKSFSTSLKN
323.	FL_18	VH CDR3	MVGYSWYAYFDY
324.	FL_18	VL CDR1	RASQISSYLN
325.	FL_18	VL CDR2	AASSLQS
326.	FL_18	VL CDR3	LQHNSYPLT
327.	FL_18	VH	QVTLKESGPTLVKPTQTLTCTVSGFSLNARMGVSWIRQPPGKALEWLANIFSNDEKSFSTSLKNRLTISKDTSKSQV

328.	FL_18	VL	VLTMNMDPVDATYYCARMVGYSGWYAYFDYWGQGTQVTVSS DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGDTFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
329.	FL_18	scFv	QVTLKESGPVLVKPTQTTLTCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMNMDPVDATYYCARMVGYSGWYAYFDYWGQGTQVTVSSGGGGGGGGSDIQMTQSPSSLSASVGRVTI TCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGDTFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
330.	FL_18	bispecific molecule	QVTLKESGPVLVKPTQTTLTCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMNMDPVDATYYCARMVGYSGWYAYFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVTI TCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGDTFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVLVESSGGLVQPGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVTI SLTVSPGGTFTLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
331.	FL_19	VH CDR1	YARMGVSV
332.	FL_19	VH CDR2	QIFSNDEKSYSTSLKS
333.	FL_19	VH CDR3	IVGYGTGWYGYFDY
334.	FL_19	VL CDR1	RASQDIGDDL
335.	FL_19	VL CDR2	AASTLQS
336.	FL_19	VL CDR3	LQHNSYPLT
337.	FL_19	VH	QVTLKESGPTLVKPTETTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIYGYGTGWYGYFDYWGQGTQVTVSS
338.	FL_19	VL	DIQMTQSPSSLSASVGRVTITCRASQDIGDDLQVYQKPKAPKRLIYAASTLQSGVPSRFSGSGSGDTFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
339.	FL_19	scFv	QVTLKESGPTLVKPTETTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIYGYGTGWYGYFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVTI TCRASQDIGDDLQVYQKPKAPKRLIYAASTLQSGVPSRFSGSGSGDTFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
340.	FL_19	bispecific molecule	QVTLKESGPTLVKPTETTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIYGYGTGWYGYFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVTI TCRASQDIGDDLQVYQKPKAPKRLIYAASTLQSGVPSRFSGSGSGDTFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVLVESSGGLVQPGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD

			RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNGNSYISYWAYWQGTLVTVSSGGGGGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
341.	FL_20	VH CDR1	NARMAVS
342.	FL_20	VH CDR2	HIFSNDEKSYSTSLKS
343.	FL_20	VH CDR3	IVGYGTGWYGFFDY
344.	FL_20	VL CDR1	RASQGIRNDLA
345.	FL_20	VL CDR2	AASSLQS
346.	FL_20	VL CDR3	LQHNSYPLT
347.	FL_20	VH	QVTLKESGPALVKPTETLTLTCTLSGFSLNARMASVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTYGFFDYWGQILVTVSS
348.	FL_20	VL	DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLAWYQQKPKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGGKVEIK
349.	FL_20	scFv	QVTLKESGPALVKPTETLTLTCTLSGFSLNARMASVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTYGFFDYWGQILVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTVIT TCRASQGIKNDLAWYQQKPKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
350.	FL_20	bispecific molecule	QVTLKESGPALVKPTETLTLTCTLSGFSLNARMASVIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTYGFFDYWGQILVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTVIT TCRASQGIKNDLAWYQQKPKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNGNSYISYWAYWQGTLVTVSSGGGGGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
351.	FL_21	VH CDR1	NARMGVS
352.	FL_21	VH CDR2	HIFSNDEKSYSTSLKS
353.	FL_21	VH CDR3	IPGYGGNFYHYGMDV

354.	FL_21	VL CDR1	RTSRGIRNDLG	
355.	FL_21	VL CDR2	AASTLQS	
356.	FL_21	VL CDR3	LQHNNFPWT	
357.	FL_21	VH	QVTLKESGPALVKPTETLTTLCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARI PGYGGNFYHYGMDVWGQTTVTVSS	
358.	FL_21	VL	DIQMTQSPSSLSASVGDRTITCRTSGIRNDLGWYQQIPGRAPKRLIYAASTLQSGVPSRFSGSGTEFTLTISLQ EDFATYYCLQHNNFPWTFGQGTKVEIK	
359.	FL_21	scFv	QVTLKESGPALVKPTETLTTLCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARI PGYGGNFYHYGMDVWGQTTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRT VTITCRTSGIRNDLGWYQQIPGRAPKRLIYAASTLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNFPWTF GQGTKVEIK	
360.	FL_21	bispecific molecule	QVTLKESGPALVKPTETLTTLCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARI PGYGGNFYHYGMDVWGQTTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRT VTITCRTSGIRNDLGWYQQIPGRAPKRLIYAASTLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNFPWTF GQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQTTLVTVSSGGGGGGGGGGGGTQTVVT QEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL	
361.	FL_22	VH CDR1	NARMGV	
362.	FL_22	VH CDR2	HIFSNDEKSYSTSLKS	
363.	FL_22	VH CDR3	MPEYSSGWSGAFDI	
364.	FL_22	VL CDR1	RASQGISNYLA	
365.	FL_22	VL CDR2	AASTLQS	
366.	FL_22	VL CDR3	LQHNTYPWT	
367.	FL_22	VH	QVTLKESGPALVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS	
368.	FL_22	VL	DIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGTEFTLTISLQ	

369.	FL_22		scFv	EDFATYYCLQHNTYPTWTFGQGTKVEIK QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGISNYLAWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTIISSLPEDFATYYCLQHNTYPTWTFGQG TKVEIK
370.	FL_22		bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGISNYLAWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTIISSLPEDFATYYCLQHNTYPTWTFGQG TKVEIKSGGGGGSEVLVESGGGLVPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI SLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTIVL
371.	FL_23		VH CDR1	NARMGV'S
372.	FL_23		VH CDR2	HIFSNDEKSYSTSLKS
373.	FL_23		VH CDR3	MPEYSSGWSGAFDI
374.	FL_23		VL CDR1	RASQDIGYDLG
375.	FL_23		VL CDR2	AASLTQS
376.	FL_23		VL CDR3	LQHNSFPWT
377.	FL_23		VH	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS
378.	FL_23		VL	DIQMTQSPSSLASVGDRTVIITCRASQDIGYDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTIISSLPQ EDFATYYCLQHNSFPWTFGQGTKVEIK
379.	FL_23		scFv	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQDIGYDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTIISSLPEDFATYYCLQHNSFPWTFGQG TKVEIK
380.	FL_23		bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQDIGYDLGWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTIISSLPEDFATYYCLQHNSFPWTFGQG TKVEIKSGGGGGSEVLVESGGGLVPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI SLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKAAALTLSGVQPEDEAEY

			YCVLWYSNRWVFGGTKLTVL
381.	FL_24	VH CDR1	NVRMGVS
382.	FL_24	VH CDR2	HIFSNDEKSYSTSLKS
383.	FL_24	VH CDR3	MPEYSSGWSGAFDI
384.	FL_24	VL CDR1	RASQDIRDDL
385.	FL_24	VL CDR2	AATLQS
386.	FL_24	VL CDR3	LQHHSYPWT
387.	FL_24	VH	QVTLKESGPALVKPTETLTITCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLILTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS
388.	FL_24	VL	DIQMTQSPSSLSASVGDRTITICRASQDIRDDLWYQQKPKGAPKRLIYAATLQSGVPSRFSGSGTEFTLTITSSLP EDFATYYCLQHHSYPWTFGQTKVEIK
389.	FL_24	scFv	QVTLKESGPALVKPTETLTITCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLILTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLWYQQKPKGAPKRLIYAATLQSGVPSRFSGSGTEFTLTITSSLPEDFATYYCLQHHSYPWTFGQ TKVEIK
390.	FL_24	bispecific molecule	QVTLKESGPALVKPTETLTITCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLILTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLWYQQKPKGAPKRLIYAATLQSGVPSRFSGSGTEFTLTITSSLPEDFATYYCLQHHSYPWTFGQ TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYICVRHGNFNSYISYWAYWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTIT SLTVSPGGTMTVTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKAAALTLGSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
391.	FL_25	VH CDR1	NARMGVS
392.	FL_25	VH CDR2	HIFSNDEKSYSTSLKS
393.	FL_25	VH CDR3	MPEYSSGWSGAFDI
394.	FL_25	VL CDR1	RASQDIRDLG

395.	FL_25	VL CDR2	AASTLQS	
396.	FL_25	VL CDR3	LQHNSFPFT	
397.	FL_25	VH	QVTLKESGPALVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS	
398.	FL_25	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRDDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFTGGSGTEFTLTISLQ EDFATYYCLOHNSFPFTFGGKVEIK	
399.	FL_25	scFv	QVTLKESGPALVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGSGGGSGTEFTLTISLQPEDFATYYCLOHNSFPFTFGG TCRASQDIRDDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFTGGSGTEFTLTISLQPEDFATYYCLOHNSFPFTFGG TKVEIK	
400.	FL_25	bispecific molecule	QVTLKESGPALVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGSGGGSGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFTGGSGTEFTLTISLQPEDFATYYCLOHNSFPFTFGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGSGGGSGGGSTVVTQEP SLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL	
401.	FL_26	VH CDR1	NARMGVS	
402.	FL_26	VH CDR2	HIFSNDEKSYSTSLKS	
403.	FL_26	VH CDR3	MPEYSSGWSGAFDI	
404.	FL_26	VL CDR1	RASQGIRNDLV	
405.	FL_26	VL CDR2	GTSTLQS	
406.	FL_26	VL CDR3	LQHNSYPLT	
407.	FL_26	VH	QVTLKESGPALVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS	
408.	FL_26	VL	DIQMTQSPSSLSASVGDRTITCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFTGGSGTEFTLTISLQ EDFATYYCLOHNSYPLTFGGKVEIK	
409.	FL_26	scFv	QVTLKESGPALVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGSGGGSGGGSDIQMTQSPSSLSASVGDRTIT	

			TCRASQGI RNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC LQHNSYPLTFFGGG TKVEIK
410.	FL_26	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGSGTEFTLTISSLQPEDFATYYC LQHNSYPLTFFGGG TCRASQGI RNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC LQHNSYPLTFFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGGGSGSGSQTVVTQEP SLTVSPGGT VTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTTKLTVL
411.	FL_27	VH CDR1	NARMGVS
412.	FL_27	VH CDR2	HIFSNDEKSYSTSLKS
413.	FL_27	VH CDR3	MPEYSSGWSGAFDI
414.	FL_27	VL CDR1	RTSQGI RNDLV
415.	FL_27	VL CDR2	AASTLQS
416.	FL_27	VL CDR3	LQHYSYPLT
417.	FL_27	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS
418.	FL_27	VL	DIQMTQSPSSLSASVGDRTITTCRTSQGI RNDLVWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC LQHYSYPLTFFGGGTTKVEIK
419.	FL_27	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGSGTEFTLTISSLQPEDFATYYC LQHNSYPLTFFGGG TCRTSQGI RNDLVWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC LQHYSYPLTFFGGG TKVEIK
420.	FL_27	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGSGTEFTLTISSLQPEDFATYYC LQHNSYPLTFFGGG TCRTSQGI RNDLVWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC LQHNSYPLTFFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGGGSGSGSQTVVTQEP SLTVSPGGT VTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTTKLTVL
421.	FL_28	VH	NARMGVS

		CDR1	
422.	FL_28	VH CDR2	HIFSNDEKSYSTSLKS
423.	FL_28	VH CDR3	MPEYSSGWSGAFDI
424.	FL_28	VL CDR1	RASQIGDDLQ
425.	FL_28	VL CDR2	ATSVLQS
426.	FL_28	VL CDR3	LQHNSYPLT
427.	FL_28	VH	QVTLKESGPVLVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVSS
428.	FL_28	VL	DIQMTQSPSSLSASVGDRTITICRASQIGIGDDLQWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGGKVEIK
429.	FL_28	scFv	QVTLKESGPVLVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
430.	FL_28	bispecific molecule	QVTLKESGPVLVKPTETLTTLCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVLVESSGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
431.	FL_29	VH CDR1	NARMGV
432.	FL_29	VH CDR2	HIFSNDEKSYRTSLKS
433.	FL_29	VH CDR3	IVGYGSGWYAYFDY
434.	FL_29	VL CDR1	RASQIRNDLG
435.	FL_29	VL CDR2	AASSLQS

436.	FL_29	VH CDR3	LQHNSYPLT QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYAYFDYWGGQTLVTVSS
437.	FL_29	VH	DIQMTQSPSSLASAVGDRVTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFGSGSGTEFTLTISLQPE EDFATYYCLQHNSYPLTFGGGTKEIK
438.	FL_29	VH	QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYAYFDYWGGQTLVTVSSGGGGGGGGDIQMTQSPSSLASAVGDRVTTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
439.	FL_29	scFv	QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYAYFDYWGGQTLVTVSSGGGGGGGGGGDIQMTQSPSSLASAVGDRVTTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
440.	FL_29	bispecific molecule	QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMNMDPVDATYYCARIVGYSGWYAYFDYWGGQTLVTVSSGGGGGGGGGGDIQMTQSPSSLASAVGDRVTTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNTATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHNGFGNSYISYWAYWGQTLVTVSSGGGGGGGGGGQTVVTTQEP SLTVSPGGTGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGILIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPDEAEY YCVLWYSNRWVFGGGTKLTVL
441.	FL_30	VH CDR1	NARMGV
442.	FL_30	VH CDR2	LIYWDDKRYSPSLKS
443.	FL_30	VH CDR3	MVGYGSGWYAYFDY
444.	FL_30	VH CDR1	RASQGIRNDLG
445.	FL_30	VH CDR2	AASSLQS
446.	FL_30	VH CDR3	LQHNSYPLT
447.	FL_30	VH	QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKRYSPSLKSRLTITKDTSKNQV VLTMNMDPVDATYYCARMVGYSGWYAYFDYWGGQTLVTVSS
448.	FL_30	VH	DIQMTQSPSSLASAVGDRVTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFGSGSGTEFTLTISLQPE EDFATYYCLQHNSYPLTFGGGTKEIK
449.	FL_30	scFv	QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKRYSPSLKSRLTITKDTSKNQV VLTMNMDPVDATYYCARMVGYSGWYAYFDYWGGQTLVTVSSGGGGGGGGGGDIQMTQSPSSLASAVGDRVTTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK

450.	FL_30	bispecific molecule	QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKALEWLALIIYNDKRYSPSLKSRLTITTKDTSKNQV VLTMNDPVDATYYCARWVGYSWYAYFDYWGQGLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPKRLIIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
451.	FL_31	VH CDR1	NARMGV
452.	FL_31	VH CDR2	HIFSNDEKSYSTSLKS
453.	FL_31	VH CDR3	IVGYGTGWYGGFDY
454.	FL_31	VL CDR1	RTSQGIRNDLG
455.	FL_31	VL CDR2	AASSLQS
456.	FL_31	VL CDR3	LQHNSYPLT
457.	FL_31	VH	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKALEWLALHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNDPVDATYYCARIVGYGTGWYGGFDYWGQGLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVI DIQMTQSPSSLSASVGDRTVITCRTSQGIRNDLGWYQQKPGKAPKRLIIYAASSLQSGVPSRFSGSGTEFTLTISLQPE EDFATYYCLQHNSYPLTFGGTKVEIK
458.	FL_31	VL	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKALEWLALHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNDPVDATYYCARIVGYGTGWYGGFDYWGQGLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVI TCRTSQGIRNDLGWYQQKPGKAPKRLIIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
459.	FL_31	scFv	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKALEWLALHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNDPVDATYYCARIVGYGTGWYGGFDYWGQGLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVI TCRTSQGIRNDLGWYQQKPGKAPKRLIIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
460.	FL_31	bispecific molecule	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKALEWLALHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMNDPVDATYYCARIVGYGTGWYGGFDYWGQGLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVI TCRTSQGIRNDLGWYQQKPGKAPKRLIIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
461.	FL_32	VH CDR1	NARMGV
462.	FL_32	VH	HIFSNDEKSYSTSLKS

			CDR2	
463.	FL_32	VH	VH	IVGYGSGWYGFDY
464.	FL_32	CDR3	VL	RASQGIRNDLV
465.	FL_32	CDR1	VL	AASTLQS
466.	FL_32	CDR2	VL	LQHYSYPLT
467.	FL_32	CDR3	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMNTMDPVDATYYCARIVGYSGWYGFDYWGQGTLLVTVSS
468.	FL_32	VL	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLVWYQQKPKGAPKRLIYAASTLQSGVPSRFSGSGSGTEFILTISLQPE EDFATYFCLQHYSYPLTFGGGTKLEIK
469.	FL_32	scFv	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMNTMDPVDATYYCARIVGYSGWYGFDYWGQGTLLVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPKGAPKRLIYAASTLQSGVPSRFSGSGSGTEFILTISLQPEDFATYFCLQHYSYPLTFGGG TKLEIK
470.	FL_32	bispecific molecule	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMNTMDPVDATYYCARIVGYSGWYGFDYWGQGTLLVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPKGAPKRLIYAASTLQSGVPSRFSGSGSGTEFILTISLQPEDFATYFCLQHYSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGSGGGGGSGTQVVTQEP SLTVSPGGTVTLTCCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
471.	FL_33	VH	VH	NARMGV'S
472.	FL_33	CDR1	CDR1	HIFSNDEKSYSTSLKS
473.	FL_33	CDR2	VH	IVGYGSGWYGFDY
474.	FL_33	CDR3	VL	RASQIGDDLG
475.	FL_33	CDR1	VL	ATSVLQS
476.	FL_33	CDR2	VL	LQHNSYPLT

477.	FL_33	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDATYYCARIYGYSGWYGYFDYWGQGTTLVTVSS
478.	FL_33	VL	DIQMTQSPSSLSASVGRVTITCRASQGIIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGGKLEIK
479.	FL_33	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDATYYCARIYGYSGWYGYFDYWGQGTTLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVTI TCRASQGIIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKLEIK
480.	FL_33	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKTTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDATYYCARIYGYSGWYGYFDYWGQGTTLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVTI TCRASQGIIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGTTLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVT SLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
481.	FL_34	VH CDR1	NARMGV
482.	FL_34	VH CDR2	HIFWNDEKSYSTSLKS
483.	FL_34	VH CDR3	IPYGGSGSYNGMDV
484.	FL_34	VL CDR1	RASQGIRNDLG
485.	FL_34	VL CDR2	AASSLQS
486.	FL_34	VL CDR3	LQHNSYPLT
487.	FL_34	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQQV VLTMTNMDPVDATYYCARIPIYGGSGSYNGMDVWGQGTTLVTVSS
488.	FL_34	VL	DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGGKLEIK
489.	FL_34	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQQV VLTMTNMDPVDATYYCARIPIYGGSGSYNGMDVWGQGTTLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVT ITCRASQGIIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG GKLEIK
490.	FL_34	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQQV VLTMTNMDPVDATYYCARIPIYGGSGSYNGMDVWGQGTTLVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGRVT ITCRASQGIIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGG

		molecule	GTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLVTVSSGGGGSGGGSGQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAE YYCVLWYSNRWVFGGTKLTVL
491.	FL_35	VH CDR1	NARMGV
492.	FL_35	VH CDR2	HIFSNDEKSYSTSLKN
493.	FL_35	VH CDR3	IVGYGTGWYGGFDY
494.	FL_35	VL CDR1	RASQDIRDDL
495.	FL_35	VL CDR2	GTSTLQS
496.	FL_35	VL CDR3	LQHHSYPLT
497.	FL_35	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTYGGFDYWGQGTQVTVSS
498.	FL_35	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRDDLWYQQKPKAPKRLIYGTSTLQSGVPSRFSGSGTEFTLTISLQ EDFATYYCLQHHSYPLTFGGGKLEIK
499.	FL_35	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTYGGFDYWGQGTQVTVSSGGGGSGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLWYQQKPKAPKRLIYGTSTLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHHSYPLTFGGG TKLEIK
500.	FL_35	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTYGGFDYWGQGTQVTVSSGGGGSGGGSDIQMTQSPSSLSASVGDRTIT TCRASQDIRDDLWYQQKPKAPKRLIYGTSTLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHHSYPLTFGGG TKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLVTVSSGGGGSGGGSGQTVVTQE SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAE YCVLWYSNRWVFGGTKLTVL
501.	FL_36	VH CDR1	YARMGV
502.	FL_36	VH CDR2	HIFSNDEKSYSTSLKS
503.	FL_36	VH	MPEYSSGWSGAFDI

			CDR3	
504.	FL_36		VL CDR1	RASQDIRNDLA
505.	FL_36		VL CDR2	AASSLQS
506.	FL_36		VL CDR3	LQHNSYPLT
507.	FL_36		VH	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSS
508.	FL_36		VL	DIQMTQSPSSLSASVGDRTITCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISLQPEDFATYYCQLHNSYPLTFGGGKLEIK
509.	FL_36		scFv	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGGGGGDIQMTQSPSSLSASVGDRTITCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISLQPEDFATYYCQLHNSYPLTFGGGKLEIK
510.	FL_36		bispecific molecule	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGGGGGDIQMTQSPSSLSASVGDRTITCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISLQPEDFATYYCQLHNSYPLTFGGGKLEIKSGGGSEVLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLVTVSSGGGGGGGGGGSGTQVTVTQEP SLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
511.	FL_37		VH CDR1	NIKMGVS
512.	FL_37		VH CDR2	HIFSNDEKSYSTSLKS
513.	FL_37		VH CDR3	MPEYSSGWSGAFDI
514.	FL_37		VL CDR1	RASQDISNYLA
515.	FL_37		VL CDR2	AASSLQS
516.	FL_37		VL CDR3	LQHNSFPLT
517.	FL_37		VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNINIKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSS

518.	FL_37	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLOHNSFPLTFGGGKLEIK
519.	FL_37	scFv	QVTLKESGPVLVKPTEETLTCTVSGFSLRNKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGSDIQMTQSPSSLSASVGDRVTI TCRASQDISNYLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLOHNSFPLTFGGG TKLEIK
520.	FL_37	bispecific molecule	QVTLKESGPVLVKPTEETLTCTVSGFSLRNKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGSDIQMTQSPSSLSASVGDRVTI TCRASQDISNYLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLOHNSFPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNINLKTEDTAVYYCVRHGNGFSYISYWAYWGQGTMTVTVSSGGGGSGGSDIQMTQSPSSLSASVGDRVTI SLTVSPGGTMTVLTCTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTIVL
521.	FL_38	VH CDR1	NARMGV
522.	FL_38	VH CDR2	HIFSNDEKSYSTSLKS
523.	FL_38	VH CDR3	MPEYSSGWSGAFDI
524.	FL_38	VL CDR1	RASQGIRNDLG
525.	FL_38	VL CDR2	AASSLQS
526.	FL_38	VL CDR3	LQHNSYPLT
527.	FL_38	VH	QVTLKESGPVLVKPTEETLTCTVSGFSLRNKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS
528.	FL_38	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGKLEIK
529.	FL_38	scFv	QVTLKESGPVLVKPTEETLTCTVSGFSLRNKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGG TKLEIK
530.	FL_38	bispecific molecule	QVTLKESGPVLVKPTEETLTCTVSGFSLRNKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNINLKTEDTAVYYCVRHGNGFSYISYWAYWGQGTMTVTVSSGGGGSGGSDIQMTQSPSSLSASVGDRVTI SLTVSPGGTMTVLTCTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTIVL

			SLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTIVL
531.	FL_39	VH CDR1	NARMGV
532.	FL_39	VH CDR2	HIFSNDEKSYSTSLKN
533.	FL_39	VH CDR3	IVGYGSGWYGFFDY
534.	FL_39	VL CDR1	RASQGI RNDLG
535.	FL_39	VL CDR2	AAS TLQS
536.	FL_39	VL CDR3	LQHNSYPLT
537.	FL_39	VH	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDATYYCARI VYGSGWYGFFDYWGQGLVTVSS
538.	FL_39	VL	DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAAS TLQSGVPSRFSGSGGTEFTLTISSLQPE DFATYYCLQHNSYPLTFGCGTKVEIK
539.	FL_39	scFv	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDATYYCARI VYGSGWYGFFDYWGQGLVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRTIT TCRASQGI RNDLGWYQQKPGKAPKRLIYAAS TLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
540.	FL_39	bispecific molecule	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDATYYCARI VYGSGWYGFFDYWGQGLVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRTIT TCRASQGI RNDLGWYQQKPGKAPKRLIYAAS TLQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGSGGGGGGSGTQVTVTQEP SLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTIVL
541.	FL_40	VH CDR1	NARMGV
542.	FL_40	VH CDR2	NIFSNDEKSYSTSLKS
543.	FL_40	VH CDR3	IVGYGSGWYGFFDY
544.	FL_40	VL	RASQDI RNDLG

		CDR1	
545.	FL_40	VL	ATSIRQS
		CDR2	
546.	FL_40	VL	LQHNSFPLT
		CDR3	
547.	FL_40	VH	QVTLKESGPTLVKPTETLTTLCTVSGFSLNARMGVSWIRQPPGKCLEWLANIFSNDEKSYSTSLKSRLTISKGTSSQV VLTMTNPNPVDGTYYCARI VGYSGWYGYFDYWGQGLTVTVSS
548.	FL_40	VL	DIQMTQSPSSLSASVGRVTITCRASQDIRNDLGWYQQKPKGAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQP EDFATYFCLQHNSFPLTFGCGTKVEIK
549.	FL_40	scFv	QVTLKESGPTLVKPTETLTTLCTVSGFSLNARMGVSWIRQPPGKCLEWLANIFSNDEKSYSTSLKSRLTISKGTSSQV VLTMTNPNPVDGTYYCARI VGYSGWYGYFDYWGQGLTVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGRVTI TCRASQDIRNDLGWYQQKPKGAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGCG TKVEIK
550.	FL_40	bispecific molecule	QVTLKESGPTLVKPTETLTTLCTVSGFSLNARMGVSWIRQPPGKCLEWLANIFSNDEKSYSTSLKSRLTISKGTSSQV VLTMTNPNPVDGTYYCARI VGYSGWYGYFDYWGQGLTVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGRVTI TCRASQDIRNDLGWYQQKPKGAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGCG TKVEIKSGGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGSGTQVTVTQEP SLTVSPGGTTLTCGSSGTGAVTSNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
551.	FL_41	VH	NARMGV
		CDR1	
552.	FL_41	VH	HIFSNDEKSFSTSLKN
		CDR2	
553.	FL_41	VH	MVGYSGWYAYFDY
		CDR3	
554.	FL_41	VL	RASQSISSYLN
		CDR1	
555.	FL_41	VL	AASSLQS
		CDR2	
556.	FL_41	VL	LQHNSYPLT
		CDR3	
557.	FL_41	VH	QVTLKESGPVLVKTQTTLTLCTVSGFSLNARMGVSWIRQPPGKCLEWLANIFSNDEKSFSTSLKNRLTISKDTSSQV VLTMTNMDPVDATYYCARMVGYSGWYAYFDYWGQGTQTVTVSS
558.	FL_41	VL	DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFTGSGSGTDFTLTISLQ EDFATYFCLQHNSYPLTFGCGTKVEIK

559.	FL_41	scFv	QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDATYYCARMWGYGSGWYAYFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
560.	FL_41	bispecific molecule	QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDATYYCARMWGYGSGWYAYFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNFGNSYISYWAYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLASVGDRTVI SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
561.	FL_42	VH CDR1	NARMAVS
562.	FL_42	VH CDR2	HIFSNDEKSYSTSLKS
563.	FL_42	VH CDR3	IVGYGTGWYGGFDY
564.	FL_42	VL CDR1	RASQGIKNDLA
565.	FL_42	VL CDR2	AASSLQS
566.	FL_42	VL CDR3	LQHNSYPLT
567.	FL_42	VH	QVTLKESGPALVKPTETLLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDATYYCARIVGYGTGWYGGFDYWGQGIILVTVSS
568.	FL_42	VL	DIQMTQSPSSLASVGDRTVITCRASQGIKNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTETTLTISLQPEDFATYYCLQHNSYPLTFGCGTKVEIK
569.	FL_42	scFv	QVTLKESGPALVKPTETLLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDATYYCARIVGYGTGWYGGFDYWGQGIILVTVSSGGGGGGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGIKNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTETTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
570.	FL_42	bispecific molecule	QVTLKESGPALVKPTETLLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDATYYCARIVGYGTGWYGGFDYWGQGIILVTVSSGGGGGGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGIKNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTETTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNFGNSYISYWAYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLASVGDRTVI SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL

571.	FL_43	VH CDR1	NARMGV
572.	FL_43	VH CDR2	HIFSNDEKSYSTSLKS
573.	FL_43	VH CDR3	MPEYSSGWSGAFDI
574.	FL_43	VL CDR1	RASQGIKNDLV
575.	FL_43	VL CDR2	GTSTLQS
576.	FL_43	VL CDR3	LQHNSYPLT
577.	FL_43	VH	QVTLKESGPVLVKPTETLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS
578.	FL_43	VL	DIQMTQSPSSLSASVGDRTITTCRASQGIKNDLVWYQQKPKAPKRLIYGTSTLQSGVPSRFSGSGTEFTLTISLQ EDFATYYCLQHNSYPLTFGGCGTKVEIK
579.	FL_43	scFv	QVTLKESGPVLVKPTETLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGGGSGGSGGSGQTVTQEP SLTVSPGGTMTLTCCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGCTKLTVL
580.	FL_43	bispecific molecule	QVTLKESGPVLVKPTETLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGSGGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVTVSSGGGGSGGSGGSGQTVTQEP SLTVSPGGTMTLTCCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGCTKLTVL
581.	FL_44	VH CDR1	NARMGV
582.	FL_44	VH CDR2	HIFSNDEKSYSTSLKS
583.	FL_44	VH CDR3	MPEYSSGWSGAFDI
584.	FL_44	VL CDR1	RTSQGIKNDLV
585.	FL_44	VL	AASTLQS

			CDR2	
586.	FL_44		VL CDR3	LQHYSYPLT
587.	FL_44		VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSS
588.	FL_44		VL	DIQMTQSPSSLSASVGDRTITCRTSQGIRNDLVWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYFCLQHYSYPLTFGCGTKVEIK
589.	FL_44		scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGGSGTEFTLTISLQPEDFATYFCLQHYSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVSSGGGGSGGGSGTAVVTQEP SLTVSPGGTMTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
590.	FL_44	bispecific molecule		QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGGSGDIQMTQSPSSLSASVGDRTITI TCRTSQGIRNDLVWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHYSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTMTVSSGGGGSGGGSGTAVVTQEP SLTVSPGGTMTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
591.	FL_45	VH		NARMGV
592.	FL_45	CDR1		
593.	FL_45	VH		HIFSNDEKSYRTSLKS
594.	FL_45	CDR2		IVGYGSGWYAYFDY
595.	FL_45	VH		
596.	FL_45	CDR3		RASQGIRNDLG
597.	FL_45	VL		AASSLQS
598.	FL_45	CDR1		
599.	FL_45	VL		LQHNSYPLT
600.	FL_45	CDR2		
601.	FL_45	VL		LQHNSYPLT
602.	FL_45	CDR3		
603.	FL_45	VH		QVTLKESGPALVKPTQTTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSS
604.	FL_45	VH		DIQMTQSPSSLSASVGDRTITCRASQGI
605.	FL_45	VL		EDFATYFCLQHNSYPLTFGCGTKVEIK
606.	FL_45	scFv		QVTLKESGPALVKPTQTTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVSSGGGGSGGGSGDIQMTQSPSSLSASVGDRTITI TCRTSQGIRNDLVWYQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPLTFGCG

600.	FL_45	bispecific molecule	TKVEIK QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLALHIFSNDEKSYRTSLKSRLTITIKDTSKNQV VLTMTNMDPVDATYYCARIVGYGSGWYAYFDYWGQGLTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL NARMGV
601.	FL_46	VH CDR1	NARMGV
602.	FL_46	VH CDR2	LIYNDDKRYSPSLKS
603.	FL_46	VH CDR3	MVGYGSGWYAYFDY
604.	FL_46	VL CDR1	RASQGI RNDLG
605.	FL_46	VL CDR2	AASSLQS
606.	FL_46	VL CDR3	LQHNSYPLT
607.	FL_46	VH	QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLALIIYNDDKRYSPSLKSRLTITIKDTSKNQV VLTMTNMDPVDATYYCARIVGYGSGWYAYFDYWGQGLTVTVSS
608.	FL_46	VL	DIQMTQSPSSLASVGDRTVITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCGTKVEIK
609.	FL_46	scFv	QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLALIIYNDDKRYSPSLKSRLTITIKDTSKNQV VLTMTNMDPVDATYYCARIVGYGSGWYAYFDYWGQGLTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
610.	FL_46	bispecific molecule	QVTLKESGPVLVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLALIIYNDDKRYSPSLKSRLTITIKDTSKNQV VLTMTNMDPVDATYYCARIVGYGSGWYAYFDYWGQGLTVTVSSGGGGSGGGGGSDIQMTQSPSSLASVGDRTVI TCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL NARMGV
611.	FL_47	VH CDR1	NARMGV

612.	FL_47	VH CDR2	HIFSNDEKSYSTSLKS
613.	FL_47	VH CDR3	IVGYGTGWYGFFDY
614.	FL_47	VL CDR1	RTSQGIRNDLG
615.	FL_47	VL CDR2	AASSLQS
616.	FL_47	VL CDR3	LQHNSYPLT
617.	FL_47	VH	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTYGFFDYWGQGILVTVSS
618.	FL_47	VL	DIQMTQSPSSLSASVGDRTITTCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISLQ EDFATYYCLOHNSYPLTFGCGTKVEIK
619.	FL_47	scFv	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTYGFFDYWGQGILVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTITI TCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLVTVSSGGGGGGGGGGGGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
620.	FL_47	bispecific molecule	QVTLKESGPALVKPTQTLLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTYGFFDYWGQGILVTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTITI TCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLVTVSSGGGGGGGGGGGGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
621.	FL_48	VH CDR1	NARMGV
622.	FL_48	VH CDR2	HIFWNDEKSYSTSLKS
623.	FL_48	VH CDR3	IPYGGSGSYNYGMDV
624.	FL_48	VL CDR1	RASQGIRNDLG
625.	FL_48	VL CDR2	AASSLQS
626.	FL_48	VL	LQHNTYPLT

		CDR3	
627.	FL_48	VH	QVTLKESGPMVLVKPTETLTLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARIPIYGGGSYNYGMDVWGQGTQTVTVSS
628.	FL_48	VL	DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTITSSSLQP EDFATYYCLQHNRYPLTFGCGTKVDIK
629.	FL_48	scFv	QVTLKESGPMVLVKPTETLTLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARIPIYGGGSYNYGMDVWGQGTQTVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRTV ITCRASQGIKNDLWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLQHNRYPLTFGC GTKVDIK
630.	FL_48	bispecific molecule	QVTLKESGPMVLVKPTETLTLTCTFSGFSLNARMGVSWIRQPPGKCLEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDATYYCARIPIYGGGSYNYGMDVWGQGTQTVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRTV ITCRASQGIKNDLWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLQHNRYPLTFGC GTKVDIKSRDSDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTQTVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRTV PSLTVSPGGTQTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGKLTVL
631.	FL_49	VH	NARMGV
632.	FL_49	CDR1	
632.	FL_49	VH	HIFSNDEKSYSTSLKN
632.	FL_49	CDR2	
633.	FL_49	VH	IVGYGTGWFYFDY
633.	FL_49	CDR3	
634.	FL_49	VL	RASQDIRTDLA
635.	FL_49	CDR1	
635.	FL_49	VL	AASSLQS
635.	FL_49	CDR2	
636.	FL_49	VL	LQHNRYPLT
636.	FL_49	CDR3	
637.	FL_49	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNMDPVDATYYCARIPIYGGGSYNYGMDVWGQGTQTVTVSS
638.	FL_49	VL	DIQMTQSPSSLSASVGDRTVITCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTITSSSLQP EDFATYYCLQHNRYPLTFGCGTKVDIK
639.	FL_49	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNMDPVDATYYCARIPIYGGGSYNYGMDVWGQGTQTVTVSSGGGSGGGGGSDIQMTQSPSSLSASVGDRTV ITCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLQHNRYPLTFGC TKVDIK
640.	FL_49	bispecific	QVTLKESGPTLVKPTETLTLTCTVSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV

		c molecule	VLMTNVPVDTATYYCARIVGYGTFWFGYFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNRYPLTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGGGGGGSGTQVTVTQEP SLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGKTLTVL
641.	FL_50	VH CDR1	NARMGV
642.	FL_50	VH CDR2	HIFSNDEKSYSTSLKS
643.	FL_50	VH CDR3	IPGYGGNFYHYHYGMDV
644.	FL_50	VL CDR1	RASQGIKNDLA
645.	FL_50	VL CDR2	AASTVQS
646.	FL_50	VL CDR3	LQHNFPWT
647.	FL_50	VH	QVTLKESGPTLVKPTETLTCTVSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLMTNMDPVDATATYYCARIIPGYGGNFYHYHYGMDVWGQGTITVTVSS
648.	FL_50	VL	DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGTEFALTISLQPEDFATYYCLQHNFPWTFGCGTKVDIK
649.	FL_50	scFv	QVTLKESGPTLVKPTETLTCTVSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLMTNMDPVDATATYYCARIIPGYGGNFYHYHYGMDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGIKNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGTEFALTISLQPEDFATYYCLQHNFPWTFGCGTKVDIK
650.	FL_50	bispecific c molecule	QVTLKESGPTLVKPTETLTCTVSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLMTNMDPVDATATYYCARIIPGYGGNFYHYHYGMDVWGQGTITVTVSSGGGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGIKNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGTEFALTISLQPEDFATYYCLQHNFPWTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGGGGGGSGTQVTVTQEP SLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLTSGVQPEDEAEY YCVLWYSNRWVFGGKTLTVL
651.	FL_51	VH CDR1	NARMGV
652.	FL_51	VH CDR2	HISNDEKSYSTSLRS

653.	FL_51	VH CDR3	MPGDSNTWRGFFDY
654.	FL_51	VL CDR1	RTSQSVNNLA
655.	FL_51	VL CDR2	GASTRAT
656.	FL_51	VL CDR3	LQHNSYPLT
657.	FL_51	VH	QVTLKESGPTLVKPTETLTCTVSGFSLRNVRMGVSWIRQPPGKCLEWLAHISSENDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDATATYCCARMPGDSNTWRGFFDYWGQGLVTVSS
658.	FL_51	VL	EIVMTQSPATLSVSPGERATLSCRTSQSVNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQPE EDFATYYCLQHNSYPLTFGCGTKVEIK
659.	FL_51	scFv	QVTLKESGPTLVKPTETLTCTVSGFSLRNVRMGVSWIRQPPGKCLEWLAHISSENDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDATATYCCARMPGDSNTWRGFFDYWGQGLVTVSSGGGGGGGGSEIVMTQSPATLSVSPGERATL SCRTSQSVNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
660.	FL_51	bispecific molecule	QVTLKESGPTLVKPTETLTCTVSGFSLRNVRMGVSWIRQPPGKCLEWLAHISSENDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDATATYCCARMPGDSNTWRGFFDYWGQGLVTVSSGGGGGGGGGGSEIVMTQSPATLSVSPGERATL SCRTSQSVNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGGSEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLIKTEDTAVYYCVRHGFNYSYI SYWAYWGQGLVTVSSGGGGGGGGGGSGTQVTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTVL
661.	FL_52	VH CDR1	YARMGV
662.	FL_52	VH CDR2	HIFSENDEKSYSTSLKS
663.	FL_52	VH CDR3	MPEYSSGWGAFDI
664.	FL_52	VL CDR1	RASQDIRNDLA
665.	FL_52	VL CDR2	AASSLQS
666.	FL_52	VL CDR3	LQHNSYPLT
667.	FL_52	VH	QVTLKESGPTLVKPTETLTCTVSGFSLRYARMGVSWIRQPPGKCLEWLAHIFSENDEKSYSTSLKSRLTISKDTSKSQV

668.	FL_52	VL	VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS DIQMTQSPSSLSASVGDRTITCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGCGTKLEIK
669.	FL_52	scFv	QVTLKESGPTLVKPTETLTCTFSGFSLRYARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTITI TCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGCG TKLEIK
670.	FL_52	bispecific molecule	QVTLKESGPTLVKPTETLTCTFSGFSLRYARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTITI TCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGCG TKLEIKSGGGGGSEVLVESGGGLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTITVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTITVTVSPGGTITLTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKGKAAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTVL
671.	FL_53	VH CDR1	SYGMH
672.	FL_53	VH CDR2	VISYDGSNEFYADSVKG
673.	FL_53	VH CDR3	GGEITMVRGVIYYYYGMDV
674.	FL_53	VL CDR1	RTSQSISSYLN
675.	FL_53	VL CDR2	AASSLQS
676.	FL_53	VL CDR3	LQHNSYPLT
677.	FL_53	VH	QVQLVESGGGVVQPGRSRLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAIVSYDGSNEFYADSVKGRFTISRDNKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYYYYGMDVWGQGTITVTVSS
678.	FL_53	VL	DIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGCGTKVDIK
679.	FL_53	scFv	QVQLVESGGGVVQPGRSRLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAIVSYDGSNEFYADSVKGRFTISRDNKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYYYYGMDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGCGTKVDIK
680.	FL_53	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAIVSYDGSNEFYADSVKGRFTISRDNKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYYYYGMDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGCGTKVDIKSGGGGSEVLVESGGGLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYA

			DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGSGGGGGSGQTV VTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGKLTIVL
681.	FL_54	VH CDR1	SYGMH
682.	FL_54	VH CDR2	VISYDGSNEFYADSVKG
683.	FL_54	VH CDR3	GGEITMVRGVIYIYYGMDV
684.	FL_54	VL CDR1	RASQGVRRNLV
685.	FL_54	VL CDR2	GASTRAT
686.	FL_54	VL CDR3	LQHNSYPLT
687.	FL_54	VH	QVQLVESGGGVQPGRSRLSCAASGFTFSYGMHWVRQAPGKCLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYIYYGMDVWGQTTVTVSS
688.	FL_54	VL	EIVMTQSPATLSVSPGERATLSCRASQGVRRNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFATYYCLQHNSYPLTFGCGTKVEIK
689.	FL_54	scFv	QVQLVESGGGVQPGRSRLSCAASGFTFSYGMHWVRQAPGKCLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYIYYGMDVWGQTTVTVSSGGGGSGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRRNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPL TFGCGTKVEIK
690.	FL_54	bispecific molecule	QVQLVESGGGVQPGRSRLSCAASGFTFSYGMHWVRQAPGKCLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYIYYGMDVWGQTTVTVSSGGGGSGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRRNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPL TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGSGGGGGSGQTV VTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGKLTIVL
691.	FL_55	VH CDR1	SYGMH
692.	FL_55	VH CDR2	VISYDGSNKYYADSVKG
693.	FL_55	VH CDR3	SYGMDV

694.	FL_55	VL CDR1	RASQGISSWLA
695.	FL_55	VL CDR2	AASSLQS
696.	FL_55	VL CDR3	QQANSFPWT
697.	FL_55	VH	QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWAVISYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQTTVTVSS
698.	FL_55	VL	DIQMTQSPSSVSASVGDRTITCRASQGISSWLA WYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQ EDFATYYCQQANSFPWTFGCGTKLEIK
699.	FL_55	scFv	QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWAVISYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQTTVTVSSGGSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGCGTKLEIK SWLA WYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGCGTKLEIK
700.	FL_55	bispecific molecule	QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWAVISYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQTTVTVSSGGSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGCGTKLEIKSGG GGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLTVTVSSGGSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGCGTKLEIK VTLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNR WFEGGGTKLTVL
701.	FL_56	VH CDR1	NVRMGVS
702.	FL_56	VH CDR2	HIFSNDEKLYTTSLSKS
703.	FL_56	VH CDR3	IVGYGTGWYGYFDY
704.	FL_56	VL CDR1	RASQDIRDDL
705.	FL_56	VL CDR2	ATSIRQS
706.	FL_56	VL CDR3	LQHHSFPLT
707.	FL_56	VH	QVTLKESGPVLVKPTETLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKLYTTSLSKRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSS
708.	FL_56	VL	DIQMTQSPSSLSASIGDRVTITCRASQDIRDDL GWYQREPGKAPKRLIYATSI RQSGVPSRFSGSGSGTDFTLTISGLQP EDFATYFCLQHHSFPLTFGGGTKVDIK

709.	FL_56	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKLYTTSLSKRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTYGFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLASASIGDRVITI TCRASQDIRDDLGWYQREP GKAPKRLIYATSI RQSGVPSRFSGSGTEFTLTISGLQPEDFATYFCLQHHSFPLTFGGG TKVDIK
710.	FL_56	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKLYTTSLSKRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTYGFDYWGQGTQVTVSSGGGGGGGGGGSDIQMTQSPSSLASASIGDRVITI TCRASQDIRDDLGWYQREP GKAPKRLIYATSI RQSGVPSRFSGSGTEFTLTISGLQPEDFATYFCLQHHSFPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISYWAYWGQGTQVTVSSGGGGGGGGGGSQTVTVTQEP SLTVSPGGTVTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGKLTIVL
711.	FL_57	VH CDR1	YARMGVSV
712.	FL_57	VH CDR2	HISNDEKSFSTALES
713.	FL_57	VH CDR3	MPGDSNTWRGFFDY
714.	FL_57	VL CDR1	RTSQTVTNSYIA
715.	FL_57	VL CDR2	GTSTRAT
716.	FL_57	VL CDR3	QKYGSSPLT
717.	FL_57	VH	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHISNDEKSFSTALESRLTISTDTSKSQM VLTMTNVDPVDATYYCARMPGDSNTWRGFFDYWGQGTQVTVSS
718.	FL_57	VL	EIVMTQSPGTLSPGERATLSRTSQTVTNSYIAWYQQRPQAPRLLIYGTSTRATGIPDRFSGSGGTDFTLTISRLE PEDFAVYCYCQYGGSSPLTFGGGKLEIK
719.	FL_57	scFv	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHISNDEKSFSTALESRLTISTDTSKSQM VLTMTNVDPVDATYYCARMPGDSNTWRGFFDYWGQGTQVTVSSGGGGGGGGGGSEIVMTQSPGTLSPGERATL SRTSQTVTNSYIAWYQQRPQAPRLLIYGTSTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYCQYGGSSPLTFGG GTKLEIK
720.	FL_57	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHISNDEKSFSTALESRLTISTDTSKSQM VLTMTNVDPVDATYYCARMPGDSNTWRGFFDYWGQGTQVTVSSGGGGGGGGGGSEIVMTQSPGTLSPGERATL SRTSQTVTNSYIAWYQQRPQAPRLLIYGTSTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYCQYGGSSPLTFGG GTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISYWAYWGQGTQVTVSSGGGGGGGGGGSQTVTVTQEP PSLTVSPGGTVTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YCVLWYSNRWVFGGKLTIVL

721.	FL_58	VH CDR1	NVRMGVS
722.	FL_58	VH CDR2	HISSNDEKSYSTSLRS
723.	FL_58	VH CDR3	MPGDSNTWRGFFDY
724.	FL_58	VL CDR1	RTSQSVNNNLA
725.	FL_58	VL CDR2	GASTRAT
726.	FL_58	VL CDR3	LQHNSYPLT
727.	FL_58	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDATYYCARMPGDSNTWRGFFDYWGQGTLLVTVSS
728.	FL_58	VL	EIVMTQSPATLSVSPGERATLSCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTITSSSLQP EDFATYYCLQHNSYPLTFGGGKVEIK
729.	FL_58	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDATYYCARMPGDSNTWRGFFDYWGQGTLLVTVSSGGGGSGGSEIIVMTQSPATLSVSPGERATL SCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTITSSLPEDFATYYCLQHNSYPLTFGGG TKVEIK
730.	FL_58	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDATYYCARMPGDSNTWRGFFDYWGQGTLLVTVSSGGGGSGGSEIIVMTQSPATLSVSPGERATL SCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTITSSLPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGGSGGSGGGGQTVVTQEP SLTVSPGGTVTLTCCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
731.	FL_59	VH CDR1	NVRMGVS
732.	FL_59	VH CDR2	HIFSNDEKSYSTSLKS
733.	FL_59	VH CDR3	MPEYSSGWSGAFDI
734.	FL_59	VL CDR1	RASQDIRDDLQ
735.	FL_59	VL	GASTLQS

		CDR2	
736.	FL_59	VL	LQHNSYPLT
737.	FL_59	CDR3	
		VH	QVTLKESGPMVLVKPTETLTTLCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSS
738.	FL_59	VL	DIQMTQSPSSLSASVGDRTITCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTITSSSLQP EDFATYYCLOHNSYPLTFGGGTRLEIK
739.	FL_59	scFv	QVTLKESGPMVLVKPTETLTTLCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTITI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLOHNSYPLTFGGG TRLEIK
740.	FL_59	bispecific molecule	QVTLKESGPMVLVKPTETLTTLCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDATATYFCARMPEYSSGWSGAFDIWGQGTMTVTVSSGGGGGGGGSDIQMTQSPSSLSASVGDRTITI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTITSSSLQPEDFATYYCLOHNSYPLTFGGG TRLEIKSGGGGSEVLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGGGGGGGSGTQVTVTQEP SLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGTKLTIVL
741.	FL_60	VH	NARMGV
742.	FL_60	CDR1	
		VH	HIFSNDEKSYSTSLKS
		CDR2	
743.	FL_60	VH	MVGYGSGWYAYFDY
		CDR3	
744.	FL_60	VL	RSSQSLHNSNGYNYLY
		CDR1	
745.	FL_60	VL	EVSNRFS
		CDR2	
746.	FL_60	VL	MQALQTPLT
		CDR3	
747.	FL_60	VH	QVTLKESGPALVKPTQTTLTCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKRQV VLTMTNMDPVDATATYFCARMVGYSGWYAYFDYWGQGTLLTVTVSS
748.	FL_60	VL	DIVMTQTPLSLSVTPGQPASISCRSSQSLHNSNGYNYLYWYLQKPGQPPQPLLIIYEVSNRFSGVPPDRFSGSGSGTDFTLKI SRVEAEDVGYYCMQALQTPLTFGGGKVEIK
749.	FL_60	scFv	QVTLKESGPALVKPTQTTLTCTFSGFSLNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKRQV VLTMTNMDPVDATATYFCARMVGYSGWYAYFDYWGQGTLLTVTVSSGGGGGGGGSDIVMTQTPLSLSVTPGQPASI SCRSSQSLHNSNGYNYLYWYLQKPGQPPQPLLIIYEVSNRFSGVPPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALQTPL

750.	FL_60	bispecific molecule	TFGGGTKVEIK QVTLKESGPALVKPTQTLLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKRQV VLTMTNMDPVDATAYCARWVGYSWYAYFDYWGQGLVTVSSGGGGSGGGSDIVMTQTPLSLSVTPGQPASI SCRSSQSLHNSNGYNLYWYLQKPGQPPQLLIYEVSNRFSGVPRFSGSGTDFTLKISRVEAEDVGYYCMQALQTPL TFGGGKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTL SGVQPE DEAEYYCVLWYSNRWVFGGGLTTLV SYGMH
751.	FL_61	VH CDR1	SYGMH
752.	FL_61	VH CDR2	VISYDGSNEFYADSVKG
753.	FL_61	VH CDR3	GGEITMVRGVIYGYGMDV
754.	FL_61	VL CDR1	RASQSISSYLN
755.	FL_61	VL CDR2	AASSLQS
756.	FL_61	VL CDR3	LQHNSYPLT
757.	FL_61	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYGYGMDVWGQGLTVTVSS
758.	FL_61	VL	DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGTEFTLTISLQ P EDFATYYC LQHNSYPLTFGGGKVEIK
759.	FL_61	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYGYGMDVWGQGLTVTVSSGGGGSGGGSDIQMTQSPSSLSASV G DRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYC LQHNSYPL TFGGGKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTL SGVQPE DEAEYYCVLWYSNRWVFGGGLTTLV TFGGGKVEIK
760.	FL_61	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIYGYGMDVWGQGLTVTVSSGGGGSGGGSDIQMTQSPSSLSASV G DRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYC LQHNSYPL TFGGGKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTL SGVQPE DEAEYYCVLWYSNRWVFGGGLTTLV
761.	FL_62	VH CDR1	SYGMH

762.	FL_62	VH CDR2	VISYDGSNEFYADSVKG
763.	FL_62	VH CDR3	GGEITMVRGVIYYYYGMDV
764.	FL_62	VL CDR1	RASQGVRRNLV
765.	FL_62	VL CDR2	GASTRAT
766.	FL_62	VL CDR3	LQHNSYPLT
767.	FL_62	VH	QVQLVESGGGVQPGRSRLSCAASGFTFSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVIYYYYGMDVWGQGT'TVTVSS
768.	FL_62	VL	EIVMTQSPATLSVSPGERATLSCRASQGVRRNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFATYYCLOHNSYPLTFGGGTKVEIK
769.	FL_62	scFv	QVQLVESGGGVQPGRSRLSCAASGFTFSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVIYYYYGMDVWGQGT'TVTVSSGGSGGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRRNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLOHNSYPL TFGGGTKVEIK
770.	FL_62	bispecific molecule	QVQLVESGGGVQPGRSRLSCAASGFTFSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVIYYYYGMDVWGQGT'TVTVSSGGSGGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRRNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLOHNSYPL TFGGGTKVEIK DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGT'TVTVSSGGSGGGGGSGGSGQTV VTQEPSTLTVSPGGT'TLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
771.	FL_63	VH CDR1	SYGMH
772.	FL_63	VH CDR2	VISYDGSNEFYADSVKG
773.	FL_63	VH CDR3	GGEITMVRGVIYYYYGMDV
774.	FL_63	VL CDR1	RTSQSISSYLN
775.	FL_63	VL CDR2	AASSLQS
776.	FL_63	VL	LQHNSYPLT

		CDR3	
777.	FL_63	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVI GYIYYGMDVWGQGTITVTVSS
778.	FL_63	VL	DIQMTQSPSSLSASVGRVTITCRTSQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTITSS LQP EDFATYYCLQHNSYPLTFGGGTKVDIK
779.	FL_63	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVI GYIYYGMDVWGQGTITVTVSSGGSGGGGGGGSDIQMTQSPSSLSASV G DRVTITCRTSQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTITSS LQPEDFATYYCLQHNSYPL TFGGGTKVDIK
780.	FL_63	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVI GYIYYGMDVWGQGTITVTVSSGGSGGGGGGGSDIQMTQSPSSLSASV G DRVTITCRTSQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTITSS LQPEDFATYYCLQHNSYPL TFGGGTKVDIKKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNINLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGSGGGGGGGSGQT V VTQEPSTVSPGGTITLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
781.	FL_64	VH	SYGMH
782.	FL_64	CDR1	VISYDGSNEFYADSVKG
783.	FL_64	VH	GGEITMVRGVI GYIYYGMDV
784.	FL_64	CDR3	RASQSISSYLN
785.	FL_64	VL	AASSLQS
786.	FL_64	CDR2	LQHNSYPLT
787.	FL_64	VL	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVI GYIYYGMDVWGQGTITVTVSS
788.	FL_64	VH	DIQMTQSPSSLSASVGNRVITICRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTITSS LQP EDFATYYCLQHNSYPLTFGGGTKVDIK
789.	FL_64	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY LQMSLRAEDTAVYYCARGGEITMVRGVI GYIYYGMDVWGQGTITVTVSSGGSGGGGGGGSDIQMTQSPSSLSASV G NRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTITSS LQPEDFATYYCLQHNSYPL TFGGGTKVDIK
790.	FL_64	bispecific	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNEFYADSVKGRFTISRDN SKNTLY

		c molecule	LQMNSLRAEDTAVYYCARGGEITMVRGVIYGYGMDVWGQGTITVTVSSGGGGGGGGGGGGSDIQMTQSPSSLSASVGNRVITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGSGQTVVTQEPSLTVSPGGTITLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTIVL
791.	FL_65	VH CDR1	SYGMH
792.	FL_65	VH CDR2	VISYDGSNKYYADSVKG
793.	FL_65	VH CDR3	SYGMDV
794.	FL_65	VL CDR1	RASQGISSWLA
795.	FL_65	VL CDR2	AASSLQS
796.	FL_65	VL CDR3	QQANSFPWT
797.	FL_65	VH	QVQLVESGGGVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSYGMDVWGQGTITVTVSS
798.	FL_65	VL	DIQMTQSPSSVSASVGDRTITICRASQGISWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQANSFPWTFGGTKLEIK
799.	FL_65	scFv	QVQLVESGGGVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSYGMDVWGQGTITVTVSSGGGGGGGGGGGGSDIQMTQSPSSVSASVGDRTITICRASQGISWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQANSFPWTFGGTKLEIK
800.	FL_65	bispecific molecule	QVQLVESGGGVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSYGMDVWGQGTITVTVSSGGGGGGGGGGGGSDIQMTQSPSSVSASVGDRTITICRASQGISWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQANSFPWTFGGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGSGQTVVTQEPSLTVSPGGTITLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTIVL
801.	Human FLT3 v1 NM_004119	human	MPALARDGGQLPLLVVFSAMIFGTITNQDLPIKCVLIHKNNDSSVGKSSSYPMVSESPEDLGCALRPQSSGTVYEAAA VEVDVSASITLQVLVDAPGNI SCLWFKHSSLNCQPHFDLQNRGVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRRPYFRKMENQDALVCI SEVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE CTRLFTIDLNQTPQTTLQPLFLKVGEPLWIRKAVHVNHGFLTWELENKALEEGNYFEMSTYSTNRTMIRILFAFVSSV ARNDTGYTCSSSKHPSSQALVTIVEKGFINATNSSEDIQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCEQKGLDNG YSISKFCNHHKHQPGEYIFHAENDDAQFTKMTLNIIRKQPQLAEASASQASCFSDGYPLPSWTWKKCSKSPNCTEEITE

802.	Cyno FLT3 x1 XM_005585544	macaque	<p>GVWNRKANRKFVQWVSSSTLNMSEAIKGFVLVKCCAYNSLGTSCETILLNSPGPFFFIQDNI SFYATIGVCLLFIVVLTL LICHYKKQFRIYESQLQWVQVTGSSDNEYFYVDFREYEDLKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIQ VAVKMLKEKADSSEREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFEYCCYGDLLNLYRSKREKFRHTWTEIFKE HNFSTYPTFQSHPNSSMPGSRVQIHPDSDQISGLHGNSFHSDEIEYENQKRLEEEEDLNVLTFEDLLCFAYQVAKGME FLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGITYTIKSDVWSYGILLWE IFSLGVNPPYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCGQLADAEAEAMYQNVDG RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS</p> <p>MPALARGGRLPLLVFSAMIFGTITNQDLPIVKCVLINHKNDSSVGKSSSYPMVSESPEDLGCALRPQSSGTVYEAAT VEVDVSASITLQVLVDTPGNI SCLWVFKHSSLNQCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRRPYFRKMENQDALVCI SE SVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE CTRLFTIDLNQTPQTTLPQLFLKVGEPLWIRKAVHVNHGFLTWELNKALEEGYFEMSTYSTNRTMIRILFAFVSSV ARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFCEQKGLDDG YSVSKFCNKHQPGEYIFHAENGDAQFTKMTLINIRKQPVLAEASASQASCSGSDGYPLPSWTWKKCSKSPNCTEDIPE GVWNRKANRKFVQWVSSSTLNMSEAMKGFVLKCCAYNSLGTSCETILLNSPGPFFFIQDNI SFYATIGVCLLFIVVLTL LICHYKKQFRIYESQLQWVQVTGSSDNEYFYVDFRDCDYDLKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIQ VAVKMLKEKADSSEREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFEYCCYGDLLNLYRSKREKFRHTWTEIFKE HNFSTYPTFQSHPNSSMPGSRDVQIHPHSDPISGLHGNSFHSDEIEYENQKRLEEEEDLNVLTFEDLLCFAYQVAKGME FLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGITYTIKSDVWSYGILLWE IFSLGVNPPYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCGQLEDAEAEAMYQNVDG RVSERPHTYQNRPPFSREMDSGPLSPKAQVEDS</p>
803.	Human FLT3 (T227M) isoform	human	<p>MPALARDGGQLPLLVFSAMIFGTITNQDLPIVKCVLINHKNDSSVGKSSSYPMVSESPEDLGCALRPQSSGTVYEAAT VEVDVSASITLQVLVDAPGNI SCLWVFKHSSLNQCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRRPYFRKMENQDALVCI SE SVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGMDIRCCARNELGRE CTRLFTIDLNQTPQTTLPQLFLKVGEPLWIRKAVHVNHGFLTWELNKALEEGYFEMSTYSTNRTMIRILFAFVSSV ARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFCEQKGLDNG YSISKFCNKHQPGEYIFHAENGDAQFTKMTLINIRKQPVLAEASASQASCSGSDGYPLPSWTWKKCSKSPNCTEEITE GVWNRKANRKFVQWVSSSTLNMSEAIKGFVLVKCCAYNSLGTSCETILLNSPGPFFFIQDNI SFYATIGVCLLFIVVLTL LICHYKKQFRIYESQLQWVQVTGSSDNEYFYVDFREYEDLKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIQ VAVKMLKEKADSSEREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFEYCCYGDLLNLYRSKREKFRHTWTEIFKE HNFSTYPTFQSHPNSSMPGSRVQIHPDSDQISGLHGNSFHSDEIEYENQKRLEEEEDLNVLTFEDLLCFAYQVAKGME FLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGITYTIKSDVWSYGILLWE IFSLGVNPPYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCGQLADAEAEAMYQNVDG RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS</p> <p>MPALARDGGQLPLLVFSAMIFGTITNQDLPIVKCVLINHKNDSSVGKSSSYPMVSESPEDLGCALRPQSSGTVYEAAT VEVDVSASITLQVLVDAPGNI SCLWVFKHSSLNQCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRRPYFRKMENQDALVCI SE SVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE CTRLFTIDLNQTPQTTLPQLFLKVGEPLWIRKAVHVNHGFLTWELNKALEEGYFEMSTYSTNRTMIRILFAFVSSV ARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFCEQKGLDNG YSISKFCNKHQPGEYIFHAENGDAQFTKMTLINIRKQPVLAEASASQASCSGSDGYPLPSWTWKKCSKSPNCTEEITE GVWNRKANRKFVQWVSSSTLNMSEAIKGFVLVKCCAYNSLGTSCETILLNSPGPFFFIQDNI SFYATIGVCLLFIVVLTL LICHYKKQFRIYESQLQWVQVTGSSDNEYFYVDFREYEDLKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIQ VAVKMLKEKADSSEREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFEYCCYGDLLNLYRSKREKFRHTWTEIFKE HNFSTYPTFQSHPNSSMPGSRVQIHPDSDQISGLHGNSFHSDEIEYENQKRLEEEEDLNVLTFEDLLCFAYQVAKGME FLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGITYTIKSDVWSYGILLWE IFSLGVNPPYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCGQLADAEAEAMYQNVDG RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS</p>
804.	Human FLT3- ITD isoform	human	<p>MPALARDGGQLPLLVFSAMIFGTITNQDLPIVKCVLINHKNDSSVGKSSSYPMVSESPEDLGCALRPQSSGTVYEAAT VEVDVSASITLQVLVDAPGNI SCLWVFKHSSLNQCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRRPYFRKMENQDALVCI SE SVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE CTRLFTIDLNQTPQTTLPQLFLKVGEPLWIRKAVHVNHGFLTWELNKALEEGYFEMSTYSTNRTMIRILFAFVSSV ARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFCEQKGLDNG YSISKFCNKHQPGEYIFHAENGDAQFTKMTLINIRKQPVLAEASASQASCSGSDGYPLPSWTWKKCSKSPNCTEEITE GVWNRKANRKFVQWVSSSTLNMSEAIKGFVLVKCCAYNSLGTSCETILLNSPGPFFFIQDNI SFYATIGVCLLFIVVLTL LICHYKKQFRIYESQLQWVQVTGSSDNEYFYVDFREYEDLKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIQ VAVKMLKEKADSSEREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFEYCCYGDLLNLYRSKREKFRHTWTEIFKE HNFSTYPTFQSHPNSSMPGSRVQIHPDSDQISGLHGNSFHSDEIEYENQKRLEEEEDLNVLTFEDLLCFAYQVAKGME FLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGITYTIKSDVWSYGILLWE IFSLGVNPPYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCGQLADAEAEAMYQNVDG RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS</p>

805.	Human KIT v1 parologue	human	FGKVMNATAYGISKTGVSIQVAVKMLKEKADSSEREALMSELKMMTQLGSHENIVNLLGACTLSGPIYLIFEYCCYGDLL NYLRSKREKFHRTWTEIFKEHNFsfyptfQSHPNSSMPGSRREVQIHPDSQISGLHGNSFHSEDEIEYENQKRLEEEEDL NVLTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVVRGNARL PVKWMAPESL FEGITYIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSPFPNLT SFLGCQLADAEEMYNQVNDGRVSECPHTYQNRFPFSREMDLGLLSPQAQVEDS MRGARGAWDFLCVLLLLLRVQTGSSQPSVSPGEPSPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDETENENKQN EWITEKAEATNTGKYCTNKHGLSNSIYFVRDPAKFLVDRSLYGKEDNDTLVRCPLTDPEVTNYSLKGCQKGKPLPKDL RFIPDPKAGIMIKSVKRAYHRLCLHCSVDQEGKSVLSEKFIKVRPAFKAFFVSVSKASYLLREGEEFTVTCTIKDVSS SVYSTWKRENSQTKLEKYNHSHHGDFNYERQATLTISSARVDFGVCYANNTFGSANVTTLLEVVDKGFNIFPFIN TTVFVNDGENVDLIVEYEAFFPKHEQQWIYMNRTFTDKWEDYKSENEIRYVSELHLTRLKGTEGGTYTFLVSNSDVN AAIAFNVYNTKPEILTYDRLVNGMLQCVAAGFPEPTIDWYFCPGEQRCASVLPVDVQTLNSSGPPFGKLVVQSSIDS SAFKHNGTVECKAYNDVGKTSAYNFNAFKGNKEQIHPHTLFTPLLI GFVIVAGMCIIVMILTYKYLQKPMYEVQWKVV EEINGNNVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSE LKVLSYLGHNHMINVNLGACTIGGPTLVI TEYCCYGDLLNFLRRKDSFICSKQEDHAEAAALYKNLLHKSKESSCSDSTNE YMDMKPGVSYYVPTKADKRRSVRIGSYIERDVTPIIMEDDELALDLEDLLSFYSYQVAKGMAFLASKNCIHRDLAARNILL THGRIITKICDFGLARDIKNDSNYVVGKNARLPVKWMAPEISFNCVYTFESDVWSYGIFLWELFSLGSSPYGMPVDSKFY KMIKEGFRMLSPEHAPAEYDIMKTCWDADPLKRPTFKQIVQLIEKQISESTNHIYSNLANCSPNRQKPVVDHVSVINSV GSTASSQPLLVHDDV
806.	Human CSF1R v1 parologue NM_005211	human	MGPVLLLLLVATAWHGQGIPIEPSVPELVVKPGATVTLRCVNGSGVEMDPPSPHWTLYSDGSSSILSTNNATFQNTG TYRTEPGDPLGSAAIHLVYKDPARPWNVLAQEVVVFEDQDALLPCLLTDVLEAGVSLVRGRPLMRHTNYSFSPWH GFTIHRAKFIQSQDYQCSALMGGRKVMISIIRLKVQKVI PGPPALTLVPAELVIRGEAAQIVCSASSVDVDFVFLQHN NTKLAIPQOSDFHNRYQKVLTLNLDQVDFQHAGNYSVCASNQGHSTSMFFRVVESAYLNLSSQNLIQEVTVGEGLN LKVMVEAYPGLQGNWTYLGPFSDHQPEPKLANATTKTDTYRHTTTLSPRLKPSEAGRYSFLARNPGGWRALTFFELTRY PPEVSVIWTFFINGSGTLLCAASGYQPQNVTLQCSGHTDRCDQAQVLQVDDPYPEVL SQEPFHKTIVQSLLTVETLEHN QTYECRAHNSVSGSWAFIPI SAGAHTHPPDEFI FT PVVAVCMSIMALLLLLLLYKYKQPKYQVRWKIIESYEGNS YTFIDPTQLPYNEKWEFPRNNLQFGKTLGAGAFGVVEATAFGLGKEDAVLKVAVKMLKSTAHADKEALMSELKIMSHL GQHENIVNLGACTHGGPVLVI TEYCCYGDLLNFLRRKAEAMLGPSLSPGQDPEGVDYKNIHLEKKYVRRDSGFSQGV DTYVEMRPVSTSSNDSFSEQDLDDKEDGRPLELRDLHLHFSSQVAQGMFLASKNCIHRDVAARNVLLTNGHVAKIGDFGLA RDIMNDSNYIVKGNARLPVKWMAPEISIFDCVYTVQSDVWSYGILLWEIFSLGLNYPGILVNSKFYKLVKDGYYQMAQPAF APKNIYSIMQACWALEPTHRPTFQQICSFLOEAQEDRRERDYTNLPSRSSRSGSGSSSELEEESSSEHLTCCEQGDIA QPLLQPNNYQFC
807.	Human PDGFRA parologue NM_006206	human	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVVQNLNSSFSLRCFGESEVSWQYPMSEESSDVEIRNEENNSGL FVTVLEVSSASAAHTGLTYCYNNHTQTEENELEGRHIYIYVPDPDVAFVPLGMDTYLIVVEDDDSAIIPCRTTDPETPVT LHNSEGVPASYSQRSQNGFTTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN EVVDLQWTPYGEVKGKIGITMLEEIKVPSIKLVYTLTVPEATQSDGYECAARQATREVEMKKVTISVHEKGYFIEIKPT FSQLEAVNLHEVKHFVVEVRAYPPIISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKIRAKEEDSGHYTIVAQNE AVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCATGPTLPDIEWMIKDIKKCNNETSWTILANNVSNIIITEIHSRD RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLLVIVISLIVLVVIWKQKPRYEIRWR VIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVGRVLGSGAFGVVEGTAYGLRSQPFVMKVAVKMLKPTARSSEKQA LMSELKIMTHLGPHLNIVNLGACTKSGPIYIITEYCFYGDVNLVYHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY VILSFENNNGDYMDMKQADTTQYVPMLERKEVSKYSIDIQRSLYDRPASYYKKKSMMLDSEVKNLLSSDDNSEGLTLLDLLSFTY

			QVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNVYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWS YGILLWEIFSLGGTPYPGMVDSTFYNKIKSGYMAKPDHATSEVEYIMVKNWSEPEKRPSEFYHLSEIIVENLLPGQYKK SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVYTKNEEDKLDWEGGLDEQRLSADSGYIIPLPDIDPVEEEDLGKRNHR SSQTSEESAIEGTSSSTFIKREDETIEDIDMDDIGIDSSDLVEDSFL
808.	Human NTM v3 paralogue	human	MGVCGYLFPLPWKCLVAVSLRLLFLVPTGVPVRSQDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSITILYAGND KWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIAT GRPEPTVTRHISPKAVGFVSEDEYLEIQGITREQSGDYECASNDVAAPVRRVKVTVNPYPISEAKGTGVPVGQKGT LQCEASAVPSAEFQWYKDDKRLIEGKKGKVENRPFLLSKLIFFNVSEHDYGNVYTCVASNKLGHTNASIMLFEVKTALTLP WKGPAVSEVSNGTSTRAGCVLLPLLLVLLLLKF
809.	Human V5 tagged FLT3- D2xEpCAM	artificial	MGWSCIIILFLVATATGVHSGKPIPNPLGLDSTSGTLRRPYFRKMENQDALVCISESVPEPIVEWVLCDSQGESCKEESP AVVKEEKVLHELFGTDIRCCARNELGRETRLTIDLNQTPQTLLPQLFLKVGEPLWIRCKAVHVNHGFLTWELENKA LEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCFSV RFKAYPQIRCTWTFSRKSFCEQKGLDNGYSISKFCNKHQPGEYIFHAENDDAQFTKMTLNIRRKPOVLAEASASQAS CFSDGYPLPSWTWKKCSDKSPNCTEEITEGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNS PGPFFFIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVVLVIRKKRMAYEKAEIKEMGEMHRELNA
810.	Human V5 tagged FLT3- D3xEpCAM	artificial	MGWSCIIILFLVATATGVHSGKPIPNPLGLDSTSGTIDLNQTPQTLLPQLFLKVGEPLWIRCKAVHVNHGFLTWELN KALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCF SVRFKAYPQIRCTWTFSRKSFCEQKGLDNGYSISKFCNKHQPGEYIFHAENDDAQFTKMTLNIRRKPOVLAEASASQ ASCFSDGYPLPSWTWKKCSDKSPNCTEEITEGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILL NSPGPFFFIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVVLVIRKKRMAYEKAEIKEMGEMHRELNA
811.	Human V5 tagged FLT3- D4xEpCAM	artificial	MGWSCIIILFLVATATGVHSGKPIPNPLGLDSTSGGINATNSSEDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPC EQKGLDNGYSISKFCNKHQPGEYIFHAENDDAQFTKMTLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKKCSDKSP NCTEEITEGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFFFIQDNISSGGGGSGAG VIAIVVVVIAIVAGIVVLVIRKKRMAYEKAEIKEMGEMHRELNA
812.	Human V5 tagged FLT3- D5xEpCAM	artificial	MGWSCIIILFLVATATGVHSGKPIPNPLGLDSTSGIRRKPOVLAEASASQASCFSDGYPLPSWTWKKCSDKSPNCTEEIT EGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFFFIQDNISSGGGGSGAGVIAIVV VIAIVAGIVVLVIRKKRMAYEKAEIKEMGEMHRELNA
813.	Human FLT3- ECD	human	MPALARDGGQLPLLVVFSAMIFGTITNQDLPIKCVLINHKNDSSVGKSSSYPMVSESPEDLGCALRPQSSGTVYEA VEVDVSASITLQVLVDPAGNISCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRRPYFRKMENQDALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE CTRLFTIDLNQTPQTLLPQLFLKVGEPLWIRCKAVHVNHGFLTWELENKALEEGNYFEMSTYSTNRTMIRILFAFVSSV ARNDTGYTCSKKHPSQSALVTIVEKGFINATNSSEDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFCEQKGLDNG YSISKFCNKHQPGEYIFHAENDDAQFTKMTLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKKCSDKSPNCTEEITE GVWNRKANRKFVGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFFFIQDNISS
814.	Human FLT3- D1	human	AAVEVDVSASITLQVLVDPAGNISCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTV SIR
815.	Human FLT3- D2	human	TLRRPYFRKMENQDALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRECTRL
816.	Human FLT3- D3	human	FTIDLNQTPQTLLPQLFLKVGEPLWIRCKAVHVNHGFLTWELENKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARND TGYYTCSKKHPSQSALVTIV

817.	Human FLT3-D4	human	GFINATNSSDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNKHQHPGEYIFHAENDDAQFTKMFLLN
818.	Human FLT3-D5	human	IRRKPQVLAEASASQASCFSDGYPLPSWTWKKCKDKSPNCTEEITEGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVLKCCAYNSLGTSCETILLNSPG
819.	hu lsp V5xFlt3-E1muxEpC-pEF DHFR	artificial	NQDLPVIKCVLINHKNDSSVGKSSSYPMVSESPEDLGALRPQSSGTVYEA
820.	hu lsp V5xFlt3-E2muxEpC-pEF DHFR	artificial	AAVEVDVSASITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDLQNRGVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSIRNTLLYT
821.	hu lsp V5xFlt3-E3muxEpC-pEF DHFR	artificial	LRRPYFRKMENQDALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEEKVLHELFGTDIRCCARNELGRECTRL
822.	hu lsp V5xFlt3-E3AmuxEpC-pEF DHFR	artificial	LRRPYFRKMENQDALVCISESVPEPIVEWVLCDSQGES
823.	hu lsp V5xFlt3-E3BmuxEpC-pEF DHFR	artificial	KEESPAVVKKEEKVLHELFGTDIRCCARNELGRECTRL
824.	hu lsp V5xFlt3-E4muxEpC-pEF DHFR	artificial	FTIDLNQTPQTTLPQLFLKVGEPLWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIV
825.	hu lsp V5xFlt3-E5muxEpC-pEF DHFR	artificial	EKGFINATNSSDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNKHQHPGEYIFHAENDDAQFTKMFLLN
826.	hu lsp V5xFlt3-E6muxEpC-pEF DHFR	artificial	IRRKPQVLAEASASQASCFSDGYPLPSWTWKKCKDKSPNCTEEITEGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVLKCCAYNSLGTSCETILLNSPGPFPIQDNI
827.	hu lsp V5xFlt3-E1muxEpC-pEF DHFR	artificial	GKPIPNPLGLDSTSGNQDLPVIKCVLISHENNGSSAGKPPSSYRMVRGSPEDLQCAPRRQSEGTVYEA AAVEVDVSASITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDLQNRGVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSIRNTLLYTLLRPFYFRKMENQDALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEEKVLHELFGTDIRCCARNELGRECTRLFTIDLNQTPQTTLPQLFLKVGEPLWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIVEKGFINATNSSDEYIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNKHQHPGEYIFHAENDDAQFTKMFLLNIRRKPQVLAEASASQASCFSDGYPLPSWTWKKCKDKSPNCTEEITEGVWNRKANRKFVGQWVSSSTLNMSEAIKGFVLKCCAYNSLGTSCETILLNSPGPFPIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVVLVSRKKRMAYEKAEIKEMGEMHRELNA
828.	hu lsp V5xFlt3-E2muxEpC-pEF DHFR	artificial	GKPIPNPLGLDSTSGNQDLPVIKCVLINHKNDSSVGKSSSYPMVSESPEDLGALRPQSSGTVYEAATVEAESGSITLQVQLATPGDLSCLWVFKHSSLGCQPHFDLQNRGIVSMAILNVETQAGEYLLHIQSEAAANYTVLFTVNRDQTLYVLLRPFYFRKMENQDALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEEKVLHELFGTDIRCCARNELGRECTRLFTIDLNQTPQTTLPQLFLKVGEPLWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYYTC

			SSSKHPSQSALVTIVEKGFINATNSSDEYEDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNHK HQPGYIFHAENDDAQFTKMTLNIRKPKQVLAESAASQASCFSDGYPLPSWTWKKCDKSPNCTEEITEGVWNRKANRK VFGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFPIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVV LVI SRKKRMAKYEKAEIKEMGEMHRELNA
829.	hu lsp V5xFl13- E3muxEpC- pEFDHFR	artificial	MGWSCIIILFLVATATGVHSGKPIPNPLLGLDSTSGNQDLPVIKCVLINHKNDSSVGKSSSPMVSESPEDLGCALRPQS SGTVYEA-AAVEVDVSASITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATN YTILFTVSI RNTLLYTLRRPYFRKMENQDALLCISEGVPEPTVEWVLCSSHRESCKEEGPAVVRKEEKVLFELFGTDIRC CARNALGRECTKLTIDLNQTPQTLPQLFLKVGEPLWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNRMTIR ILFAFVSSVARNDTGYYTCCSSKHPQSALVTIVEKGFINATNSSDEYEDQYEEFCFSVRFKAYPQIRCTWTFSRKSF CEQKGLDNGYSISKFCNHKHQPGYIFHAENDDAQFTKMTLNIRKPKQVLAESAASQASCFSDGYPLPSWTWKKCDKS PNCTEEITEGVWNRKANRKVFGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFPIQDNISSGGGGSGA GVIAIVVVVIAIVAGIVV LVI SRKKRMAKYEKAEIKEMGEMHRELNA
830.	hu lsp V5xFl13- E3AmuxEpC- pEFDHFR	artificial	GKPIPNPLLGLDSTSGNQDLPVIKCVLINHKNDSSVGKSSSPMVSESPEDLGCALRPQSSSGTVYEA-AAVEVDVSASIT LQVLVDAPGNI SCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRR PYFRKMENQDALLCISEGVPEPTVEWVLCSSHRESCKEESPAVVRKEEKVLFELFGTDIRCCARNALGRECTRLFTIDLN QTPQTLPQLFLKVGEPLWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNRMTIRILFAFVSSVARNDTGYYTC SSSKHPSQSALVTIVEKGFINATNSSDEYEDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNHK HQPGYIFHAENDDAQFTKMTLNIRKPKQVLAESAASQASCFSDGYPLPSWTWKKCDKSPNCTEEITEGVWNRKANRK VFGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFPIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVV LVI SRKKRMAKYEKAEIKEMGEMHRELNA
831.	hu lsp V5xFl13- E3BmuxEpC- pEFDHFR	artificial	GKPIPNPLLGLDSTSGNQDLPVIKCVLINHKNDSSVGKSSSPMVSESPEDLGCALRPQSSSGTVYEA-AAVEVDVSASIT LQVLVDAPGNI SCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRR PYFRKMENQDALVCI SE SVPEPIVEWVLCDSQGESCKEEGPAVVRKEEKVLFELFGTDIRCCARNALGRECTKLTIDLN QTPQTLPQLFLKVGEPLWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNRMTIRILFAFVSSVARNDTGYYTC SSSKHPSQSALVTIVEKGFINATNSSDEYEDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNHK HQPGYIFHAENDDAQFTKMTLNIRKPKQVLAESAASQASCFSDGYPLPSWTWKKCDKSPNCTEEITEGVWNRKANRK VFGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFPIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVV LVI SRKKRMAKYEKAEIKEMGEMHRELNA
832.	hu lsp V5xFl13- E4muxEpC- pEFDHFR	artificial	GKPIPNPLLGLDSTSGNQDLPVIKCVLINHKNDSSVGKSSSPMVSESPEDLGCALRPQSSSGTVYEA-AAVEVDVSASIT LQVLVDAPGNI SCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSEATNYTILFTVSI RNTLLYTLRR PYFRKMENQDALVCI SE SVPEPIVEWVLCDSQGESCKEESPAVVRKEEKVLFELFGTDIRCCARNALGRECTRLFTIDLN QAPQSTLPQLFLKVGEPLWIRCKAIVHNHGFLTWELNKALEEGSYFEMSTYSTNRMTIRILFAFVSSVGRNDTGYYTC SSSKHPSQSALVTIVEKGFINATNSSDEYEDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCQKGLDNGYSISKFCNHK HQPGYIFHAENDDAQFTKMTLNIRKPKQVLAESAASQASCFSDGYPLPSWTWKKCDKSPNCTEEITEGVWNRKANRK VFGQWVSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSPGPFPIQDNISSGGGGSGAGVIAIVVVVIAIVAGIVV LVI SRKKRMAKYEKAEIKEMGEMHRELNA
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835.	Fc monomer-1 +c/-g	artificial	DKHTTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
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837.	Fc monomer-3 -c/+g	artificial	DKHTTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
838.	Fc monomer-4 - c/+g/delGK	artificial	DKHTTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP
839.	Fc monomer-5 -c/-g	artificial	DKHTTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
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841.	Fc monomer-7 +c/+g	artificial	DKHTTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYNSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

842.	Fc monomer-8 +c/+g/delG K	artificial	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYNSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLITVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP
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845.	scFc-3	artificial	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLITVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGG GSGGGGGGGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLITVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL SPGK
846.	scFc-4	artificial	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLITVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGG GSGGGGGGGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLITVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP
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849.	scFc-7	artificial	GGGGSGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSP DKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYNSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGG GSGGGSGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSL SPGK
850.	scFc-8	artificial	DKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYNSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGG GGGGSGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSP
851.	Peptide linker	(G ₄ S) ₄ linker	GGGGSGGGSGGGSGGGGS
852.	Peptide linker	(G ₄ S) ₅ linker	GGGGSGGGSGGGSGGGSGGGGS
853.	Peptide linker	(G ₄ S) ₆ linker	GGGGSGGGSGGGSGGGSGGGSGGGGS
854.	Peptide linker	(G ₄ S) ₇ linker	GGGGSGGGSGGGSGGGSGGGSGGGSGGGGS
855.	Peptide linker	(G ₄ S) ₈ linker	GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGGS
856.	FL_16xCD 3-scFc	Bispecific c HLE molecule	QVTLKESGPVLVKPTETTLTCTVSGFSLRNARMAVSWIRQPPGKTTLEWLAIHFSNDEKSYSTSLKSRLTI SKDTSKSQV VLTMTNMDPVDATYYCARIYGYSGWYGYFDYWGQGTLLTVSSGGSGGGSGGGSDIQMTQSPSSVSAVSGDRVTI TCRASQDIRYDLAWYQQKPKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNFYPLTFGGG TKVEIKSGGGSGSEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVROAPGKGLEWVARIRSKYNNIATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDAVYYCVRHNGFNSYI SYWAYWGQGTLLTVSSGGSGGGSGGGSGGGSGQTVVTTQEP SLTVSPGGTVTLTSGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPTARFSGSLGKAAALTL SGVQPEDEAEY YCVLWYSNRWVFGGKTLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNH YTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVSCVMHEALHNHYTQKSLSLSPGK
857.	FL_16xCD	Bispecific	QVTLKESGPVLVKPTETTLTCTVSGFSLRNARMAVSWIRQPPGKTTLEWLAIHFSNDEKSYSTSLKSRLTI SKDTSKSQV

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<151> 2015-07-31

<150> 62/290861

<151> 2016-02-03

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35

40

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Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
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Ser Val Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
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Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
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 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
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Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
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Ser Val Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
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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
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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

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Trp	Val	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Gly	Leu	Ile	Gly	Gly
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Thr	Lys	Phe	Leu	Ala	Pro	Gly	Thr	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Leu
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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> 20
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 20

Gly	Ser	Ser	Thr	Gly	Ala	Val	Thr	Ser	Gly	Tyr	Tyr	Pro	Asn
1				5					10				

<210> 21
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 21

Gly	Thr	Lys	Phe	Leu	Ala	Pro
1				5		

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 22

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 23

Lys Tyr Ala Met Asn
1 5

<210> 24
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 24

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 25
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 25

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 26

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 26

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> 27

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 27

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> 28

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 28

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> 29

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 29

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 30

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 31
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 31

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 32
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 32

Ser Tyr Ala Met Asn
1 5

<210> 33
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 33

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 34
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 34

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Phe Trp Ala Tyr
1 5 10

<210> 35
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 35

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> 36
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 36

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> 37
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 37

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> 38
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 38

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 39

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 40

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

<220>
<223> Synthetic peptide

<400> 40

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

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

<220>
<223> Synthetic peptide

<400> 41

Arg Tyr Ala Met Asn
1 5

<210> 42
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 42

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 43

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Tyr Phe Ala Tyr
 1 5 10

<210> 44
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 44

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> 45
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 45

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> 46

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 46

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> 47

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 47

Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 48

Ala Thr Asp Met Arg Pro Ser
1 5

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 49

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 50

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 50

Val Tyr Ala Met Asn
1 5

<210> 51

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

<220>
<223> Synthetic peptide

<400> 51

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Lys

<210> 52
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 52

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Trp Trp Ala Tyr
1 5 10

<210> 53
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 53

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> 54

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 54

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> 55
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 55

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> 56
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 56

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
 1 5 10

<210> 57
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 57

Gly Thr Lys Phe Leu Ala Pro
 1 5

<210> 58
 <211> 9
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 58

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 59

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 59

Lys Tyr Ala Met Asn
1 5

<210> 60

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 60

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Ser

<210> 61

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 61

His Gly Asn Phe Gly Asn Ser Tyr Thr Ser Tyr Tyr Ala Tyr

1 5 10

<210> 62
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 62

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> 63
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 63

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> 64
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 64

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> 65
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 65

Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 66

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 66

Ala Thr Asp Met Arg Pro Ser
1 5

<210> 67

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 67

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 68

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 68

Gly Tyr Ala Met Asn
1 5

<210> 69

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 69

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Glu

<210> 70

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 70

His Arg Asn Phe Gly Asn Ser Tyr Leu Ser Trp Phe Ala Tyr
1 5 10

<210> 71

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 71

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> 72
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 72

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> 73
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 73

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> 74
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 74

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

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

<220>
<223> Synthetic peptide

<400> 75

Gly Thr Lys Phe Leu Ala Pro
1 5

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

<220>

<223> Synthetic peptide

<400> 76

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 77

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 77

Val Tyr Ala Met Asn
1 5

<210> 78

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 78

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Lys

<210> 79

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 79

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Trp Trp Ala Tyr
1 5 10

<210> 80
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 80

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> 81
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 81

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> 82
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 82

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> 83
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 83

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 84

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 84

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 85

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 85

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 86

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 86

Ser Tyr Ala Met Asn
1 5

<210> 87

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 87

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 88

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 88

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp Ala Tyr
1 5 10

<210> 89

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 89

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> 90
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 90

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> 91

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

<220>
<223> Synthetic peptide

<400> 91

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> 92
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 92

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 1 5 10

<210> 93
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 93

Gly Thr Lys Phe Leu Ala Pro
 1 5

<210> 94
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 94

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 95

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 95

Lys Tyr Ala Met Asn
1 5

<210> 96

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 96

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 97

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 97

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 98

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

<220>
<223> Synthetic peptide

<400> 98

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> 99
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 99

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> 100
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 100

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> 101
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 101

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> 102
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 102

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> 103
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 103

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> 104
<211> 585
<212> PRT
<213> Homo sapiens

<400> 104

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> 105
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 105

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> 106
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 106

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> 107
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 107

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 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> 108
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 108

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

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

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

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

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Gly Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

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

Ala Ala Ser Gln Ala Ala Leu Gly Leu
 580 585

<210> 109
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 109

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> 110
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 110

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> 111
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 111

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> 112
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 112

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> 113
 <211> 585

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 113

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 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> 114
<211> 585
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 114

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

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

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

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

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 115
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 115

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> 116
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 116

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> 117
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 117

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> 118
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 118

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> 119
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 119

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> 120
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 120

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> 121
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 121

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> 122
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 122

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> 123
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 123

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> 124
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 124

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> 125
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 125

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> 126
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 126

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> 127
<211> 585
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 127

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> 128
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 128

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> 129
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 129

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> 130
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 130

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> 131
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 131

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> 132
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 132

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> 133
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 133

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> 134
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 134

Arg Asp Trp Asp Phe Asp Val Phe Gly Gly Gly Thr Pro Val Gly Gly
1 5 10 15

<210> 135
<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> 135

Gln Arg Phe Val Thr Gly His Phe Gly Gly Leu Xaa Pro Ala Asn Gly
1 5 10 15

<210> 136
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 136

Gln	Arg	Phe	Val	Thr	Gly	His	Phe	Gly	Gly	Leu	Tyr	Pro	Ala	Asn	Gly
1				5				10						15	

<210> 137
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 137

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

<210> 138
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 138

Thr	Gly	His	Phe	Gly	Gly	Leu	His	Pro
1				5				

<210> 139
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 139

Gln Arg Phe Cys Thr Gly His Phe Gly Gly Leu His Pro Cys Asn Gly
 1 5 10 15

<210> 140
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 140

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> 141
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 141

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> 142
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 142

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> 143
 <211> 338
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 143

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> 144
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 144

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> 145
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 145

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> 146
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 146

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> 147
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 147

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> 148
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 148

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> 149
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 149

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> 150
<211> 217
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 150

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> 151
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 151

Asn Ala Arg Met Gly Val Ser
1 5

<210> 152
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 152

His Ile Phe Ser Asn Ala Glu Lys Ser Tyr Arg Thr Ser Leu Lys Ser
1 5 10 15

<210> 153
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 153

Ile Pro Gly Tyr Gly Gly Asn Gly Asp Tyr His Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 154
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 154

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

<210> 155
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 155

Ala Ser Ser Thr Leu Gln Ser
1 5

<210> 156
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 156

Leu Gln His Asn Asn Phe Pro Trp Thr
1 5

<210> 157
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 157

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 Ile Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys Ser Tyr Arg 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 Ile Pro Gly Tyr Gly Gly Asn Gly Asp Tyr His Tyr Tyr
100 105 110

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

<210> 158
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 158

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

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

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

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

<210> 159
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 159

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 Ile Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys Ser Tyr Arg 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 Ile Pro Gly Tyr Gly Gly Asn Gly Asp Tyr His Tyr Tyr
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 Leu Gly Asp Arg
 145 150 155 160

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

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

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

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

Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn Phe Pro Trp Thr Phe
 225 230 235 240

Gly Gln Gly Thr Lys Val Glu Ile Lys
 245

<210> 160
 <211> 504
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 160

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 Ile Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys Ser Tyr Arg 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 Ile Pro Gly Tyr Gly Gly Asn Gly Asp Tyr His Tyr Tyr
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 Leu Gly Asp Arg
145 150 155 160

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

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

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

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

Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn Phe Pro Trp Thr Phe
225 230 235 240

Gly Gln 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> 161
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 161

Asn Ala Arg Met Gly Val Ser
1 5

<210> 162
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 162

His Ile Phe Ser Asn Asp Glu Lys Thr Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 163
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 163

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

<210> 164
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 164

Arg Ala Ser Gln Asp Ile Arg Asn Asp Phe Gly
1 5 10

<210> 165

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 165

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 166

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 166

Leu Gln Tyr Asn Thr Tyr Pro Trp Thr
1 5

<210> 167

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 167

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 Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Thr Tyr Ser Thr Ser
50 55 60

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

Val Leu Thr Met Thr Lys Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Pro Tyr Tyr Gly Ser Gly Ser His Asn Tyr Gly Met
100 105 110

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

<210> 168
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 168

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30

Phe Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Arg Leu Leu
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 169
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 169

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 Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Thr Tyr Ser Thr Ser
50 55 60

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

Val Leu Thr Met Thr Lys Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Pro Tyr Tyr Gly Ser Gly Ser His Asn Tyr Gly Met
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Asp Ile Arg Asn Asp Phe Gly Trp Tyr
165 170 175

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

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

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

Thr Tyr Tyr Cys Leu Gln Tyr Asn Thr Tyr Pro Trp Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 170
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 170

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 Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Thr Tyr Ser Thr Ser
50 55 60

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

Val Leu Thr Met Thr Lys Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Pro Tyr Tyr Gly Ser Gly Ser His Asn Tyr Gly Met
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Asp Ile Arg Asn Asp Phe Gly Trp Tyr
165 170 175

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

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

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

Thr Tyr Tyr Cys Leu Gln Tyr Asn Thr Tyr Pro Trp Thr Phe Gly Gln
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Lys Leu Thr Val Leu
500

<210> 171
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 171

Asn Ala Arg Met Ala Val Ser
1 5

<210> 172
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 172

His Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 173
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 173

Ile Val Gly Tyr Ser Asp Trp Leu Leu Pro Phe Asp His
1 5 10

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 174

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

<210> 175

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 175

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 176

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 176

Leu Gln His Asn Ser Tyr Pro Trp Thr
1 5

<210> 177

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 177

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

Trp Leu Ala His Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Thr Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Ile Val Gly Tyr Ser Asp Trp Leu Leu Pro Phe Asp His
100 105 110

Trp Gly Gln Gly Ile Met Val Thr Val Ser Ser
115 120

<210> 178
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 178

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 Asn Ile Asn Arg Phe
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 Leu Gln His Asn Ser Tyr Pro Trp
85 90 95

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

<210> 179
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 179

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

Trp Leu Ala His Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Thr Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Ile Val Gly Tyr Ser Asp Trp Leu Leu Pro Phe Asp His
100 105 110

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
130 135 140

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

Cys Arg Ala Ser Gln Asn Ile Asn Arg Phe Leu Asn Trp Tyr Gln Gln
 165 170 175

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

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

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

Tyr Cys Leu Gln His Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr
 225 230 235 240

Lys Val Asp Ile Lys
 245

<210> 180
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 180

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

Trp Leu Ala His Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Thr Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Ile Val Gly Tyr Ser Asp Trp Leu Leu Pro Phe Asp His
100 105 110

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
130 135 140

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

Cys Arg Ala Ser Gln Asn Ile Asn Arg Phe Leu Asn Trp Tyr Gln Gln
165 170 175

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

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

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

Tyr Cys Leu Gln His Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr
225 230 235 240

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

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

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

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

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

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

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
 340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
 355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly 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 Ala Lys 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 Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 183
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 183

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 184
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 184

Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Gly
1 5 10

<210> 185

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 185

Gly Ala Ser Thr Leu Gln Ser
1 5

<210> 186

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 186

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 187

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 187

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<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 Asp Ile Arg Asp Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Gly Ala Ser Thr 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 189
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 189

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 190
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 190

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly 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> 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 Trp Asn 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

Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp Val
1 5 10 15

<210> 194
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 194

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

<210> 195
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 195

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 196
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 196

Leu Gln His Asn Thr Tyr Pro Leu 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 Met Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr 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 Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Thr Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp 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 Met Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Gly Ile Arg Asn Asp Leu Gly Trp Tyr
165 170 175

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

Thr Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Asp 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 Met Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Gly Ile Arg Asn Asp Leu Gly Trp Tyr
165 170 175

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

Thr Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Asp 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> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 201

Asn Ala Arg Met Ala Val Ser
1 5

<210> 202
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 202

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Pro Ser Leu Lys Ser
1 5 10 15

<210> 203
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 203

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

<210> 204
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 204

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

<210> 205
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 205

Ala Ala Ser Val Leu Gln Ser
1 5

<210> 206
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 206

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 207
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 207

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Pro 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Val 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 209
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 209

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Pro 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 Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Gly Trp Phe Gln
 165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 210
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 210

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Pro 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Gly Trp Phe Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly 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> 211
 <211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 211

Asn Ala Arg Met Gly Val Ser
1 5

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

<220>
<223> Synthetic peptide

<400> 212

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Asn
1 5 10 15

<210> 213
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 213

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

<210> 214
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 214

Arg Ala Ser Gln Asp Ile Arg Thr Asp Leu Ala
1 5 10

<210> 215
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 215

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 216
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 216

Leu Gln His Asn Arg Tyr Pro Leu Thr
1 5

<210> 217
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 217

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

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

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 218
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 218

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Thr Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Arg Tyr Pro Leu
85 90 95

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

<210> 219
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 219

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

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

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

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

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Arg Thr Asp Leu Ala Trp Tyr Gln
 165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Arg Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 220
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 220

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

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

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Arg Thr Asp Leu Ala Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Arg Tyr Pro Leu Thr Phe Gly Gly 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> 221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 221

Tyr Ala Arg Met Gly Val Ser
1 5

<210> 222

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 222

Gln Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 223

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 223

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

<210> 224

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 224

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

<210> 225

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 225

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 226
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 226

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 227
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 227

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

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

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

Trp Leu Ala Gln Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Asn Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 228
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 228

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 229
<211> 246

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 229

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

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

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

Trp Leu Ala Gln Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Asn Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 230
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 230

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

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

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

Trp Leu Ala Gln Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Asn Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly 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> 231

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 231

Asn Ala Arg Met Gly Val Ser
1 5

<210> 232

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 232

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 233

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 233

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

Val

<210> 234

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 234

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

<210> 235
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 235

Ala Ala Ser Thr Val Gln Ser
1 5

<210> 236
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 236

Leu Gln His Asn Ser Phe Pro Trp Thr
1 5

<210> 237
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 237

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
100 105 110

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

<210> 238
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 238

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 Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Thr Val Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 239
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 239

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
 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 Gly Ile Arg Asn Asp Leu Ala
 165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Val Asp Ile Lys
245

<210> 240
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 240

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
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 Gly Ile Arg Asn Asp Leu Ala
165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Val Asp 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> 241
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 241

Asn Ala Arg Met Gly Val Ser
1 5

<210> 242

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 242

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 243

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 243

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 244

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 244

Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Gly
1 5 10

<210> 245

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 245

Gly Ala Ser Thr Leu Gln Ser
1 5

<210> 246
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 246

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 247
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 247

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 248
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 248

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Gly Ala Ser Thr 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 249
<211> 246

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 249

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 250
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 250

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly 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> 251

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 251

Asn Ala Lys Met Gly Val Ser
1 5

<210> 252

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 252

Gln Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 253

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 253

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 254

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 254

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

<210> 255

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 255

Gly Ala Ser Thr Leu Gln Ser
1 5

<210> 256

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 256

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 257

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 257

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 Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala Gln Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 258
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 258

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 Arg Asn Asp
20 25 30

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

Tyr Gly Ala Ser Thr 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 259
<211> 246
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 259

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 Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala Gln Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 260
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 260

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 Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala Gln Ile Phe Ser Asn Gly Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 261
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 261

Asn Ala Arg Met Gly Val Ser
1 5

<210> 262

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 262

Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 263

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 263

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 264

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 264

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

<210> 265

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 265

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 266

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 266

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 267

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 267

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 268
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 268

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 269
<211> 246
<212> PRT
<213> Artificial Sequence

<220> 236

<223> Synthetic peptide

<400> 269

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 270
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 270

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
 500

<210> 271
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 271

Asn Ala Arg Met Gly Val Ser
1 5

<210> 272
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 272

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Asn
1 5 10 15

<210> 273
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 273

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp Tyr
1 5 10

<210> 274
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 274

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

<210> 275
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 275

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 276

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 276

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 277

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 277

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 278
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 278

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 Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 279
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 279

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 280
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 280

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 281
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 281

Asn Ala Arg Met Ala Val Ser
1 5

<210> 282
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 282

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 283
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 283

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 284
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 284

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

<210> 285
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 285

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 286
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 286

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 287
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 287

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 288
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 288

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 289
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 289

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 290
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 290

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 291
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 291

Asn Ala Arg Met Ala Val Ser
1 5

<210> 292
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 292

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 293
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 293

Ile	Val	Gly	Tyr	Gly	Ser	Gly	Trp	Tyr	Gly	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 294
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 294

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

<210> 295
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 295

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 296
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 296

Leu Gln His Asn Ser Tyr Pro Leu Thr
 1 5

<210> 297
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 297

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 298
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 298

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 299
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 299

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30
 Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Thr Leu Glu
 35 40 45
 Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
 100 105 110
 Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Gly Asn Asp Leu Gly Trp Tyr Gln
 165 170 175
 Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
 180 185 190
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 300
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 300

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Gly Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 301

Asn Ala Arg Met Ala Val Ser
1 5

<210> 302
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 302

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 303
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 303

Ile	Val	Gly	Tyr	Gly	Ser	Gly	Trp	Tyr	Gly	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 304
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 304

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

<210> 305
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 305

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 306
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 306

Leu Gln His Asn Phe Tyr Pro Leu Thr
1 5

<210> 307
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 307

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 Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 308
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 308

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Tyr Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Phe Tyr Pro Leu
85 90 95

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

<210> 309
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 309

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 Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg Tyr Asp Leu Ala Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Phe Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 310
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 310

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 Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg Tyr Asp Leu Ala Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Phe Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
 500

<210> 311
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 311

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 312
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 312

Asn	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 313

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 313

Ile	Val	Gly	Tyr	Gly	Ser	Gly	Trp	Tyr	Gly	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 314

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 314

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

<210> 315

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 315

Ala	Thr	Ser	Ile	Arg	Gln	Ser
1				5		

<210> 316

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 316

Leu Gln His Asn Ser Phe Pro Leu Thr
1 5

<210> 317
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 317

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asn Pro Val Asp Thr Gly Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 318
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 318

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30

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

Tyr Ala Thr Ser Ile Arg Gln Ser Gly Val Pro Ser Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

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

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

<210> 319
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 319

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asn Pro Val Asp Thr Gly Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Phe Cys Leu Gln His Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 320
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 320

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asn Pro Val Asp Thr Gly Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Phe Cys Leu Gln His Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
 500

<210> 321
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 321

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 322
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 322

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Phe	Ser	Thr	Ser	Leu	Lys	Asn
1				5					10					15	

<210> 323

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 323

Met	Val	Gly	Tyr	Gly	Ser	Gly	Trp	Tyr	Ala	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 324

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 324

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

<210> 325

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 325

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 326

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 326

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 327

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 327

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser
50 55 60

Leu Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 328

<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 328

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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 329
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 329

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser
50 55 60

Leu Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

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

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

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

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

Thr Lys Val Glu Ile Lys
245

<210> 330
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 330

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser
50 55 60

Leu Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
 500

<210> 331
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 331

Tyr Ala Arg Met Gly Val Ser
 1 5

<210> 332
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 332

Gln Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 333

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 333

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

<210> 334

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 334

Arg Ala Ser Gln Asp Ile Gly Asp Asp Leu Gly
1 5 10

<210> 335

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 335

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 336

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 336

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 337

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 337

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

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

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

Trp Leu Ala Gln Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 338

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 338

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asp Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Phe 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 339

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 339

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

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

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

Trp Leu Ala Gln Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Gly Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

Thr Lys Val Glu Ile Lys
245

<210> 340
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 340

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

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

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

Trp Leu Ala Gln Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

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

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Gly Asp Asp Leu Gly Trp Tyr Gln
 165 170 175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 341
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 341

Asn Ala Arg Met Ala Val Ser
1 5

<210> 342
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 342

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 343
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 343

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

<210> 344
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 344

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

<210> 345
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 345

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 346
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 346

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 347

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 347

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 348

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 348

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 Arg Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 349

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 349

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 350

<211> 501

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 350

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

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 351
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 351

Asn Ala Arg Met Gly Val Ser
1 5

<210> 352
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 352

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 353
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 353

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

Val

<210> 354
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 354

Arg Thr Ser Arg Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 355
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 355

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 356
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 356

Leu Gln His Asn Asn Phe Pro Trp Thr
1 5

<210> 357

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 357

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
100 105 110

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

<210> 358

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 358

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 Thr Ser Arg Gly Ile Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn Phe Pro Trp
85 90 95

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

<210> 359

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 359

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
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 Thr Ser Arg Gly Ile Arg Asn Asp Leu Gly
165 170 175

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

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

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

Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn Phe Pro Trp Thr Phe
225 230 235 240

Gly Gln Gly Thr Lys Val Glu Ile Lys
245

<210> 360
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 360

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
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 Thr Ser Arg Gly Ile Arg Asn Asp Leu Gly
165 170 175

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

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

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

Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn Phe Pro Trp Thr Phe
225 230 235 240

Gly Gln 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> 361
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 361

Asn Ala Arg Met Gly Val Ser
1 5

<210> 362
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 362

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 363
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 363

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 364
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 364

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

<210> 365
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 365

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 366
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 366

Leu Gln His Asn Thr Tyr Pro Trp Thr
1 5

<210> 367

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 367

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 368

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 368

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Trp
85 90 95

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

<210> 369

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 369

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 370

<211> 501

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 370

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 371
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 371

Asn Ala Arg Met Gly Val Ser
1 5

<210> 372
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 372

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 373
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 373

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 374
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 374

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

<210> 375
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 375

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 376
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 376

Leu Gln His Asn Ser Phe Pro Trp Thr
1 5

<210> 377
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 377

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 378
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 378

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Tyr Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 379

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 379

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Gly Tyr Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 380
<211> 501
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 380

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Gly Tyr Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 381
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 381

Asn Val Arg Met Gly Val Ser
1 5

<210> 382
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 382

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 383
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 383

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 384
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 384

Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Val
1 5 10

<210> 385
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 385

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 386
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 386

Leu Gln His His Ser Tyr Pro Trp Thr
1 5

<210> 387
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 387

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 388
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 388

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
 20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

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

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

<210> 389
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 389

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Val Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His His Ser Tyr Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 390
<211> 501
<212> PRT
<213> Artificial Sequence

<220> 321

<223> Synthetic peptide

<400> 390

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Val Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His His Ser Tyr Pro Trp Thr Phe Gly Gln Gly
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 391
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 391

Asn Ala Arg Met Gly Val Ser
1 5

<210> 392
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 392

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 393
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 393

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 394
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 394

Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Gly
1 5 10

<210> 395
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 395

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 396
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 396

Leu Gln His Asn Ser Phe Pro Phe Thr
1 5

<210> 397
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 397

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 398
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 398

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Thr Gly
50 55 60

Gly 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 Leu Gln His Asn Ser Phe Pro Phe
85 90 95

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

<210> 399
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 399

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Phe Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 400
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 400

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Phe Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 401
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 401

Asn Ala Arg Met Gly Val Ser
1 5

<210> 402
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 402

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 403
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 403

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 404

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 404

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

<210> 405

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 405

Gly Thr Ser Thr Leu Gln Ser
1 5

<210> 406

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 406

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 407

<211> 124

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 407

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 408
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 408

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 Arg Asn Asp
20 25 30

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

Tyr Gly Thr Ser Thr 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 409
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 409

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Arg Asn Asp Leu Val Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 410
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 410

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 Phe Arg Asn Ala
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Arg Asn Asp Leu Val Trp Tyr Gln
 165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 411
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 411

Asn Ala Arg Met Gly Val Ser
1 5

<210> 412
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 412

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 413
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 413

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 414

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 414

Arg Thr Ser Gln Gly Ile Arg Asn Asp Leu Val
1 5 10

<210> 415

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 415

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 416

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 416

Leu Gln His Tyr Ser Tyr Pro Leu Thr
1 5

<210> 417

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 417

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 418

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 418

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 Thr Ser Gln Gly Ile Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 419

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 419

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

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

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

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

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

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

Thr Lys Val Glu Ile Lys
245

<210> 420
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 420

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 Phe Arg Asn Ala
 20 25 30
 Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95
 Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110
 Ile Trp Gly Gln Gly Thr Met 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Val Trp Tyr Gln
 165 170 175
 Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
 180 185 190
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
500

<210> 421
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 421

Asn Ala Arg Met Gly Val Ser
1 5

<210> 422
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 422

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 423
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 423

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 424

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 424

Arg Ala Ser Gln Gly Ile Gly Asp Asp Leu Gly
1 5 10

<210> 425

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 425

Ala Thr Ser Val Leu Gln Ser
1 5

<210> 426

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 426

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 427

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 427

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 428

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 428

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 Gly Asp Asp
20 25 30

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

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

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

<210> 429
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 429

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Gly Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 430
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 430

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 Phe Arg Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Gly Asp Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
 500

<210> 431
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 431

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 432
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 432

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Arg Thr Ser Leu Lys Ser
 1 5 10 15

<210> 433
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 433

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

<210> 434
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 434

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

<210> 435
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 435

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 436
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 436

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 437
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 437

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 438

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 438

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 439
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 439

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 440
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 440

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
 500

<210> 441
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 441

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 442
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 442

Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser Leu Lys Ser
 1 5 10 15

<210> 443
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 443

Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp Tyr
 1 5 10

<210> 444
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 444

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

<210> 445
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 445

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 446
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 446

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 447
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 447

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
 20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
 50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 448
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 448

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

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

<210> 449
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 449

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 450
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 450

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

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

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

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

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

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

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 451
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 451

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 452
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 452

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
 1 5 10 15

<210> 453
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 453

Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp Tyr
 1 5 10

<210> 454
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 454

Arg Thr Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 455
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 455

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 456
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 456

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 457
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 457

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 458
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 458

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 459
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 459

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 460
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 460

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 461
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 461

Asn Ala Arg Met Gly Val Ser
1 5

<210> 462
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 462

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 463
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 463

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 464
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 464

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Val
1 5 10

<210> 465
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 465

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 466
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 466

Leu Gln His Tyr Ser Tyr Pro Leu Thr
1 5

<210> 467
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 467

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 468
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 468

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Leu Gln His Tyr Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 469
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 469

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Val Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Phe Cys Leu Gln His Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 470
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 470

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Val Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Phe Cys Leu Gln His Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 471
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 471

Asn Ala Arg Met Gly Val Ser
1 5

<210> 472
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 472

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 473
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 473

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 474
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 474

Arg Ala Ser Gln Gly Ile Gly Asp Asp Leu Gly
1 5 10

<210> 475

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 475

Ala Thr Ser Val Leu Gln Ser
1 5

<210> 476

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 476

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 477

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 477

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 Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Thr Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 478
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 478

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Asp Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Ile Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Thr Ser Val 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 479
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 479

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 Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Thr Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Gly Asp Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Ile Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Thr Ser Val
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Leu Glu Ile Lys
 245

<210> 480
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 480

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 Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Thr Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Gly 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Gly Asp Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Ile Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Thr Ser Val
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 481
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 481

Asn Ala Arg Met Gly Val Ser
1 5

<210> 482
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 482

His Ile Phe Trp Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 483
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 483

Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp Val
1 5 10 15

<210> 484
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 484

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 485

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 485

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 486

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 486

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 487

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 487

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 488
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 488

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 489
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 489

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Gly Ile Arg Asn Asp Leu Gly Trp Tyr
 165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 210 215 220

Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly
 225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
 245

<210> 490
 <211> 502
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 490

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Gly Ile Arg Asn Asp Leu Gly Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Leu 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> 491
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 491

Asn Ala Arg Met Gly Val Ser
1 5

<210> 492
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 492

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Asn
1 5 10 15

<210> 493
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 493

Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp Tyr
1 5 10

<210> 494
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 494

Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Val
1 5 10

<210> 495

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 495

Gly Thr Ser Thr Leu Gln Ser
1 5

<210> 496

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 496

Leu Gln His His Ser Tyr Pro Leu Thr
1 5

<210> 497

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 497

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 498
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 498

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Gly Thr Ser Thr 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 Leu Gln His His Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 499
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 499

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Arg Asp Asp Leu Val Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Gly Thr Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 500
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 500

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Arg Asp Asp Leu Val Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Gly Thr Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 501
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 501

Tyr Ala Arg Met Gly Val Ser
1 5

<210> 502
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 502

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 503
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 503

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 504
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 504

Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Ala
1 5 10

<210> 505
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 505

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 506
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 506

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 507
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 507

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 508
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 508

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 509
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 509

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 510
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 510

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 511
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 511

Asn Ile Lys Met Gly Val Ser
1 5

<210> 512
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 512

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 513
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 513

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 514
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 514

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Ala
1 5 10

<210> 515
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 515

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 516
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 516

Leu Gln His Asn Ser Phe Pro Leu Thr
1 5

<210> 517
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 517

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 Arg Asn Ile
20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 518
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 518

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 519
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 519

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 Arg Asn Ile
 20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Ser Asn Tyr Leu Ala Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 520
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 520

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 Arg Asn Ile
20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Ser Asn Tyr Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 521

<211> 7

414

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 521

Asn Ala Arg Met Gly Val Ser
1 5

<210> 522
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 522

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 523
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 523

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 524
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 524

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 525
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 525

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 526
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 526

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 527
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 527

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 Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 528
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 528

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 529
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 529

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 Phe Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 530
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 530

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 Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 531
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 531

Asn Ala Arg Met Gly Val Ser
1 5

<210> 532

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 532

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Asn
1 5 10 15

<210> 533

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 533

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp Tyr
1 5 10

<210> 534

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 534

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 535

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 535

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 536
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 536

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 537
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 537

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 538
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 538

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 539
<211> 246

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 539

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 540
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 540

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 541

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 541

Asn Ala Arg Met Gly Val Ser
1 5

<210> 542

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 542

Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 543

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 543

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 544

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 544

Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Gly
1 5 10

<210> 545

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 545

Ala Thr Ser Ile Arg Gln Ser
1 5

<210> 546

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 546

Leu Gln His Asn Ser Phe Pro Leu Thr
1 5

<210> 547

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 547

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asn Pro Val Asp Thr Gly Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 548
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 548

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Thr Ser Ile Arg Gln Ser Gly Val Pro Ser Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Leu Gln His Asn Ser Phe Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 549
<211> 246
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 549

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asn Pro Val Asp Thr Gly Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Thr Ser Ile
180 185 190

Arg Gln Ser Gly Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Phe Cys Leu Gln His Asn Ser Phe Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 550
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 550

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala Asn Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Gly Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asn Pro Val Asp Thr Gly Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Thr Ser Ile
180 185 190

Arg Gln Ser Gly Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Phe Cys Leu Gln His Asn Ser Phe Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 551
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 551

Asn Ala Arg Met Gly Val Ser
1 5

<210> 552

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 552

His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser Leu Lys Asn
1 5 10 15

<210> 553

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 553

Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp Tyr
1 5 10

<210> 554

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 554

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 555

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 555

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 556

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 556

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 557

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 557

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser
50 55 60

Leu Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 558
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 558

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 559
<211> 246
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 559

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser
50 55 60

Leu Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 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 Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 560
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 560

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Phe Ser Thr Ser
 50 55 60

Leu Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 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 Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 561
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 561

Asn Ala Arg Met Ala Val Ser
1 5

<210> 562
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 562

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 563
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 563

Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp Tyr
1 5 10

<210> 564
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 564

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Ala
1 5 10

<210> 565
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 565

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 566

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 566

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 567

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 567

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 568
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 568

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 Arg Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 569
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 569

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 570
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 570

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Asn Asn Ala
 20 25 30

Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 571
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 571

Asn Ala Arg Met Gly Val Ser
1 5

<210> 572
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 572

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 573
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 573

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 574
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 574

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Val
1 5 10

<210> 575
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 575

Gly Thr Ser Thr Leu Gln Ser
1 5

<210> 576
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 576

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 577
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 577

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 Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 578
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 578

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Gly Thr Ser Thr 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 579
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 579

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 Phe Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Arg Asn Asp Leu Val Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Gly Thr Ser Thr
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 580
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 580

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 Phe Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Arg Asn Asp Leu Val Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Gly Thr Ser Thr
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 581
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 581

Asn Ala Arg Met Gly Val Ser
1 5

<210> 582
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 582

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 583
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 583

Met	Pro	Glu	Tyr	Ser	Ser	Gly	Trp	Ser	Gly	Ala	Phe	Asp	Ile
1				5					10				

<210> 584
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 584

Arg	Thr	Ser	Gln	Gly	Ile	Arg	Asn	Asp	Leu	Val
1				5					10	

<210> 585
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 585

Ala	Ala	Ser	Thr	Leu	Gln	Ser
1				5		

<210> 586
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 586

Leu Gln His Tyr Ser Tyr Pro Leu Thr
1 5

<210> 587
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 587

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 Phe Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 588
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 588

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Leu Gln His Tyr Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 589
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 589

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 Phe Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Val Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Phe Cys Leu Gln His Tyr Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 590
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 590

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 Phe Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Val Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Phe Cys Leu Gln His Tyr Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 591
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 591

Asn Ala Arg Met Gly Val Ser
1 5

<210> 592
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 592

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Arg	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 593
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 593

Ile	Val	Gly	Tyr	Gly	Ser	Gly	Trp	Tyr	Ala	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 594
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 594

Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp	Leu	Gly
1				5					10	

<210> 595
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 595

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 596
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 596

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 597
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 597

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Arg 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 598
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 598

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 599
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 599

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Arg 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 600
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 600

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Arg 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 601
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 601

Asn Ala Arg Met Gly Val Ser
1 5

<210> 602
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 602

Leu	Ile	Tyr	Trp	Asn	Asp	Asp	Lys	Arg	Tyr	Ser	Pro	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 603

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 603

Met	Val	Gly	Tyr	Gly	Ser	Gly	Trp	Tyr	Ala	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 604

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 604

Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp	Leu	Gly
1				5					10	

<210> 605

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 605

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 606

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 606

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 607
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 607

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 608
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 608

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 609
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 609

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45
 Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
 100 105 110
 Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175
 Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
 180 185 190
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220
 Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 610
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 610

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 611
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 611

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 612
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 612

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 613

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 613

Ile	Val	Gly	Tyr	Gly	Thr	Gly	Trp	Tyr	Gly	Phe	Phe	Asp	Tyr
1				5					10				

<210> 614

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 614

Arg	Thr	Ser	Gln	Gly	Ile	Arg	Asn	Asp	Leu	Gly
1				5						10

<210> 615

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 615

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 616

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 616

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 617

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 617

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 618

<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 618

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 619
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 619

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 620
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 620

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Asp Met Asp Pro Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Thr Ser Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 621
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 621

Asn Ala Arg Met Gly Val Ser
1 5

<210> 622
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 622

His Ile Phe Trp Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 623

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 623

Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp Val
1 5 10 15

<210> 624

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 624

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 625

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 625

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 626

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 626

Leu Gln His Asn Thr Tyr Pro Leu Thr
1 5

<210> 627

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 627

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 Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 628

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 628

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Thr Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys
100 105

<210> 629

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 629

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 Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Gly Ile Arg Asn Asp Leu Gly Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Leu Thr Phe Gly Cys
225 230 235 240

Gly Thr Lys Val Asp Ile Lys
245

<210> 630
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 630

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 Phe Ser Gly Phe Ser Leu Arg Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asn 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 Ile Pro Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile 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 Gly Ile Arg Asn Asp Leu Gly Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Leu Thr Phe Gly Cys
225 230 235 240

Gly Thr Lys Val Asp 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> 631
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 631

Asn Ala Arg Met Gly Val Ser
1 5

<210> 632
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 632

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Asn
1 5 10 15

<210> 633
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 633

Ile Val Gly Tyr Gly Thr Gly Trp Phe Gly Tyr Phe Asp Tyr
1 5 10

<210> 634
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 634

Arg Ala Ser Gln Asp Ile Arg Thr Asp Leu Ala
1 5 10

<210> 635
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 635

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 636
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 636

Leu Gln His Asn Arg Tyr Pro Leu Thr
1 5

<210> 637

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 637

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Phe Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 638

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 638

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Thr Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Arg Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys
100 105

<210> 639

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 639

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Phe Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Arg Thr Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Arg Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 640

<211> 501

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 640

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Phe Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln 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 Asp Ile Arg Thr Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Arg Tyr Pro Leu Thr Phe Gly Cys 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> 641
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 641

Asn Ala Arg Met Gly Val Ser
1 5

<210> 642
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 642

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 643
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 643

Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 644
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 644

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Ala
1 5 10

<210> 645
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 645

Ala Ala Ser Thr Val Gln Ser
1 5

<210> 646
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 646

Leu Gln His Asn Ser Phe Pro Trp Thr
1 5

<210> 647

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 647

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 648

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 648

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 Arg Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Val Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys
100 105

<210> 649

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 649

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
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 Gly Ile Arg Asn Asp Leu Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala
180 185 190

Ala Ser Thr Val Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Glu Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp Thr Phe
225 230 235 240

Gly Cys Gly Thr Lys Val Asp Ile Lys
245

<210> 650
 <211> 504
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 650

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr 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 Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Pro Gly Tyr Gly Gly Asn Phe Tyr Tyr His Tyr Tyr
 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 Gly Ile Arg Asn Asp Leu Ala
 165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala
180 185 190

Ala Ser Thr Val Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Glu Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp Thr Phe
225 230 235 240

Gly Cys Gly Thr Lys Val Asp 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> 651
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 651

Asn Val Arg Met Gly Val Ser
1 5

<210> 652
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 652

His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Arg Ser
1 5 10 15

<210> 653
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 653

Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp Tyr
1 5 10

<210> 654
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 654

Arg Thr Ser Gln Ser Val Asn Asn Asn Leu Ala
1 5 10

<210> 655
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 655

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 656
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 656

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 657

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 657

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Ser Thr 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 Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 658

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 658

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Gln Ser Val Asn Asn Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 659

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 659

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Ser Thr 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 Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
145 150 155 160

Ser Cys Arg Thr Ser Gln Ser Val Asn Asn Asn Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr
180 185 190

Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 660

<211> 501

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 660

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Ser Thr 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 Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
145 150 155 160

Ser Cys Arg Thr Ser Gln Ser Val Asn Asn Asn Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr
180 185 190

Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 661
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 661

Tyr Ala Arg Met Gly Val Ser
1 5

<210> 662
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 662

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 663
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 663

Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp Ile
1 5 10

<210> 664
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 664

Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Ala
1 5 10

<210> 665
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 665

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 666
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 666

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 667
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 667

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 668
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 668

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 669

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 669

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 670
<211> 501
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 670

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 671
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 671

Ser Tyr Gly Met His
1 5

<210> 672
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 672

Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 673
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 673

Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 674
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 674

Arg Thr Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 675
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 675

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 676
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 676

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 677

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 677

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 678
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 678

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys
100 105

<210> 679
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 679

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys
245 250

<210> 680
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 680

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
 385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
 405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
 420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
 435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
 450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
 465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
 485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 681
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 681

Ser Tyr Gly Met His
 1 5

<210> 682
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 682

Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 683

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 683

Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 684

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 684

Arg Ala Ser Gln Gly Val Arg Asn Asn Leu Val
1 5 10

<210> 685

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 685

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 686

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 686

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 687

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 687

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 688
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 688

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Asn Asn
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 689
<211> 251
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 689

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
145 150 155 160

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Asn Asn
165 170 175

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
180 185 190

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 690
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 690

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
145 150 155 160

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Asn Asn
165 170 175

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
180 185 190

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 691
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 691

Ser Tyr Gly Met His
1 5

<210> 692

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 692

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 693

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 693

Ser Tyr Gly Met Asp Val
1 5

<210> 694

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 694

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 695

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 695

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 696
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 696

Gln Gln Ala Asn Ser Phe Pro Trp Thr
1 5

<210> 697
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 697

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 698
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 698

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala 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 Ala Asn Ser Phe Pro Trp
85 90 95

Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 699
<211> 237

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 699

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser
130 135 140

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser
145 150 155 160

Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
165 170 175

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
180 185 190

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
195 200 205

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe
210 215 220

Pro Trp Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
225 230 235

<210> 700
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 700

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser
130 135 140

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser
145 150 155 160

Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
165 170 175

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
180 185 190

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
195 200 205

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe
210 215 220

Pro Trp Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly
225 230 235 240

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
245 250 255

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
260 265 270

Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
275 280 285

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
290 295 300

Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
305 310 315 320

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
325 330 335

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
340 345 350

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
355 360 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
370 375 380

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
385 390 395 400

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
405 410 415

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
420 425 430

Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser
435 440 445

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
450 455 460

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg
465 470 475 480

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490

<210> 701
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 701

Asn Val Arg Met Gly Val Ser
1 5

<210> 702
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 702

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Leu	Tyr	Thr	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 703
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 703

Ile	Val	Gly	Tyr	Gly	Thr	Gly	Trp	Tyr	Gly	Tyr	Phe	Asp	Tyr
1				5					10				

<210> 704
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 704

Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asp	Asp	Leu	Gly
1				5					10	

<210> 705
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 705

Ala	Thr	Ser	Ile	Arg	Gln	Ser
1				5		

<210> 706
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 706

Leu Gln His His Ser Phe Pro Leu Thr
 1 5

<210> 707
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 707

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 Arg Asn Val
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Leu Tyr Thr 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 Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 708
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 708

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
20 25 30

Leu Gly Trp Tyr Gln Arg Glu Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Thr Ser Ile Arg 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 Gly Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Leu Gln His His Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 709
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 709

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 Arg Asn Val
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Leu Tyr Thr 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 Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Gln 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 Ile Gly Asp Arg Val Thr Ile
 145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
 165 170 175

Arg Glu Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Thr Ser Ile
 180 185 190

Arg Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Phe Cys Leu Gln His His Ser Phe Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Val Asp Ile Lys
 245

<210> 710
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 710

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 Arg Asn Val
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Leu Tyr Thr 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 Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Gln 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 Ile Gly Asp Arg Val Thr Ile
 145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
 165 170 175

Arg Glu Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Thr Ser Ile
 180 185 190

Arg Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Phe Cys Leu Gln His His Ser Phe Pro Leu Thr Phe Gly Gly 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> 711
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 711

Tyr Ala Arg Met Gly Val Ser
1 5

<210> 712
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 712

His	Ile	Ser	Ser	Asn	Asp	Glu	Lys	Ser	Phe	Ser	Thr	Ala	Leu	Glu	Ser
1				5					10					15	

<210> 713
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 713

Met	Pro	Gly	Asp	Ser	Asn	Thr	Trp	Arg	Gly	Phe	Phe	Asp	Tyr
1				5					10				

<210> 714
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 714

Arg	Thr	Ser	Gln	Thr	Val	Thr	Asn	Ser	Tyr	Ile	Ala
1				5					10		

<210> 715
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 715

Gly	Thr	Ser	Thr	Arg	Ala	Thr
1				5		

<210> 716
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 716

Gln Lys Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 717
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 717

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Phe Ser Thr Ala
50 55 60

Leu Glu Ser Arg Leu Thr Ile Ser Thr Asp Thr Ser Lys Ser Gln Met
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 718
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 718

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 Thr Ser Gln Thr Val Thr Asn Ser
20 25 30

Tyr Ile Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Thr Ser Thr 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 Lys Tyr Gly Ser Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 719
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 719

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
 20 25 30
 Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Phe Ser Thr Ala
 50 55 60
 Leu Glu Ser Arg Leu Thr Ile Ser Thr Asp Thr Ser Lys Ser Gln Met
 65 70 75 80
 Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
 100 105 110
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
 130 135 140
 Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
 145 150 155 160
 Ser Cys Arg Thr Ser Gln Thr Val Thr Asn Ser Tyr Ile Ala Trp Tyr
 165 170 175
 Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Thr Ser
 180 185 190
 Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
 195 200 205
 Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
 210 215 220
 Val Tyr Tyr Cys Gln Lys Tyr Gly Ser Ser Pro Leu Thr Phe Gly Gly
 225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 720
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 720

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Phe Ser Thr Ala
50 55 60

Leu Glu Ser Arg Leu Thr Ile Ser Thr Asp Thr Ser Lys Ser Gln Met
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
145 150 155 160

Ser Cys Arg Thr Ser Gln Thr Val Thr Asn Ser Tyr Ile Ala Trp Tyr
165 170 175

Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Thr Ser
180 185 190

Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Gln Lys Tyr Gly Ser Ser Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Leu 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> 721
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 721

Asn Val Arg Met Gly Val Ser
 1 5

<210> 722
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 722

His	Ile	Ser	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Arg	Ser
1				5					10					15	

<210> 723

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 723

Met	Pro	Gly	Asp	Ser	Asn	Thr	Trp	Arg	Gly	Phe	Phe	Asp	Tyr
1				5					10				

<210> 724

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 724

Arg	Thr	Ser	Gln	Ser	Val	Asn	Asn	Asn	Leu	Ala
1				5					10	

<210> 725

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 725

Gly	Ala	Ser	Thr	Arg	Ala	Thr
1				5		

<210> 726

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 726

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 727
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 727

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Ser Thr 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 Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 728
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 728

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Gln Ser Val Asn Asn Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 729
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 729

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Ser Thr 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 Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
145 150 155 160

Ser Cys Arg Thr Ser Gln Ser Val Asn Asn Asn Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr
180 185 190

Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 730
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 730

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Ser Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Ser Thr 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 Met Pro Gly Asp Ser Asn Thr Trp Arg Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
145 150 155 160

Ser Cys Arg Thr Ser Gln Ser Val Asn Asn Asn Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr
180 185 190

Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 731
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 731

Asn Val Arg Met Gly Val Ser
 1 5

<210> 732
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 732

His	Ile	Phe	Ser	Asn	Asp	Glu	Lys	Ser	Tyr	Ser	Thr	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 733

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 733

Met	Pro	Glu	Tyr	Ser	Ser	Gly	Trp	Ser	Gly	Ala	Phe	Asp	Ile
1				5					10				

<210> 734

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 734

Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asp	Asp	Leu	Gly
1				5					10	

<210> 735

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 735

Gly	Ala	Ser	Thr	Leu	Gln	Ser
1				5		

<210> 736

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 736

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 737

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 737

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 Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 738

<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 738

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Gly Ala Ser Thr 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 Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 739
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 739

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 Arg Asn Val
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Asn Ala Pro Lys Arg Leu Ile Tyr Gly Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Arg Leu Glu Ile Lys
245

<210> 740
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 740

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 Arg Asn Val
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Asn Ala Pro Lys Arg Leu Ile Tyr Gly Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 741
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 741

Asn Ala Arg Met Gly Val Ser
 1 5

<210> 742
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 742

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 743

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 743

Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp Tyr
1 5 10

<210> 744

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 744

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Tyr
1 5 10 15

<210> 745

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 745

Glu Val Ser Asn Arg Phe Ser
1 5

<210> 746

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 746

Met Gln Ala Leu Gln Thr Pro Leu Thr
1 5

<210> 747

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 747

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Arg 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 748

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 748

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 Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr 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 Met Gln Ala
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 749

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 749

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Arg 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Val Met Thr
130 135 140

Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
145 150 155 160

Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
165 170 175

Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile
180 185 190

Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
210 215 220

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 750
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 750

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Arg 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Val Met Thr
 130 135 140

Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
 145 150 155 160

Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
 165 170 175

Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile
180 185 190

Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
210 215 220

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 751
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 751

Ser Tyr Gly Met His
1 5

<210> 752
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 752

Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Glu	Phe	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 753
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 753

Gly	Gly	Glu	Ile	Thr	Met	Val	Arg	Gly	Val	Ile	Gly	Tyr	Tyr	Tyr	Tyr
1				5					10					15	

Gly	Met	Asp	Val
			20

<210> 754
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 754

Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn
1				5					10	

<210> 755
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 755

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 756
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 756

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 757
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 757

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 758
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 758

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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 759
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 759

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
 100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
 225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 760
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 760

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
 100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
 225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
 245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
 275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
 305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
 325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
 340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 761
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 761

Ser Tyr Gly Met His
1 5

<210> 762
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 762

Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 763
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 763

Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 764
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 764

Arg Ala Ser Gln Gly Val Arg Asn Asn Leu Val
1 5 10

<210> 765
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 765

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 766

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 766

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 767

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 767

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 768
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 768

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Asn Asn
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 769
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 769

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
 100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 145 150 155 160

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Asn Asn
 165 170 175

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
180 185 190

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 770
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 770

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
145 150 155 160

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Asn Asn
165 170 175

Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
180 185 190

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 771
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 771

Ser Tyr Gly Met His
1 5

<210> 772

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 772

Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 773

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 773

Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 774

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 774

Arg Thr Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 775

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 775

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 776

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 776

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 777

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 777

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 778
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 778

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 Thr 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 779
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 779

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
 165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
 225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
 245 250

<210> 780
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 780

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 781
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 781

Ser Tyr Gly Met His
1 5

<210> 782
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 782

Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 783
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 783

Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 784
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 784

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 785
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 785

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 786
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 786

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 787
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 787

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 788
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 788

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asn 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 789
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 789

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145 150 155 160

Asn Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
245 250

<210> 790
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 790

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145 150 155 160

Asn Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 791
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 791

Ser Tyr Gly Met His
1 5

<210> 792
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 792

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 793
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 793

Ser Tyr Gly Met Asp Val
1 5

<210> 794

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 794

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 795

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 795

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 796

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 796

Gln Gln Ala Asn Ser Phe Pro Trp Thr
1 5

<210> 797

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 797

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 798

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 798

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala 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 Ala Asn Ser Phe Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 799
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 799

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser
130 135 140

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser
145 150 155 160

Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
165 170 175

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
180 185 190

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
195 200 205

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe
210 215 220

Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225 230 235

<210> 800
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 800

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser
130 135 140

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser
145 150 155 160

Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
165 170 175

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
180 185 190

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
195 200 205

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe
210 215 220

Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly
225 230 235 240

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
245 250 255

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
260 265 270

Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
275 280 285

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
290 295 300

Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
305 310 315 320

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
325 330 335

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
340 345 350

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
355 360 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
370 375 380

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
385 390 395 400

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
405 410 415

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
420 425 430

Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser
435 440 445

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
450 455 460

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg
 465 470 475 480

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490

<210> 801
 <211> 993
 <212> PRT
 <213> Homo sapiens

<400> 801

Met Pro Ala Leu Ala Arg Asp Gly Gly Gln Leu Pro Leu Leu Val Val
 1 5 10 15

Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
 20 25 30

Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
 35 40 45

Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
 50 55 60

Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
 65 70 75 80

Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
 85 90 95

Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
 100 105 110

Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
 115 120 125

Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
 130 135 140

Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile

145		150		155		160									
Arg	Asn	Thr	Leu	Leu	Tyr	Thr	Leu	Arg	Arg	Pro	Tyr	Phe	Arg	Lys	Met
			165						170					175	
Glu	Asn	Gln	Asp	Ala	Leu	Val	Cys	Ile	Ser	Glu	Ser	Val	Pro	Glu	Pro
			180					185					190		
Ile	Val	Glu	Trp	Val	Leu	Cys	Asp	Ser	Gln	Gly	Glu	Ser	Cys	Lys	Glu
		195					200					205			
Glu	Ser	Pro	Ala	Val	Val	Lys	Lys	Glu	Glu	Lys	Val	Leu	His	Glu	Leu
	210					215					220				
Phe	Gly	Thr	Asp	Ile	Arg	Cys	Cys	Ala	Arg	Asn	Glu	Leu	Gly	Arg	Glu
225					230					235					240
Cys	Thr	Arg	Leu	Phe	Thr	Ile	Asp	Leu	Asn	Gln	Thr	Pro	Gln	Thr	Thr
			245						250					255	
Leu	Pro	Gln	Leu	Phe	Leu	Lys	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys
		260						265					270		
Lys	Ala	Val	His	Val	Asn	His	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu
	275						280					285			
Asn	Lys	Ala	Leu	Glu	Glu	Gly	Asn	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser
	290					295					300				
Thr	Asn	Arg	Thr	Met	Ile	Arg	Ile	Leu	Phe	Ala	Phe	Val	Ser	Ser	Val
305				310						315					320
Ala	Arg	Asn	Asp	Thr	Gly	Tyr	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro
			325						330					335	
Ser	Gln	Ser	Ala	Leu	Val	Thr	Ile	Val	Glu	Lys	Gly	Phe	Ile	Asn	Ala
		340						345					350		
Thr	Asn	Ser	Ser	Glu	Asp	Tyr	Glu	Ile	Asp	Gln	Tyr	Glu	Glu	Phe	Cys
	355						360					365			

Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
 370 375 380

Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly
 385 390 395 400

Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
 405 410 415

Ile Phe His Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr
 420 425 430

Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
 435 440 445

Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp
 450 455 460

Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu
 465 470 475 480

Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
 485 490 495

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val
 500 505 510

Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
 515 520 525

Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Phe
 530 535 540

Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Leu
 545 550 555 560

Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu
 565 570 575

Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr Val

580	585	590
Asp Phe Arg Glu Tyr Glu Tyr	Asp Leu Lys Trp Glu Phe Pro Arg Glu	
595	600	605
Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val		
610	615	620
Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln		
625	630	635
Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Ser Glu Arg Glu		
645	650	655
Ala Leu Met Ser Glu Leu Lys Met Met Thr Gln Leu Gly Ser His Glu		
660	665	670
Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Ile Tyr		
675	680	685
Leu Ile Phe Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu Arg		
690	695	700
Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu		
705	710	715
His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His Pro Asn Ser Ser		
725	730	735
Met Pro Gly Ser Arg Glu Val Gln Ile His Pro Asp Ser Asp Gln Ile		
740	745	750
Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp Glu Ile Glu Tyr		
755	760	765
Glu Asn Gln Lys Arg Leu Glu Glu Glu Glu Asp Leu Asn Val Leu Thr		
770	775	780
Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu		
785	790	795
		800

Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn
805 810 815

Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu
820 825 830

Ala Arg Asp Ile Met Ser Asp Ser Asn Tyr Val Val Arg Gly Asn Ala
835 840 845

Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile
850 855 860

Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu
865 870 875 880

Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala
885 890 895

Asn Phe Tyr Lys Leu Ile Gln Asn Gly Phe Lys Met Asp Gln Pro Phe
900 905 910

Tyr Ala Thr Glu Glu Ile Tyr Ile Ile Met Gln Ser Cys Trp Ala Phe
915 920 925

Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly
930 935 940

Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
945 950 955 960

Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg Arg Pro Phe Ser
965 970 975

Arg Glu Met Asp Leu Gly Leu Leu Ser Pro Gln Ala Gln Val Glu Asp
980 985 990

Ser

<210> 802

<211> 993
 <212> PRT
 <213> Macaca fascicularis

<400> 802

Met Pro Ala Leu Ala Arg Gly Gly Gly Arg Leu Pro Leu Leu Val Val
 1 5 10 15

Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
 20 25 30

Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
 35 40 45

Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
 50 55 60

Cys Ala Leu Arg Pro Gln Ser Ala Gly Thr Val Tyr Glu Ala Ala Thr
 65 70 75 80

Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
 85 90 95

Thr Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
 100 105 110

Asn Cys Gln Pro His Phe Asp Val Gln Asn Arg Gly Val Val Ser Met
 115 120 125

Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
 130 135 140

Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
 145 150 155 160

Arg Asn Thr Leu Leu Phe Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
 165 170 175

Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
 180 185 190

Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
195 200 205

Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
210 215 220

Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
225 230 235 240

Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr
245 250 255

Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys
260 265 270

Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu
275 280 285

Asn Lys Ala Leu Glu Glu Gly Ser Tyr Phe Glu Met Ser Thr Tyr Ser
290 295 300

Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val
305 310 315 320

Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro
325 330 335

Ser Gln Ser Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala
340 345 350

Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
355 360 365

Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
370 375 380

Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asp Gly
385 390 395 400

Tyr Ser Val Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
405 410 415

Ile Phe His Ala Glu Asn Gly Asp Ala Gln Phe Thr Lys Met Phe Thr
420 425 430

Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
435 440 445

Gln Ala Ser Cys Ser Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp
450 455 460

Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Asp Ile Pro Glu
465 470 475 480

Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
485 490 495

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Met Lys Gly Phe Leu Val
500 505 510

Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
515 520 525

Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Ser Ile Ser Phe
530 535 540

Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Met
545 550 555 560

Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu
565 570 575

Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr Val
580 585 590

Asp Phe Arg Asp Cys Asp Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu
595 600 605

Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val
610 615 620

Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln
625 630 635 640

Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Ser Glu Arg Glu
645 650 655

Ala Leu Met Ser Glu Leu Lys Met Met Thr Gln Leu Gly Ser His Glu
660 665 670

Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Ile Tyr
675 680 685

Leu Ile Phe Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu Arg
690 695 700

Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu
705 710 715 720

His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His Pro Asn Ser Ser
725 730 735

Met Pro Gly Ser Arg Asp Val Gln Ile His Pro His Ser Asp Pro Ile
740 745 750

Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp Glu Ile Glu Tyr
755 760 765

Glu Asn Gln Lys Arg Leu Glu Glu Glu Glu Asp Leu Asn Val Leu Thr
770 775 780

Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu
785 790 795 800

Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn
805 810 815

Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu
820 825 830

Ala Arg Asp Ile Met Ser Asp Ser Asn Tyr Val Val Arg Gly Asn Ala
835 840 845

Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile
850 855 860

Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu
865 870 875 880

Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala
885 890 895

Asn Phe Tyr Lys Leu Ile Arg Asn Gly Phe Lys Met Asp Gln Pro Phe
900 905 910

Tyr Ala Thr Glu Glu Ile Tyr Ile Ile Met Gln Ser Cys Trp Ala Phe
915 920 925

Asp Ser Arg Lys Arg Pro Ser Phe Pro His Leu Thr Ser Phe Leu Gly
930 935 940

Cys Gln Leu Glu Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
945 950 955 960

Arg Val Ser Glu Arg Pro His Ile Tyr Gln Asn Arg Arg Pro Phe Ser
965 970 975

Arg Glu Met Asp Ser Gly Pro Leu Ser Pro Lys Ala Gln Val Glu Asp
980 985 990

Ser

<210> 803
<211> 993
<212> PRT
<213> Homo sapiens

<400> 803

Met Pro Ala Leu Ala Arg Asp Gly Gly Gln Leu Pro Leu Leu Val Val
1 5 10 15

Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val

20

25

30

Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
 35 40 45

Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
 50 55 60

Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
 65 70 75 80

Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
 85 90 95

Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
 100 105 110

Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
 115 120 125

Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
 130 135 140

Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
 145 150 155 160

Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
 165 170 175

Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
 180 185 190

Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
 195 200 205

Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
 210 215 220

Phe Gly Met Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
 225 230 235 240

Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr
245 250 255

Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys
260 265 270

Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu
275 280 285

Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser
290 295 300

Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val
305 310 315 320

Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro
325 330 335

Ser Gln Ser Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala
340 345 350

Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
355 360 365

Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
370 375 380

Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly
385 390 395 400

Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
405 410 415

Ile Phe His Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr
420 425 430

Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
435 440 445

Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp

450

455

460

Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu
 465 470 475 480

Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
 485 490 495

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val
 500 505 510

Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
 515 520 525

Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Phe
 530 535 540

Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Leu
 545 550 555 560

Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu
 565 570 575

Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr Val
 580 585 590

Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu
 595 600 605

Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val
 610 615 620

Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln
 625 630 635 640

Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Ser Glu Arg Glu
 645 650 655

Ala Leu Met Ser Glu Leu Lys Met Met Thr Gln Leu Gly Ser His Glu
 660 665 670

Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Ile Tyr
675 680 685

Leu Ile Phe Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu Arg
690 695 700

Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu
705 710 715 720

His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His Pro Asn Ser Ser
725 730 735

Met Pro Gly Ser Arg Glu Val Gln Ile His Pro Asp Ser Asp Gln Ile
740 745 750

Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp Glu Ile Glu Tyr
755 760 765

Glu Asn Gln Lys Arg Leu Glu Glu Glu Glu Asp Leu Asn Val Leu Thr
770 775 780

Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu
785 790 795 800

Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn
805 810 815

Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu
820 825 830

Ala Arg Asp Ile Met Ser Asp Ser Asn Tyr Val Val Arg Gly Asn Ala
835 840 845

Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile
850 855 860

Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu
865 870 875 880

Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala

885

890

895

Asn Phe Tyr Lys Leu Ile Gln Asn Gly Phe Lys Met Asp Gln Pro Phe
 900 905 910

Tyr Ala Thr Glu Glu Ile Tyr Ile Ile Met Gln Ser Cys Trp Ala Phe
 915 920 925

Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly
 930 935 940

Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
 945 950 955 960

Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg Arg Pro Phe Ser
 965 970 975

Arg Glu Met Asp Leu Gly Leu Leu Ser Pro Gln Ala Gln Val Glu Asp
 980 985 990

Ser

<210> 804
 <211> 1013
 <212> PRT
 <213> Homo sapiens

<400> 804

Met Pro Ala Leu Ala Arg Asp Gly Gly Gln Leu Pro Leu Leu Val Val
 1 5 10 15

Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
 20 25 30

Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
 35 40 45

Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
 50 55 60

Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
65 70 75 80

Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
85 90 95

Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
100 105 110

Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
115 120 125

Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
130 135 140

Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
145 150 155 160

Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
165 170 175

Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
180 185 190

Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
195 200 205

Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
210 215 220

Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
225 230 235 240

Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr
245 250 255

Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys
260 265 270

Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu
275 280 285

Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser
 290 295 300

Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val
 305 310 315 320

Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro
 325 330 335

Ser Gln Ser Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala
 340 345 350

Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
 355 360 365

Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
 370 375 380

Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly
 385 390 395 400

Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
 405 410 415

Ile Phe His Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr
 420 425 430

Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
 435 440 445

Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp
 450 455 460

Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu
 465 470 475 480

Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
 485 490 495

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val
500 505 510

Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
515 520 525

Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Phe
530 535 540

Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Leu
545 550 555 560

Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu
565 570 575

Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr Val
580 585 590

Asp Phe Arg Glu Tyr Glu Tyr Ser Ser Ser Asp Asn Glu Tyr Phe Tyr
595 600 605

Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Asp Leu Lys Trp Glu
610 615 620

Phe Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala
625 630 635 640

Phe Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly
645 650 655

Val Ser Ile Gln Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser
660 665 670

Ser Glu Arg Glu Ala Leu Met Ser Glu Leu Lys Met Met Thr Gln Leu
675 680 685

Gly Ser His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser
690 695 700

Gly Pro Ile Tyr Leu Ile Phe Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
705 710 715 720

Asn Tyr Leu Arg Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu
725 730 735

Ile Phe Lys Glu His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His
740 745 750

Pro Asn Ser Ser Met Pro Gly Ser Arg Glu Val Gln Ile His Pro Asp
755 760 765

Ser Asp Gln Ile Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp
770 775 780

Glu Ile Glu Tyr Glu Asn Gln Lys Arg Leu Glu Glu Glu Glu Asp Leu
785 790 795 800

Asn Val Leu Thr Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala
805 810 815

Lys Gly Met Glu Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu
820 825 830

Ala Ala Arg Asn Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys
835 840 845

Asp Phe Gly Leu Ala Arg Asp Ile Met Ser Asp Ser Asn Tyr Val Val
850 855 860

Arg Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu
865 870 875 880

Phe Glu Gly Ile Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile
885 890 895

Leu Leu Trp Glu Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile
900 905 910

Pro Val Asp Ala Asn Phe Tyr Lys Leu Ile Gln Asn Gly Phe Lys Met
915 920 925

Asp Gln Pro Phe Tyr Ala Thr Glu Glu Ile Tyr Ile Ile Met Gln Ser
 930 935 940

Cys Trp Ala Phe Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr
 945 950 955 960

Ser Phe Leu Gly Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln
 965 970 975

Asn Val Asp Gly Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg
 980 985 990

Arg Pro Phe Ser Arg Glu Met Asp Leu Gly Leu Leu Ser Pro Gln Ala
 995 1000 1005

Gln Val Glu Asp Ser
 1010

<210> 805
 <211> 976
 <212> PRT
 <213> Homo sapiens

<400> 805

Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu Leu
 1 5 10 15

Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
 20 25 30

Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
 35 40 45

Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
 50 55 60

Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn
 65 70 75 80

Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr Asn Thr Gly Lys Tyr Thr
 85 90 95

Cys Thr Asn Lys His Gly Leu Ser Asn Ser Ile Tyr Val Phe Val Arg
100 105 110

Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Ser Leu Tyr Gly Lys Glu
115 120 125

Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Thr Asp Pro Glu Val Thr
130 135 140

Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pro Leu Pro Lys Asp Leu
145 150 155 160

Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Met Ile Lys Ser Val Lys
165 170 175

Arg Ala Tyr His Arg Leu Cys Leu His Cys Ser Val Asp Gln Glu Gly
180 185 190

Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Lys Val Arg Pro Ala Phe
195 200 205

Lys Ala Val Pro Val Val Ser Val Ser Lys Ala Ser Tyr Leu Leu Arg
210 215 220

Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Ile Lys Asp Val Ser Ser
225 230 235 240

Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Ser Gln Thr Lys Leu Gln
245 250 255

Glu Lys Tyr Asn Ser Trp His His Gly Asp Phe Asn Tyr Glu Arg Gln
260 265 270

Ala Thr Leu Thr Ile Ser Ser Ala Arg Val Asn Asp Ser Gly Val Phe
275 280 285

Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Ala Asn Val Thr Thr Thr
290 295 300

Leu Glu Val Val Asp Lys Gly Phe Ile Asn Ile Phe Pro Met Ile Asn

305		310		315		320
Thr Thr Val Phe	Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu					
	325			330		335
Tyr Glu Ala Phe	Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn					
	340			345		350
Arg Thr Phe Thr	Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu					
	355			360		365
Ser Asn Ile Arg	Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly					
	370			375		380
Thr Glu Gly Gly	Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn					
385				390		400
Ala Ala Ile Ala	Phe Asn Val Tyr Val Asn Thr Lys Pro Glu Ile Leu					
	405			410		415
Thr Tyr Asp Arg	Leu Val Asn Gly Met Leu Gln Cys Val Ala Ala Gly					
	420			425		430
Phe Pro Glu Pro	Thr Ile Asp Trp Tyr Phe Cys Pro Gly Thr Glu Gln					
	435			440		445
Arg Cys Ser Ala	Ser Val Leu Pro Val Asp Val Gln Thr Leu Asn Ser					
	450			455		460
Ser Gly Pro Pro	Phe Gly Lys Leu Val Val Gln Ser Ser Ile Asp Ser					
465				470		480
Ser Ala Phe Lys	His Asn Gly Thr Val Glu Cys Lys Ala Tyr Asn Asp					
	485			490		495
Val Gly Lys Thr	Ser Ala Tyr Phe Asn Phe Ala Phe Lys Gly Asn Asn					
	500			505		510
Lys Glu Gln Ile	His Pro His Thr Leu Phe Thr Pro Leu Leu Ile Gly					
	515			520		525

Phe Val Ile Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr
530 535 540

Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln Trp Lys Val Val
545 550 555 560

Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu
565 570 575

Pro Tyr Asp His Lys Trp Glu Phe Pro Arg Asn Arg Leu Ser Phe Gly
580 585 590

Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Val Val Glu Ala Thr Ala
595 600 605

Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met
610 615 620

Leu Lys Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu
625 630 635 640

Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val Asn Leu
645 650 655

Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Leu Val Ile Thr Glu Tyr
660 665 670

Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu Arg Arg Lys Arg Asp Ser
675 680 685

Phe Ile Cys Ser Lys Gln Glu Asp His Ala Glu Ala Ala Leu Tyr Lys
690 695 700

Asn Leu Leu His Ser Lys Glu Ser Ser Cys Ser Asp Ser Thr Asn Glu
705 710 715 720

Tyr Met Asp Met Lys Pro Gly Val Ser Tyr Val Val Pro Thr Lys Ala
725 730 735

Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile Glu Arg Asp Val

740

745

750

Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu Asp Leu Glu Asp
755 760 765

Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gly Met Ala Phe Leu Ala
770 775 780

Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu
785 790 795 800

Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp
805 810 815

Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro
820 825 830

Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Cys Val Tyr Thr Phe
835 840 845

Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Leu Trp Glu Leu Phe Ser
850 855 860

Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Val Asp Ser Lys Phe Tyr
865 870 875 880

Lys Met Ile Lys Glu Gly Phe Arg Met Leu Ser Pro Glu His Ala Pro
885 890 895

Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Trp Asp Ala Asp Pro Leu
900 905 910

Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Leu Ile Glu Lys Gln Ile
915 920 925

Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Leu Ala Asn Cys Ser Pro
930 935 940

Asn Arg Gln Lys Pro Val Val Asp His Ser Val Arg Ile Asn Ser Val
945 950 955 960

Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu Leu Val His Asp Asp Val
965 970 975

<210> 806
<211> 972
<212> PRT
<213> Homo sapiens

<400> 806

Met Gly Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His
1 5 10 15

Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
20 25 30

Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
35 40 45

Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
50 55 60

Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly
65 70 75 80

Thr Tyr Arg Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala
85 90 95

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
100 105 110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
115 120 125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
130 135 140

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145 150 155 160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
165 170 175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
180 185 190

Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
195 200 205

Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
210 215 220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225 230 235 240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
245 250 255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
260 265 270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
275 280 285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
290 295 300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305 310 315 320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
325 330 335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
340 345 350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
355 360 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
370 375 380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
 385 390 395 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
 405 410 415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
 420 425 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
 435 440 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
 450 455 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
 465 470 475 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
 485 490 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
 500 505 510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
 515 520 525

Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
 530 535 540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
 545 550 555 560

Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
 565 570 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
 580 585 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
 595 600 605

Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
610 615 620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625 630 635 640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
645 650 655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
660 665 670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
675 680 685

Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
690 695 700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705 710 715 720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
725 730 735

Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
740 745 750

Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
755 760 765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
770 775 780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785 790 795 800

Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
805 810 815

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
820 825 830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
835 840 845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
850 855 860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865 870 875 880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
885 890 895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
900 905 910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
915 920 925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
930 935 940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945 950 955 960

Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
965 970

<210> 807
<211> 1089
<212> PRT
<213> Homo sapiens

<400> 807

Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr
1 5 10 15

Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro
20 25 30

Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg
35 40 45

Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu
50 55 60

Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu
65 70 75 80

Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly
85 90 95

Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
100 105 110

Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
115 120 125

Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
130 135 140

Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
145 150 155 160

Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln
165 170 175

Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
180 185 190

Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
195 200 205

Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
210 215 220

Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
225 230 235 240

Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys

245	250	255
Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val 260	265	270
Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr 275	280	285
Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys 290	295	300
Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr 305	310	315
Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val 325	330	335
Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn 340	345	350
Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu 355	360	365
Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala 370	375	380
Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp 385	390	395
Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser 405	410	415
Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr 420	425	430
Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met 435	440	445
Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile 450	455	460

Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
465 470 475 480

Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
485 490 495

Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
500 505 510

Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
515 520 525

Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val
530 535 540

Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
545 550 555 560

Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
565 570 575

Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
580 585 590

Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
595 600 605

Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
610 615 620

Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
625 630 635 640

Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
645 650 655

Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
660 665 670

Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys

675	680	685
Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu		
690	695	700
Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr		
705	710	715 720
Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln		
	725	730 735
Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser		
	740	745 750
Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr		
	755	760 765
Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp		
	770	775 780
Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe Thr Tyr		
785	790	795 800
Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His		
	805	810 815
Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val		
	820	825 830
Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn		
	835	840 845
Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro		
	850	855 860
Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser		
865	870	875 880
Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr		
	885	890 895

Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
900 905 910

Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
915 920 925

Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
930 935 940

His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys
945 950 955 960

Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
965 970 975

Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
980 985 990

Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
995 1000 1005

Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro
1010 1015 1020

Asp Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg Asn
1025 1030 1035

Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly
1040 1045 1050

Ser Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu
1055 1060 1065

Asp Ile Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu
1070 1075 1080

Val Glu Asp Ser Phe Leu
1085

<210> 808

<211> 355
 <212> PRT
 <213> Homo sapiens

<400> 808

Met Gly Val Cys Gly Tyr Leu Phe Leu Pro Trp Lys Cys Leu Val Val
 1 5 10 15

Val Ser Leu Arg Leu Leu Phe Leu Val Pro Thr Gly Val Pro Val Arg
 20 25 30

Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val Thr Val Arg
 35 40 45

Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp Asn Arg Val Thr
 50 55 60

Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp
 65 70 75 80

Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr
 85 90 95

Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
 100 105 110

Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
 115 120 125

His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
 130 135 140

Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
 145 150 155 160

Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
 165 170 175

Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
 180 185 190

Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
195 200 205

Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
210 215 220

Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
225 230 235 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
245 250 255

Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu
260 265 270

Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
275 280 285

Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
290 295 300

Asn Ala Ser Ile Met Leu Phe Glu Val Lys Thr Thr Ala Leu Thr Pro
305 310 315 320

Trp Lys Gly Pro Gly Ala Val Ser Glu Val Ser Asn Gly Thr Ser Arg
325 330 335

Arg Ala Gly Cys Val Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu
340 345 350

Leu Lys Phe
355

<210> 809
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 809

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 Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln
35 40 45

Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro Ile Val Glu
50 55 60

Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu Glu Ser Pro
65 70 75 80

Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Thr
85 90 95

Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu Cys Thr Arg
100 105 110

Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr Leu Pro Gln
115 120 125

Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys Lys Ala Val
130 135 140

His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu Asn Lys Ala
145 150 155 160

Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser Thr Asn Arg
165 170 175

Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val Ala Arg Asn
180 185 190

Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro Ser Gln Ser
195 200 205

Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala Thr Asn Ser
210 215 220

Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys Phe Ser Val
 225 230 235 240

Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr Phe Ser Arg
 245 250 255

Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly Tyr Ser Ile
 260 265 270

Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr Ile Phe His
 275 280 285

Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr Leu Asn Ile
 290 295 300

Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser Gln Ala Ser
 305 310 315 320

Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys Cys
 325 330 335

Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu Gly Val Trp
 340 345 350

Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val Ser Ser Ser
 355 360 365

Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val Lys Cys Cys
 370 375 380

Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu Leu Asn Ser
 385 390 395 400

Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Ser Gly Gly Gly
 405 410 415

Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala
 420 425 430

Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met
 435 440 445

Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg
 450 455 460

Glu Leu Asn Ala
 465

<210> 810
 <211> 390
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 810

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 Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr Leu
 35 40 45

Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys Lys
 50 55 60

Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu Asn
 65 70 75 80

Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser Thr
 85 90 95

Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val Ala
 100 105 110

Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro Ser
 115 120 125

Gln Ser Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala Thr
130 135 140

Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys Phe
145 150 155 160

Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr Phe
165 170 175

Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly Tyr
180 185 190

Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr Ile
195 200 205

Phe His Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr Leu
210 215 220

Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser Gln
225 230 235 240

Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys
245 250 255

Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu Gly
260 265 270

Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val Ser
275 280 285

Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val Lys
290 295 300

Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu Leu
305 310 315 320

Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Ser Gly
325 330 335

Gly Gly Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val Val Val
340 345 350

Ile Ala Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg Lys Lys
 355 360 365

Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly Glu Met
 370 375 380

His Arg Glu Leu Asn Ala
 385 390

<210> 811
 <211> 287
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 811

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 Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu
 35 40 45

Ile Asp Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr
 50 55 60

Pro Gln Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys
 65 70 75 80

Glu Gln Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn
 85 90 95

His Lys His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp
 100 105 110

Ala Gln Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln
 115 120 125

Val Leu Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly
130 135 140

Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro
145 150 155 160

Asn Cys Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn
165 170 175

Arg Lys Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser
180 185 190

Glu Ala Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu
195 200 205

Gly Thr Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro
210 215 220

Phe Ile Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly
225 230 235 240

Val Ile Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile
245 250 255

Val Val Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys
260 265 270

Ala Glu Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
275 280 285

<210> 812
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 812

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 Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala
35 40 45

Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr
50 55 60

Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr
65 70 75 80

Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp
85 90 95

Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu
100 105 110

Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile
115 120 125

Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser
130 135 140

Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val
145 150 155 160

Val Val Ile Ala Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg
165 170 175

Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly
180 185 190

Glu Met His Arg Glu Leu Asn Ala
195 200

<210> 813
<211> 543
<212> PRT
<213> Homo sapiens

<400> 813

Met Pro Ala Leu Ala Arg Asp Gly Gly Gln Leu Pro Leu Leu Val Val
1 5 10 15

Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
20 25 30

Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
35 40 45

Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
50 55 60

Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
65 70 75 80

Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
85 90 95

Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
100 105 110

Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
115 120 125

Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
130 135 140

Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
145 150 155 160

Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
165 170 175

Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
180 185 190

Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
195 200 205

Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
210 215 220

Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
225 230 235 240

Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr
245 250 255

Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys
260 265 270

Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu
275 280 285

Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser
290 295 300

Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val
305 310 315 320

Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro
325 330 335

Ser Gln Ser Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala
340 345 350

Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
355 360 365

Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
370 375 380

Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly
385 390 395 400

Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
405 410 415

Ile Phe His Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr

420

425

430

Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
 435 440 445

Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp
 450 455 460

Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu
 465 470 475 480

Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
 485 490 495

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val
 500 505 510

Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
 515 520 525

Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser
 530 535 540

<210> 814
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 814

Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu
 1 5 10 15

Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser
 20 25 30

Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val
 35 40 45

Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu
 50 55 60

Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val
65 70 75 80

Ser Ile Arg

<210> 815
<211> 78
<212> PRT
<213> Homo sapiens

<400> 815

Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu
1 5 10 15

Val Cys Ile Ser Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu
20 25 30

Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val
35 40 45

Lys Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg
50 55 60

Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu
65 70 75

<210> 816
<211> 101
<212> PRT
<213> Homo sapiens

<400> 816

Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu
1 5 10 15

Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys Lys Ala Val His
20 25 30

Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu
35 40 45

Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr
50 55 60

Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val Ala Arg Asn Asp
65 70 75 80

Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro Ser Gln Ser Ala
85 90 95

Leu Val Thr Ile Val
100

<210> 817
<211> 87
<212> PRT
<213> Homo sapiens

<400> 817

Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln
1 5 10 15

Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile
20 25 30

Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys
35 40 45

Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His
50 55 60

Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln Phe
65 70 75 80

Thr Lys Met Phe Thr Leu Asn
85

<210> 818
<211> 99
<212> PRT
<213> Homo sapiens

<400> 818

Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser Gln Ala
1 5 10 15

Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys
20 25 30

Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu Gly Val
35 40 45

Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val Ser Ser
50 55 60

Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val Lys Cys
65 70 75 80

Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu Leu Asn
85 90 95

Ser Pro Gly

<210> 819
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 819

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
1 5 10 15

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
20 25 30

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
35 40 45

Val Tyr Glu Ala
50

<210> 820
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 820

Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu
1 5 10 15

Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser
20 25 30

Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val
35 40 45

Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu
50 55 60

Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val
65 70 75 80

Ser Ile Arg Asn Thr Leu Leu Tyr Thr
85

<210> 821
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 821

Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val
1 5 10 15

Cys Ile Ser Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys
20 25 30

Asp Ser Gln Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys
35 40 45

Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys
50 55 60

Cys Ala Arg Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu
65 70 75

<210> 822
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 822

Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val
1 5 10 15

Cys Ile Ser Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys
20 25 30

Asp Ser Gln Gly Glu Ser Cys
35

<210> 823
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 823

Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His
1 5 10 15

Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly
20 25 30

Arg Glu Cys Thr Arg Leu
35

<210> 824
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 824

Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu
1 5 10 15

Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys Lys Ala Val His
20 25 30

Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu
35 40 45

Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr
50 55 60

Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val Ala Arg Asn Asp
65 70 75 80

Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro Ser Gln Ser Ala
85 90 95

Leu Val Thr Ile Val
100

<210> 825
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 825

Glu Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile
1 5 10 15

Asp Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro
20 25 30

Gln Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu
35 40 45

Gln Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His
50 55 60

Lys His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala
65 70 75 80

Gln Phe Thr Lys Met Phe Thr Leu Asn
85

<210> 826
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 826

Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser Gln Ala
1 5 10 15

Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys
20 25 30

Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu Gly Val
35 40 45

Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val Ser Ser
50 55 60

Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val Lys Cys
65 70 75 80

Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu Leu Asn
85 90 95

Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser
100 105

<210> 827
 <211> 589
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 827

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
 1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser His Glu Asn
 20 25 30

Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met Val Arg Gly
 35 40 45

Ser Pro Glu Asp Leu Gln Cys Ala Pro Arg Arg Gln Ser Glu Gly Thr
 50 55 60

Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr
 65 70 75 80

Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val
 85 90 95

Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn
 100 105 110

Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala
 115 120 125

Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile
 130 135 140

Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg
 145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val Cys Ile Ser
 165 170 175

Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys Asp Ser Gln
180 185 190

Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu
195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
210 215 220

Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn
225 230 235 240

Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His Gly Phe Gly
260 265 270

Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe
275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Phe
290 295 300

Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
305 310 315 320

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Val Glu
325 330 335

Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp
340 345 350

Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln
355 360 365

Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln
370 375 380

Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys
385 390 395 400

His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln
405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln Val Leu
420 425 430

Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
450 455 460

Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys
465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
485 490 495

Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr
500 505 510

Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
580 585

<210> 828

<211> 589

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 828

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
20 25 30

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
35 40 45

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
50 55 60

Val Tyr Glu Ala Ala Thr Val Glu Val Ala Glu Ser Gly Ser Ile Thr
65 70 75 80

Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys Leu Trp Val
85 90 95

Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp Leu Gln Asn
100 105 110

Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu Thr Gln Ala
115 120 125

Gly Glu Tyr Leu Leu His Ile Gln Ser Glu Ala Ala Asn Tyr Thr Val
130 135 140

Leu Phe Thr Val Asn Val Arg Asp Thr Gln Leu Tyr Val Leu Arg Arg
145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val Cys Ile Ser
165 170 175

Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys Asp Ser Gln
180 185 190

Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu
195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
210 215 220

Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn
225 230 235 240

Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His Gly Phe Gly
260 265 270

Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe
275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Phe
290 295 300

Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
305 310 315 320

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Val Glu
325 330 335

Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp
340 345 350

Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln
355 360 365

Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln
370 375 380

Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys
385 390 395 400

His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln
405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln Val Leu
420 425 430

Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
450 455 460

Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys
465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
485 490 495

Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr
500 505 510

Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
580 585

<210> 829
<211> 608
<212> PRT
<213> artificial

<220>

<223> hu lsp V5xFlt3-E3muxEpC-pEFDHFR

<400> 829

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 Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn
35 40 45

His Lys Asn Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met
50 55 60

Val Ser Glu Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser
65 70 75 80

Ser Gly Thr Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala
85 90 95

Ser Ile Thr Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys
100 105 110

Leu Trp Val Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp
115 120 125

Leu Gln Asn Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu
130 135 140

Thr Gln Ala Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn
145 150 155 160

Tyr Thr Ile Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr
165 170 175

Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Leu
180 185 190

Cys Ile Ser Glu Gly Val Pro Glu Pro Thr Val Glu Trp Val Leu Cys
195 200 205

Ser Ser His Arg Glu Ser Cys Lys Glu Glu Gly Pro Ala Val Val Arg
210 215 220

Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys
225 230 235 240

Cys Ala Arg Asn Ala Leu Gly Arg Glu Cys Thr Lys Leu Phe Thr Ile
245 250 255

Asp Leu Asn Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys
260 265 270

Val Gly Glu Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His
275 280 285

Gly Phe Gly Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly
290 295 300

Asn Tyr Phe Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg
305 310 315 320

Ile Leu Phe Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr
325 330 335

Tyr Thr Cys Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr
340 345 350

Ile Val Glu Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr
355 360 365

Glu Ile Asp Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala
370 375 380

Tyr Pro Gln Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro
385 390 395 400

Cys Glu Gln Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys
405 410 415

Asn His Lys His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp
420 425 430

Asp Ala Gln Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro
435 440 445

Gln Val Leu Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp
450 455 460

Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser
465 470 475 480

Pro Asn Cys Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala
485 490 495

Asn Arg Lys Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met
500 505 510

Ser Glu Ala Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser
515 520 525

Leu Gly Thr Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe
530 535 540

Pro Phe Ile Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala
545 550 555 560

Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly
565 570 575

Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu
580 585 590

Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
595 600 605

<210> 830
<211> 589
<212> PRT
<213> artificial

<220>

<223> hu lsp V5xFlt3-E3AmuxEpC-pEFDHFR

<400> 830

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
20 25 30

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
35 40 45

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
50 55 60

Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr
65 70 75 80

Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val
85 90 95

Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn
100 105 110

Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala
115 120 125

Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile
130 135 140

Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg
145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Leu Cys Ile Ser
165 170 175

Glu Gly Val Pro Glu Pro Thr Val Glu Trp Val Leu Cys Ser Ser His
180 185 190

Arg Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu
195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
210 215 220

Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn
225 230 235 240

Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His Gly Phe Gly
260 265 270

Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe
275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Phe
290 295 300

Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
305 310 315 320

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Val Glu
325 330 335

Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp
340 345 350

Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln
355 360 365

Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln
370 375 380

Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys
385 390 395 400

His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln
405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln Val Leu
420 425 430

Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
450 455 460

Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys
465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
485 490 495

Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr
500 505 510

Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
580 585

<210> 831
<211> 589
<212> PRT
<213> artificial

<220>
<223> hu lsp V5xFlt3-E3BmuxEpC-pEFDHFR

<400> 831

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
 1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
 20 25 30

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
 35 40 45

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
 50 55 60

Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr
 65 70 75 80

Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val
 85 90 95

Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn
 100 105 110

Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala
 115 120 125

Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile
 130 135 140

Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg
 145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val Cys Ile Ser
 165 170 175

Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys Asp Ser Gln
 180 185 190

Gly Glu Ser Cys Lys Glu Glu Gly Pro Ala Val Val Arg Lys Glu Glu
 195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
 210 215 220

Asn Ala Leu Gly Arg Glu Cys Thr Lys Leu Phe Thr Ile Asp Leu Asn
 225 230 235 240

Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
 245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His Gly Phe Gly
 260 265 270

Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe
 275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Phe
 290 295 300

Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
 305 310 315 320

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Val Glu
 325 330 335

Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp
 340 345 350

Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln
 355 360 365

Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln
 370 375 380

Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys
 385 390 395 400

His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln
 405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln Val Leu
 420 425 430

Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
450 455 460

Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys
465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
485 490 495

Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr
500 505 510

Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
580 585

<210> 832
<211> 589
<212> PRT
<213> artificial

<220>
<223> hu lsp V5xF1t3-E4muxEpC-pEFDHFR

<400> 832

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
20 25 30

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
35 40 45

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
50 55 60

Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr
65 70 75 80

Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val
85 90 95

Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn
100 105 110

Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala
115 120 125

Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile
130 135 140

Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg
145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val Cys Ile Ser
165 170 175

Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys Asp Ser Gln
180 185 190

Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu
195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
210 215 220

Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn
225 230 235 240

Gln Ala Pro Gln Ser Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Ile His Val Asn His Gly Phe Gly
260 265 270

Leu Thr Trp Glu Leu Glu Asp Lys Ala Leu Glu Glu Gly Ser Tyr Phe
275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Leu
290 295 300

Ala Phe Val Ser Ser Val Gly Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
305 310 315 320 325

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Leu Glu
325 330 335

Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp
340 345 350

Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln
355 360 365

Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln
370 375 380

Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys
385 390 395 400

His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln
405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln Val Leu
420 425 430

Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
 450 455 460

Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys
 465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
 485 490 495

Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr
 500 505 510

Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
 515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
 530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
 545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
 565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
 580 585

<210> 833
 <211> 589
 <212> PRT
 <213> artificial

<220>
 <223> hu lsp V5xFlt3-E5muxEpC-pEFDHFR

<400> 833

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
 1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
 20 25 30

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
35 40 45

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
50 55 60

Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr
65 70 75 80

Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val
85 90 95

Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn
100 105 110

Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala
115 120 125

Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile
130 135 140

Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg
145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val Cys Ile Ser
165 170 175

Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys Asp Ser Gln
180 185 190

Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu
195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
210 215 220

Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn
225 230 235 240

Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His Gly Phe Gly
260 265 270

Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe
275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Phe
290 295 300

Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
305 310 315 320

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Val Glu
325 330 335

Lys Gly Phe Ile Asn Ala Thr Ser Ser Gln Glu Glu Tyr Glu Ile Asp
340 345 350

Pro Tyr Glu Lys Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Arg
355 360 365

Ile Arg Cys Thr Trp Ile Phe Ser Gln Ala Ser Phe Pro Cys Glu Gln
370 375 380

Arg Gly Leu Glu Asp Gly Tyr Ser Ile Ser Lys Phe Cys Asp His Lys
385 390 395 400

Asn Lys Pro Gly Glu Tyr Ile Phe Tyr Ala Glu Asn Asp Asp Ala Gln
405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Arg Lys Pro Gln Val Leu
420 425 430

Ala Glu Ala Ser Ala Ser Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
450 455 460

Thr Glu Glu Ile Thr Glu Gly Val Trp Asn Arg Lys Ala Asn Arg Lys
 465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
 485 490 495

Ile Lys Gly Phe Leu Val Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr
 500 505 510

Ser Cys Glu Thr Ile Leu Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
 515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
 530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
 545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
 565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
 580 585

<210> 834
 <211> 589
 <212> PRT
 <213> artificial

<220>
 <223> hu lsp V5xFlt3-E6muxEpC-pEFDHFR

<400> 834

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Ser Gly
 1 5 10 15

Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Asn His Lys Asn
 20 25 30

Asn Asp Ser Ser Val Gly Lys Ser Ser Ser Tyr Pro Met Val Ser Glu
 35 40 45

Ser Pro Glu Asp Leu Gly Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr
50 55 60

Val Tyr Glu Ala Ala Ala Val Glu Val Asp Val Ser Ala Ser Ile Thr
65 70 75 80

Leu Gln Val Leu Val Asp Ala Pro Gly Asn Ile Ser Cys Leu Trp Val
85 90 95

Phe Lys His Ser Ser Leu Asn Cys Gln Pro His Phe Asp Leu Gln Asn
100 105 110

Arg Gly Val Val Ser Met Val Ile Leu Lys Met Thr Glu Thr Gln Ala
115 120 125

Gly Glu Tyr Leu Leu Phe Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile
130 135 140

Leu Phe Thr Val Ser Ile Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg
145 150 155 160

Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Val Cys Ile Ser
165 170 175

Glu Ser Val Pro Glu Pro Ile Val Glu Trp Val Leu Cys Asp Ser Gln
180 185 190

Gly Glu Ser Cys Lys Glu Glu Ser Pro Ala Val Val Lys Lys Glu Glu
195 200 205

Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg
210 215 220

Asn Glu Leu Gly Arg Glu Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn
225 230 235 240

Gln Thr Pro Gln Thr Thr Leu Pro Gln Leu Phe Leu Lys Val Gly Glu
245 250 255

Pro Leu Trp Ile Arg Cys Lys Ala Val His Val Asn His Gly Phe Gly
260 265 270

Leu Thr Trp Glu Leu Glu Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe
275 280 285

Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg Ile Leu Phe
290 295 300

Ala Phe Val Ser Ser Val Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys
305 310 315 320

Ser Ser Ser Lys His Pro Ser Gln Ser Ala Leu Val Thr Ile Val Glu
325 330 335

Lys Gly Phe Ile Asn Ala Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp
340 345 350

Gln Tyr Glu Glu Phe Cys Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln
355 360 365

Ile Arg Cys Thr Trp Thr Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln
370 375 380

Lys Gly Leu Asp Asn Gly Tyr Ser Ile Ser Lys Phe Cys Asn His Lys
385 390 395 400

His Gln Pro Gly Glu Tyr Ile Phe His Ala Glu Asn Asp Asp Ala Gln
405 410 415

Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Lys Lys Pro Gln Val Leu
420 425 430

Ala Asn Ala Ser Ala Ser Gln Ala Ser Cys Ser Ser Asp Gly Tyr Pro
435 440 445

Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys
450 455 460

Thr Glu Glu Ile Pro Glu Gly Val Trp Asn Lys Lys Ala Asn Arg Lys
465 470 475 480

Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met Ser Glu Ala
485 490 495

Gly Lys Gly Leu Leu Val Lys Cys Cys Ala Tyr Asn Ser Met Gly Thr
500 505 510

Ser Cys Glu Thr Ile Phe Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile
515 520 525

Gln Asp Asn Ile Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile
530 535 540

Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val
545 550 555 560

Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu
565 570 575

Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
580 585

<210> 835
<211> 227
<212> PRT
<213> artificial

<220>
<223> Fc monomer-1

<400> 835

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> 836
<211> 225
<212> PRT
<213> artificial

<220>
<223> Fc monomer-2

<400> 836

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> 837
<211> 227
<212> PRT
<213> artificial

<220>
<223> Fc monomer-3

<400> 837

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> 838
<211> 225
<212> PRT
<213> artificial

<220>
<223> Fc monomer-4

<400> 838

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> 839
<211> 227
<212> PRT
<213> artificial

<220>
<223> Fc monomer-5

<400> 839

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> 840
 <211> 225
 <212> PRT
 <213> artificial

<220>
 <223> Fc monomer-6

<400> 840

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> 841
<211> 227
<212> PRT
<213> artificial

<220>
<223> Fc monomer-7

<400> 841

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> 842
 <211> 225
 <212> PRT
 <213> artificial

<220>
 <223> Fc monomer-8

<400> 842

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> 843
<211> 484
<212> PRT
<213> artificial

<220>

<223> scFc-1

<400> 843

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> 844
<211> 480
<212> PRT
<213> artificial

<220>
<223> scFc-2

<400> 844

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr
65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
325 330 335

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

<210> 845
<211> 484
<212> PRT
<213> artificial

<220>
<223> scFc-3

<400> 845

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> 846
 <211> 480
 <212> PRT
 <213> artificial

<220>
 <223> scFc-4

<400> 846

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> 847
<211> 484
<212> PRT
<213> artificial

<220>
<223> scFc-5

<400> 847

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> 848
 <211> 480
 <212> PRT
 <213> artificial

<220>
 <223> scFc-6

<400> 848

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
1				5					10					15	

Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			20					25					30		

Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		35					40					45			

Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	50					55					60				

His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Gly	Ser	Thr	Tyr
65					70					75					80

Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
				85					90					95	

Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			100					105					110		

Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		115					120					125			

Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
	130					135					140				

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480

<210> 849
 <211> 484
 <212> PRT
 <213> artificial

<220>
 <223> scFc-7

<400> 849

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
245 250 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
260 265 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
275 280 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
290 295 300

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr
325 330 335

Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
370 375 380

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
385 390 395 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
405 410 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
420 425 430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
435 440 445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
450 455 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465 470 475 480

Ser Pro Gly Lys

<210> 850
 <211> 480
 <212> PRT
 <213> artificial

<220>
 <223> scFc-8

<400> 850

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 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> 851
 <211> 20
 <212> PRT
 <213> artificial

<220>
 <223> (G4S)4 linker

<400> 851

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser
 20

<210> 852
 <211> 25
 <212> PRT
 <213> artificial

<220>
 <223> (G4S)5 linker

<400> 852

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> 853
<211> 30
<212> PRT
<213> artificial

<220>
<223> (G4S)6 linker

<400> 853

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> 854
<211> 35
<212> PRT
<213> artificial

<220>
<223> (G4S)7 linker

<400> 854

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> 855
<211> 40
<212> PRT
<213> artificial

<220>
<223> (G4S)8 linker

<400> 855

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> 856

<211> 989

<212> PRT

<213> artificial

<220>

<223> FL_16xCD3-scFc

<400> 856

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 Arg Asn Ala
20 25 30

Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Thr Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg Tyr Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Phe Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 857
 <211> 987
 <212> PRT
 <213> artificial

<220>
 <223> FL_16xCD3-scFc_delGK

<400> 857

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 Arg Asn Ala
 20 25 30

Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Thr Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg Tyr Asp Leu Ala Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Phe Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
 500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
 580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 858
<211> 989
<212> PRT
<213> artificial

<220>
<223> FL_23xCD3-scFc

<400> 858

Gln Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Phe Arg Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
 85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Gly Tyr Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Ile Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Gly Tyr Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Ile Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
 225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

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35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Thr
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
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Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
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Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
 465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
 500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Arg Met Ala Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Glu Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Val Gly Tyr Gly Thr Gly Trp Tyr Gly Phe Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Ile Leu 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 Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
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Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
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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
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Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
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Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
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Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
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Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
 580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn 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 Met Val Gly Tyr Gly Ser Gly Trp Tyr Ala Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu 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 Arg Asn Asp Leu Gly Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
 225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
 305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
 385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

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<400> 868

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Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

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<400> 869

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Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Tyr Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn 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 Leu Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Met Pro Glu Tyr Ser Ser Gly Trp Ser Gly Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met 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 Asp Ile Arg Asn Asp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
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Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Glu Phe Tyr Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
 225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
 245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
 275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
 305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
 325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
 340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
 355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
 385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
 405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
 420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
 435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
 450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
 465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
 485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys
 500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 565 570 575

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
755 760 765

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
770 775 780

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
785 790 795 800

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
805 810 815

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
820 825 830

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
835 840 845

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
850 855 860

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
865 870 875 880

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
885 890 895

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
900 905 910

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
915 920 925

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
930 935 940

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
945 950 955 960

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
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Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Glu Phe Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Ile Thr Met Val Arg Gly Val Ile Gly Tyr Tyr
 100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
245 250 255

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
260 265 270

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
275 280 285

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
290 295 300

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
340 345 350

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
355 360 365

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
565 570 575

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr
755 760 765

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
770 775 780

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
785 790 795 800

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
805 810 815

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
820 825 830

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
835 840 845

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
850 855 860

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
865 870 875 880

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
885 890 895

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
900 905 910

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
915 920 925

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
930 935 940

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
945 950 955 960

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
965 970 975

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985 990

Claims

1. A bispecific antibody construct comprising a first binding domain which binds to human and macaque FLT3 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 FLT3 which is comprised within the extracellular region of FLT3 as depicted in SEQ ID NOs: 801-804.
2. The antibody construct according to claim 1, wherein the first binding domain binds to an epitope of FLT3 which is comprised within the region of the human FLT3 having a sequence as depicted in SEQ ID NO: 814 (cluster 1) or SEQ ID NO: 816 (cluster 3).
3. 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 those formats.
4. The antibody construct according to claim 2 or 3, 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:
 SEQ ID NOs: 151-156, SEQ ID NOs: 161-166, SEQ ID NOs: 171-176, SEQ ID NOs: 181-186, SEQ ID NOs: 191-196, SEQ ID NOs: 201-206, SEQ ID NOs: 211-216, SEQ ID NOs: 221-226, SEQ ID NOs: 231-236, SEQ ID NOs: 241-246, SEQ ID NOs: 251-256, SEQ ID NOs: 261-266, SEQ ID NOs: 271-276, SEQ ID NOs: 281-286, SEQ ID NOs: 291-296, SEQ ID NOs: 301-306, SEQ ID NOs: 311-316, SEQ ID NOs: 321-326, SEQ ID NOs: 331-336, SEQ ID NOs: 341-346, SEQ ID NOs: 351-356, SEQ ID NOs: 361-366, SEQ ID NOs: 371-376, SEQ ID NOs: 381-386, SEQ ID NOs: 391-396, SEQ ID NOs: 401-406, SEQ ID NOs: 411-416, SEQ ID NOs: 421-426, SEQ ID NOs: 431-436, SEQ ID NOs: 441-446, SEQ ID NOs: 451-456, SEQ ID NOs: 461-466, SEQ ID NOs: 471-476, SEQ ID NOs: 481-486, SEQ ID NOs: 491-496, SEQ ID NOs: 501-506, SEQ ID NOs: 511-516, SEQ ID NOs: 521-526, SEQ ID NOs: 531-536, SEQ ID NOs: 541-546, SEQ ID NOs: 551-556, SEQ ID NOs: 561-566, SEQ ID NOs: 571-576, SEQ ID NOs: 581-586, SEQ ID NOs: 591-596, SEQ ID NOs: 601-606, SEQ ID NOs: 611-616, SEQ ID NOs: 621-626, SEQ ID NOs: 631-636, SEQ ID NOs: 641-646, SEQ ID NOs: 651-656, SEQ ID NOs: 661-666, SEQ ID

NOs: 671-676, SEQ ID NOs: 681-686, SEQ ID NOs: 691-696, SEQ ID NOs: 701-706, SEQ ID NOs: 711-716, SEQ ID NOs: 721-726, SEQ ID NOs: 731-736, SEQ ID NOs: 741-746, SEQ ID NOs: 751-756, SEQ ID NOs: 761-766, SEQ ID NOs: 771-776, SEQ ID NOs: 781-786, SEQ ID NOs: 791-796.

5. The antibody construct according to claim 4, wherein the first binding domain comprises a VH region selected from the group consisting of those depicted in SEQ ID NO: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, and SEQ ID NO: 797.
6. The antibody construct according to any one of claims 4 or 5, wherein the first binding domain comprises a VL region selected from the group consisting of those depicted in SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598,

SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788, and SEQ ID NO: 798.

7. The antibody construct according to any one of claims 4 to 6, 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 NO: 157+158, SEQ ID NO: 167+168, SEQ ID NO: 177+178, SEQ ID NO: 187+188, SEQ ID NO: 197+198, SEQ ID NO: 207+208, SEQ ID NO: 217+218, SEQ ID NO: 227+228, SEQ ID NO: 237+238, SEQ ID NO: 247+248, SEQ ID NO: 257+258, SEQ ID NO: 267+268, SEQ ID NO: 277+278, SEQ ID NO: 287+288, SEQ ID NO: 297+298, SEQ ID NO: 307+308, SEQ ID NO: 317+318, SEQ ID NO: 327+328, SEQ ID NO: 337+338, SEQ ID NO: 347+348, SEQ ID NO: 357+358, SEQ ID NO: 367+368, SEQ ID NO: 377+378, SEQ ID NO: 387+388, SEQ ID NO: 397+398. , SEQ ID NO: 407+408, SEQ ID NO: 417+418, SEQ ID NO: 427+428, SEQ ID NO: 437+438, SEQ ID NO: 447+448, SEQ ID NO: 457+458, SEQ ID NO: 467+468, SEQ ID NO: 477+478, SEQ ID NO: 487+488, SEQ ID NO: 497+498, SEQ ID NO: 507+508, SEQ ID NO: 517+518, SEQ ID NO: 527+528, SEQ ID NO: 537+538, SEQ ID NO: 547+548, SEQ ID NO: 557+558, SEQ ID NO: 567+568, SEQ ID NO: 577+578, SEQ ID NO: 587+588, SEQ ID NO: 597+598, SEQ ID NO: 607+608, SEQ ID NO: 617+618, SEQ ID NO: 627+628, SEQ ID NO: 637+638, SEQ ID NO: 647+648, SEQ ID NO: 657+658, SEQ ID NO: 667+668, SEQ ID NO: 677+678, SEQ ID NO: 687+688, SEQ ID NO: 697+698, SEQ ID NO: 707+708, SEQ ID NO: 717+718, SEQ ID NO: 727+728, SEQ ID NO: 737+738, SEQ ID NO: 747+748, SEQ ID NO: 757+758, SEQ ID NO: 767+768, SEQ ID NO: 777+778, SEQ ID NO: 787+788, and SEQ ID NO: 797+798.
8. The antibody construct according to any one of claims 4 to 7, wherein the first binding domain comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329,

SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799.

9. The antibody construct according to any one of claims 1 to 8, wherein the second binding domain binds to human CD3 epsilon and to *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus* CD3 epsilon.
10. The antibody construct according to any one of claims 1 to 9, comprising:
 - (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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and

SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 10;
- (b) a polypeptide comprising in following order starting from the N-terminus:
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103

- optionally a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 104-134; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 10;
- (c) a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having the amino acid sequence QRFVTGHFGGLX₁PANG (SEQ ID NO: 135) whereas X₁ is Y or H; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103;
 - a polypeptide having the amino acid sequence QRFVTGHFGGLHPANG (SEQ ID NO: 137) or QRFCTGHFGGLHPCNG (SEQ ID NO: 139); and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 10;

(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: 17, SEQ ID NO: 26, SEQ ID NO: 35, SEQ ID NO: 44, SEQ ID NO: 53, SEQ ID NO: 62, SEQ ID NO: 71, SEQ ID NO: 80, SEQ ID NO: 89, SEQ ID NO: 98, and SEQ ID NO: 101;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788, and SEQ ID NO: 798 and a serine residue at the C-terminus;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 140; 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: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547,

SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, and SEQ ID NO: 797;

- a peptide linker having the amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 27, SEQ ID NO: 36, SEQ ID NO: 45, SEQ ID NO: 54, SEQ ID NO: 63, SEQ ID NO: 72, SEQ ID NO: 81, SEQ ID NO: 90, SEQ ID NO: 99, and SEQ ID NO: 102 and a serine residue at the C-terminus;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 141;
- (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: 17, SEQ ID NO: 26, SEQ ID NO: 35, SEQ ID NO: 44, SEQ ID NO: 53, SEQ ID NO: 62, SEQ ID NO: 71, SEQ ID NO: 80, SEQ ID NO: 89, SEQ ID NO: 98, and SEQ ID NO: 101;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 8;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788, and SEQ ID NO: 798;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 142; 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: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, and SEQ ID NO: 797;
- a peptide linker having an amino acid sequence depicted in SEQ ID NO: 8;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 27, SEQ ID NO: 36, SEQ ID NO: 45, SEQ ID NO: 54, SEQ ID NO: 63, SEQ ID NO: 72, SEQ ID NO: 81, SEQ ID NO: 90, SEQ ID NO: 99, and SEQ ID NO: 102 and a serine residue at the C-terminus;
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 143;

(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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and

SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 144; and a polypeptide having the amino acid sequence depicted in SEQ ID NO: 145;
- (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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 146; 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: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 147;

(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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 148; 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: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 149; 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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189,

SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103; and
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 150.

(j) 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: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, and SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, and SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, and SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, and SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, and SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, and SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, and SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, and SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, and SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, and SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, and

SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, and SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, and SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, and SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, and SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, and SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, and SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, and SEQ ID NO: 789, and SEQ ID NO: 799;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 37, SEQ ID NO: 46, SEQ ID NO: 55, SEQ ID NO: 64, SEQ ID NO: 73, SEQ ID NO: 82, SEQ ID NO: 91, SEQ ID NO: 100, and SEQ ID NO: 103;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-9; and; and
 - the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 843-850.
11. The antibody construct according to any one of claims 1 to 10, comprising or consisting of a polypeptide as depicted in SEQ ID NOs: 856 to 871.
12. The antibody construct according to any one of claims 1 to 11, wherein the binding of the first binding domain to human FLT3 is reduced by FLT3-ligand by $\leq 25\%$, preferably $\leq 20\%$, more preferably $\leq 15\%$, further preferably $\leq 10\%$, even more preferably $\leq 8\%$, more preferably $\leq 6\%$ and most preferably $\leq 2\%$.
13. A polynucleotide encoding an antibody construct as defined in any one of the preceding claims.
14. A vector comprising a polynucleotide as defined in claim 13.
15. A host cell transformed or transfected with the polynucleotide as defined in claim 13 or with the vector as defined in claim 14.

16. A process for the production of an antibody construct according to any one of claims 1 to 12, said process comprising culturing a host cell as defined in claim 15, under conditions allowing the expression of the antibody construct as defined in any one of claims 1 to 12 and recovering the produced antibody construct from the culture.
17. A pharmaceutical composition comprising an antibody construct according to any one of claims 1 to 12, or produced according to the process of claim 16.
18. The antibody construct according to any one of claims 1 to 12, or produced according to the process of claim 16, for use in the prevention, treatment or amelioration of a *hematological cancer* disease or a metastatic cancer disease.
19. A method for the treatment or amelioration of a *hematological 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 12, or produced according to the process of claim 16.
20. The method according to claim 19 or the antibody construct according to claim 18, wherein the *hematological cancer* disease is AML or a metastatic cancer disease derived from any of the foregoing.
21. A kit comprising an antibody construct according to any one of claims 1 to 12, an antibody construct produced according to the process of claim 16, a polynucleotide as defined in claim 13, a vector as defined in claim 14, and/or a host cell as defined in claim 15.