TITLE OF THE INVENTION

Binding molecules against SARS-coronavirus and uses thereof

FIELD OF THE INVENTION

The invention relates to medicine. In particular the invention relates to binding molecules capable of specifically binding to SARS-coronavirus (SARS-CoV). The binding molecules are useful in the diagnosis of SARS CoV and the prophylaxis and/or treatment of a condition resulting from SARS-CoV.

BACKGROUND OF THE INVENTION

Recently a new and in several cases deadly clinical syndrome was observed in the human population, now called severe acute respiratory syndrome (SARS) (Holmes, 2003). The syndrome is caused by a novel coronavirus (Ksiazek *et al.*, 2003), referred to as the SARS-CoV. The genome sequence of SARS-CoV has been determined (Rota *et al.*, 2003; Marra *et al.*, 2003). However, much remains to be learnt about this virus, and means and methods for diagnostics, prophylaxis and/or treatment of the virus and the syndrome are needed. The present invention provides means and methods for use in diagnostics, prevention and/or treatment of SARS-CoV.

DESCRIPTION OF THE FIGURES

Figure 1 shows results from an ELISA, wherein the binding of the single-chain phage antibodies called SC03-001, SC03-002, SC03-003, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 to an immobilized SARS-CoV preparation (left column) or immobilised FBS (right column) was measured. The binding of the control single-chain phage antibody called SC02-006 is also shown. On the y-axis the absorbance (OD) at 492nm is shown.

Figure 2 shows results from an ELISA, wherein the binding of the single-chain phage antibodies called SC03-016, SC03-017 and SC03-018 to an immobilized SARS-CoV preparation (left column) or immobilised FBS (right column) was measured. The binding of the control single-chain phage antibody called SC02-300 is also shown. On the y-axis the absorbance (OD) at 492 nm is shown.

Figure 3 shows the construction of the bivalent scFv expression vector pPICZbiFVH. In figure 3A the vector pPICZαB is shown and in figure 3B the bivalent scFv expression vector pPicZbiFVH is shown. Figure 3C shows the cloning strategy of scFv's into pPicZbiFVH.

Figure 4 shows a competition ELISA of the SARS-CoV specific single-chain phage antibodies called SC03-001, SC03-002, SC03-003, SC03-004, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-010, SC03-012, SC03-013, SC03-014, SC03-015, SC03-016, SC03-017 and SC03-018 and the human monoclonal anti-SARS-CoV antibodies called (from left to right for each single chain antibody) 03-001, 03-002, 03-009, 03-013, 03-014 and 03-018. The antibody called 02-361 is a control antibody (second column from the right side). On the X-axis the single-chain phage antibodies that were tested are shown and on the Y-axis the residual binding (in %) of the single-chain phage antibodies to the SARS-CoV preparation in the presence of human monoclonal anti-SARS-CoV antibodies is shown. The binding value in the absence of human monoclonal anti-SARS-CoV antibody is set at 100%. This value can be found at the right side of each single-chain phage antibody (no IgG).

Figure 5 shows the binding of the human monoclonal anti-SARS-CoV antibodies called 03-001, 03-002, 03-009, 03-013, 03-014, 03-018 and the control antibody called 02-027 (a human monoclonal anti-EPCAM antibody) to an UV- or gamma-irradiated SARS-CoV preparation. From each antibody 1 and 5 µg/ml was tested. On the X-axis the antibodies and on the Y-axis the absorbance (OD) at 492 nm is shown. For each anti-SARS-CoV antibody is shown from left to right the binding of 5 µg/ml of the antibody to the gamma-irradiated preparation, the binding of 5 µg/ml of the antibody to the UV-irradiated preparation, the binding of 1 µg/ml of the antibody to the gamma-irradiated preparation and the binding of 1 µg/ml of the antibody to the UV-irradiated preparation. The binding of the control antibody to the UV- and gamma-irradiated SARS-CoV preparation was only tested at a concentration of 5 µg/ml.

Figures 6A-D show sandwich ELISAs of the immobilized recombinant human monoclonal anti-SARS-CoV antibodies called 03-001, 03-002, 03-009, 03-013, 03-014, 03-018 and the control antibody 02-300 (an antibody directed against CD46) with from left to right a SARS-CoV preparation, a denatured SARS-CoV preparation and BSA. On the Y-axis the absorbance (OD) at 492 nm is shown. In Figure 6A detection was performed with a polyclonal rabbit antiserum recognizing the complete SARS-CoV. In Figure 6B detection was performed with a polyclonal rabbit antiserum (IMG-542) recognizing the spike protein of SARS-CoV. In Figure 6C detection was performed with a polyclonal rabbit antiserum (IMG-543) recognizing the nucleocapsid (N) protein of SARS-CoV and in Figure 6D detection was performed with another polyclonal rabbit antiserum (IMG-557) recognizing the spike protein of SARS-CoV.

Figure 7 shows the vector pDV-C05.

Figure 8 shows the ELISA binding of SC03-009, SC03-014 and the control SC02-006 to a SARS-CoV preparation, the S565 fragment (amino acids 1-565 of the S protein of SARS-CoV), the nucleocapsid protein of SARS-CoV and a control protein. On the Y-axis the absorbance (OD) at 492 nm is shown.

Figure 9 shows the ELISA binding of antibodies 03-001, 03-002, 03-006, 03-009, 03-013, 03-014, 03-015, 03-018 and the control antibody 02-027 (anti-EPCAM) to the nucleocapsid protein of SARS-CoV and a control protein. On the Y-axis the absorbance (OD) at 492 nm is shown.

Figure 10 shows the ELISA binding of dilutions of antibodies 03-009, 03-018 and the control antibody 02-027 to the nucleocapsid protein of SARS-CoV. On the Y-axis the absorbance (OD) at 492 nm is shown and on the X-axis the amount of antibody in M.

Figure 11 shows a competition ELISA for binding to the nucleocapsid protein of SARS-CoV between biotinylated antibody 03-009 without competing antibody or with 25 or 50 µg/ml competing antibody 03-009 or 03-018. On the Y-axis the % of maximal binding is shown and on the X-axis the amount of the competing antibody in µg/ml.

Figure 12 shows FACS binding of the antibodies 03-001, 03-002, 03-006, 03-009, 03-013, 03-014, 03-015, 03-018 and the control antibody 02-027 (anti-EPCAM) to the full length S protein expressed on HEK293T cells (left column) and ELISA binding of these antibodies to the S565 fragment (amino acids 1-565 of

the S protein of SARS-CoV; middle column) and S318-510 fragment (amino acids 318-510 of the S protein of SARS-CoV; right column). On the right Y-axis the absorbance (OD) at 492 nm is shown and on the left Y-axis the mean fluorescense intensity is shown.

Figure 13 shows the ELISA binding of dilutions of antibodies 03-006, 03-013, 03-014 and the control antibody 02-027 to the S565 fragment of the S protein of SARS-CoV. On the Y-axis the absorbance (OD) at 492 nm is shown and on the X-axis the amount of antibody in M.

Figure 14 shows a competition ELISA for binding the S565 fragment of the S protein of SARS-CoV between biotinylated antibody 03-014 without competing antibody or with 25 or 50 µg/ml competing antibody 03-006 or 03-014. On the Y-axis the % of maximal binding is shown and on the X-axis the amount of the competing antibody in µg/ml is indicated.

Figure 15 shows the flow cytometric analysis of the binding of the S565 fragment of the S protein of SARS-CoV to Vero cells in the presence or absence of antibody 03-014. The dotted line indicates Vero cells incubated with a myc-tagged control protein, *i.e.* bivalent scFv 02-006. The normal line and bold line indicate Vero cells incubated with a myc-tagged S565 fragment in the absence or presence of antibody 03-014, respectively.

Figure 16 shows the flow cytometric analysis of the binding of the S565 fragment of the S protein of SARS-CoV to Vero cells in the presence or absence of antibody 03-018. The dotted line indicates Vero cells incubated with a myc-tagged control

protein, *i.e.* bivalent scFv 02-006. The normal line and bold line indicate Vero cells incubated with a myc-tagged S565 fragment in the absence or presence of antibody 03-018, respectively.

Figure 17 shows the flow cytometric analysis of the binding of the S565 fragment of the S protein of SARS-CoV to Vero cells in the presence or absence of the control anti-EPCAM antibody 02-027. The dotted line indicates Vero cells incubated with a myc-tagged control protein, *i.e.* bivalent scFv 02-006. The normal line and bold line indicate Vero cells incubated with a myc-tagged S565 fragment in the absence or presence of antibody 02-027, respectively.

Figure 18 shows SARS-CoV secretion at days 2, 4 and 7 of ferrets inoculated with a virus-control antibody mixture or a virus-03-014 antibody mixture.

Figure 19 shows SARS-CoV lung titers at days 4 and 7 of ferrets inoculated with a virus-control antibody mixture or a virus-03-014 antibody mixture. The dashed line represents the detection limit of the assay.

Figure 20 shows the lung pathology score at days 4 and 7 of ferrets inoculated with a virus-control antibody mixture or a virus-03-014 antibody mixture.

Figure 21 shows SARS-CoV titration in lung homogenates on day 4 after challenge. SARS-CoV lung titers of ferrets administered with control antibody (named control) or with antibody 03-014 (named CR3014) are shown.

Figure 22 shows SARS-CoV excretion measured by RT/PCR in nasopharyngeal swabs on days 2 and 4, expressed as SARS-CoV genome equivalents. In the 03-014-treated group (named CR3014) three animals had no SARS-CoV excretion and are superimposed.

Figure 23 shows electron micrographs of SARS-CoV incubated with the monoclonal anti-SARS-CoV 03-014 IgG1 antibody (see section a) or a human monoclonal control IgG1 antibody (see section b). The bar is 100 nm.

Figure 24 shows electron micrographs of ultra-thin sections of Vero cells infected with SARS-CoV. Figure 24A: unstained (control) sections; Figure 24B: sections stained with the human monoclonal control IgG1 antibody 02-027 (anti-Epcam antibody); Figure 24C: sections stained with the monoclonal anti-SARS-CoV IgG1 antibody 03-009; and Figure 24D: sections stained with the monoclonal anti-SARS-CoV IgG1 antibody 03-018.

Figure 25 shows binding of the monoclonal anti-SARS-CoV IgG1 antibody 03-014 and a control monoclonal anti-His6 antibody to the amino acid region of 318-510 of the S protein of the SARS-CoV strain Frankfurt 1 (called WT S318-510) and variant S318-510 fragments (variant A, mutation K344R; variant B, mutation S353F; variant C, mutation R426G and N437D; variant D, mutation Y436H; variant E, mutation Y442S; variant F, mutation N479S; variant G, mutation K344R, F360S, L472P, D480G, and T487S; variant H, mutation K344R, F501Y). The control is an irrelevant myc-His tagged protein. On the Y-axis is depicted the binding as percentage of binding to WT 318-510, which was set at 100% for both antibodies.

DESCRIPTION OF THE INVENTION

Herebelow follow definitions of terms as used in the invention

DEFINITIONS

Amino acid sequence

The term "amino acid sequence" as used herein refers to naturally occuring or synthetic molecules and to a peptide, oligopeptide, polypeptide or protein sequence.

Binding molecule

As used herein the term "binding molecule" refers to an intact immunoglobulin including monoclonal antibodies, such as chimeric, humanised or human monoclonal antibodies, or to an antigen-binding and/or variable domain comprising fragment of an immunoglobulin that competes with the intact immunoglobulin for specific binding to the binding partner of the immunoglobulin, *e.g.* the SARS-CoV. Regardless of structure, the antigen-binding fragment binds with the same antigen that is recognised by the intact immunoglobulin. An antigen-binding fragment can comprise a peptide or polypeptide comprising an amino acid sequence of at least 2 contiguous amino acid residues, at least 5 contiguous amino acid residues, at least 10 contiguous amino acid residues, at least 15 contiguous amino acid residues, at least 20 contiguous amino acid residues, at least 25 contiguous amino acid residues, at least 30 contiguous amino acid residues, at least 35 contiguous amino acid residues, at least 40 contiguous amino acid residues, at least 50 contiguous amino acid residues, at least 60 contiguous amino residues, at least 70 contiguous amino acid residues, at least contiguous 80 amino acid residues, at least contiguous 90 amino acid residues, at least contiguous

100 amino acid residues, at least contiguous 125 amino acid residues, at least 150 contiguous amino acid residues, at least contiguous 175 amino acid residues, at least 200 contiguous amino acid residues, or at least contiguous 250 amino acid residues of the amino acid sequence of the binding molecule.

The term "binding molecule", as used herein includes all immunoglobulin classes and subclasses known in the art. Depending on the amino acid sequence of the constant domain of their heavy chains, binding molecules can be divided into the five major classes of intact antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), *e.g.*, IgA1, IgA2, IgG1, IgG2, IgG3 and IgG4.

Antigen-binding fragments include, *inter alia*, Fab, F(ab'), $F(ab')_2$, Fv, dAb, Fd, complementarity determining region (CDR) fragments, single-chain antibodies (scFv), bivalent single-chain antibodies, single-chain phage antibodies, diabodies, triabodies, tetrabodies, (poly)peptides that contain at least a fragment of an immunoglobulin that is sufficient to confer specific antigen binding to the (poly)peptide, etc. The above fragments may be produced synthetically or by enzymatic or chemical cleavage of intact immunoglobulins or they may be genetically engineerd by recombinant DNA techniques. The methods of production are well known in the art and are described, for example, in Antibodies: A Laboratory Manual, Edited by: E. Harlow and D, Lane (1988), Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, which is incorporated herein by reference. A binding molecule or antigen-binding fragment thereof may have one or more binding sites. If there is more than one binding

site, the binding sites may be identical to one another or they may be different.

The binding molecule can be a naked or unconjugated binding molecule but can also be part of an immunoconjugate. A naked or unconjugated binding molecule is intended to refer to a binding molecule that is not conjugated, operatively linked or otherwise physically or functionally associated with an effector moiety or tag, such as *inter alia* a toxic substance, a radioactive substance, a liposome, an enzyme. It will be understood that naked or unconjugated binding molecules do not exclude binding molecules that have been stabilized, multimerized, humanized or in any other way manipulated, other than by the attachment of an effector moiety or tag. Accordingly, all post-translationally modified naked and unconjugated binding molecules are included herewith, including where the modifications are made in the natural binding molecule-producing cell environment, by a recombinant binding molecule-producing cell, and are introduced by the hand of man after initial binding molecule preparation. Of course, the term naked or unconjugated binding molecule does not exclude the ability of the binding molecule to form functional associations with effector cells and/or molecules after administration to the body, as some of such interactions are necessary in order to exert a biological effect. The lack of associated effector group or tag is therefore applied in definition to the naked or unconjugated binding molecule *in vitro*, not *in vivo*.

Biological sample

As used herein, the term "biological sample" encompasses a variety of sample types, including blood and other liquid samples of biological origin, solid tissue samples such as a

biopsy specimen or tissue cultures, or cells derived therefrom and the progeny thereof. The term also includes samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components, such as proteins or polynucleotides. The term encompasses various kinds of clinical samples obtained from any species, and also includes cells in culture, cell supernatants and cell lysates.

Complementary determining regions (CDR)

The term "complementary determining regions" as used herein means sequences within the variable regions of binding molecules, such as immunoglobulins, that usually contribute to a large extent to the antigen binding site which is complementary in shape and charge distribution to the epitope recognised on the antigen. The CDR regions can be specific for linear epitopes, discontinuous epitopes, or conformational epitopes of proteins or protein fragments, either as present on the protein in its native conformation or, in some cases, as present on the proteins as denatured, *e.g.*, by solubilization in SDS. Epitopes may also consist of posttranslational modifications of proteins.

Deletion

The term "deletion", as used herein, denotes a change in either amino acid or nucleotide sequence in which one or more amino acid or nucleotide residues, respectively, are absent as compared to the parent, often the naturally occurring, molecule.

Expression-regulating nucleic acid sequence

The term "expression-regulating nucleic acid sequence" as used herein refers to polynucleotide sequences necessary for and/or affecting the expression of an operably linked coding sequence in a particular host organism. The expression-regulating nucleic acid sequences, such as *inter alia* appropriate transcription initiation, termination, promoter, enhancer sequences; repressor or activator sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (*e.g.*, ribosome binding sites); sequences that enhance protein stability; and when desired, sequences that enhance protein secretion, can be any nucleic acid sequence showing activity in the host organism of choice and can be derived from genes encoding proteins, which are either homologous or heterologous to the host organism. The identification and employment of expression-regulating sequences is routine to the person skilled in the art.

Functional variant

The term "functional variant", as used herein, refers to a binding molecule that comprises a nucleotide and/or amino acid sequence that is altered by one or more nucleotides and/or amino acids compared to the nucleotide and/or amino acid sequences of the parent binding molecule and that is still capable of competing for binding to the binding partner, *e.g.* SARS-CoV, with the parent binding molecule. In other words, the modifications in the amino acid and/or nucleotide sequence of the parent binding molecule do not significantly affect or alter the binding characteristics of the binding molecule encoded by the nucleotide sequence or containing the amino acid sequence, *i.e.* the binding molecule is still able to recognize and bind its target. The functional variant may have

conservative sequence modifications including nucleotide and amino acid substitutions, additions and deletions. These modifications can be introduced by standard techniques known in the art, such as site-directed mutagenesis and random PCR-mediated mutagenesis, and may comprise natural as well as non-natural nucleotides and amino acids.

Conservative amino acid substitutions include the ones in which the amino acid residue is replaced with an amino acid residue having similar structural or chemical properties. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cystine, tryptophan), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). It will be clear to the skilled artisan that other classifications of amino acid residue families than the one used above can also be employed. Furthermore, a variant may have non-conservative amino acid substitutions, *e.g.*, replacement of an amino acid with an amino acid residue having different structural or chemical properties. Similar minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing immunological activity may be found using computer programs well known in the art.

A mutation in a nucleotide sequence can be a single alteration made at a locus (a point mutation), such as

transition or transversion mutations, or alternatively, multiple nucleotides may be inserted, deleted or changed at a single locus. In addition, one or more alterations may be made at any number of loci within a nucleotide sequence. The mutations may be performed by any suitable method known in the art.

Host

The term "host", as used herein, is intended to refer to an organism or a cell into which a vector such as a cloning vector or an expression vector has been introduced. The organism or cell can be prokaryotic or eukaryotic. It should be understood that this term is intended to refer not only to the particular subject organism or cell, but to the progeny of such an organism or cell as well. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent organism or cell, but are still included within the scope of the term "host" as used herein.

Human

The term "human", when applied to binding molecules as defined herein, refers to molecules that are either directly derived from a human or based upon a human sequence. When a binding molecule is derived from or based on a human sequence and subsequently modified, it is still to be considered human as used throughout the specification. In other words, the term human, when applied to binding molecules is intended to include binding molecules having variable and constant regions derived from human germline immunoglobulin sequences based on variable or constant regions either or not occuring in a human

or human lymphocyte or in modified form. Thus, the human binding molecules may include amino acid residues not encoded by human germline immunoglobulin sequences, comprise substitutions and/or deletions (*e.g.*, mutations introduced by for instance random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*). "Based on" as used herein refers to the situation that a nucleic acid sequence may be exactly copied from a template, or with minor mutations, such as by error-prone PCR methods, or synthetically made matching the template exactly or with minor modifications. Semisynthetic molecules based on human sequences are also considered to be human as used herein.

Insertion

The term "insertion", also known as the term "addition", denotes a change in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid or nucleotide residues, respectively, as compared to the parent, often the naturally occurring, molecule.

Isolated

The term "isolated", when applied to binding molecules as defined herein, refers to binding molecules that are substantially free of other proteins or polypeptides, particularly free of other binding molecules having different antigenic specificities, and are also substantially free of other cellular material and/or chemicals. For example, when the binding molecules are recombinantly produced, they are preferably substantially free of culture medium, and when the binding molecules are produced by chemical synthesis, they are preferably substantially free of chemical precursors or other chemicals, *i.e.*, they are separated from chemical precursors

or other chemicals which are involved in the synthesis of the protein. The term "isolated" when applied to nucleic acid molecules encoding binding molecules as defined herein, is intended to refer to nucleic acid molecules in which the nucleotide sequences encoding the binding molecules are free of other nucleotide sequences, particularly nucleotide sequences encoding binding molecules that bind binding partners other than SARS-CoV. Furthermore, the term "isolated" refers to nucleic acid molecules that are substantially separated from other cellular components that naturally accompany the native nucleic acid molecule in its natural host, *e.g.*, ribosomes, polymerases, or genomic sequences with which it is naturally associated. Moreover, "isolated" nucleic acid molecules, such as a cDNA molecules, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

Monoclonal antibody

The term "monoclonal antibody" as used herein refers to a preparation of antibody molecules of single molecular composition. A monoclonal antibody displays a single binding specificity and affinity for a particular epitope. Accordingly, the term "human monoclonal antibody" refers to an antibody displaying a single binding specificity which have variable and constant regions derived from or based on human germline immunoglobulin sequences or derived from completely synthetic sequences. The method of preparing the monoclonal antibody is not relevant.

Naturally occuring

The term "naturally-occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally-occurring.

Nucleic acid molecule

The term "nucleic acid molecule" as used in the present invention refers to a polymeric form of nucleotides and includes both sense and antisense strands of RNA, cDNA, genomic DNA, and synthetic forms and mixed polymers of the above. A nucleotide refers to a ribonucleotide, deoxynucleotide or a modified form of either type of nucleotide. The term also includes single- and double-stranded forms of DNA. In addition, a polynucleotide may include either or both naturally-occurring and modified nucleotides linked together by naturally-occurring and/or non-naturally occurring nucleotide linkages. The nucleic acid molecules may be modified chemically or biochemically or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those of skill in the art. Such modifications include, for example, labels, methylation, substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates, etc.), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen, etc.), chelators, alkylators, and modified linkages

(*e.g.*, alpha anomeric nucleic acids, etc.). The above term is also intended to include any topological conformation, including single-stranded, double-stranded, partially duplexed, triplex, hairpinned, circular and padlocked conformations. Also included are synthetic molecules that mimic polynucleotides in their ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules are known in the art and include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule. A reference to a nucleic acid sequence encompasses its complement unless otherwise specified. Thus, a reference to a nucleic acid molecule having a particular sequence should be understood to encompass its complementary strand, with its complementary sequence. The complementary strand is also useful, *e.g.*, for antisense therapy, hybridization probes and PCR primers.

Operably linked

The term "operably linked" refers to two or more nucleic acid sequence elements that are usually physically linked and are in a functional relationship with each other. For instance, a promoter is operably linked to a coding sequence if the promoter is able to initiate or regulate the transcription or expression of a coding sequence, in which case the coding sequence should be understood as being "under the control of" the promoter.

Pharmaceutically acceptable excipient

By "pharmaceutically acceptable excipient" is meant any inert substance that is combined with an active molecule such as a drug, agent, or binding molecule for preparing an agreeable or convenient dosage form. The "pharmaceutically acceptable

excipient" is an excipient that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation comprising the drug, agent or binding molecule.

Specifically Binding

The term "specifically binding", as used herein, in reference to the interaction of a binding molecule, *e.g.* an antibody, and its binding partner, *e.g.* an antigen, means that the interaction is dependent upon the presence of a particular structure, *e.g.* an antigenic determinant or epitope, on the binding partner. In other words, the antibody preferentially binds or recognizes the binding partner even when the binding partner is present in a mixture of other molecules or organisms. The binding may be mediated by covalent or non-covalent interactions or a combination of both. In yet other words, the term "specifically binding" means immunospecifically binding to an antigen or a fragment thereof and not immunospecifically binding to other antigens. A binding molecule that immunospecifically binds to an antigen may bind to other peptides or polypeptides with lower affinity as determined by, *e.g.*, radioimmunoassays (RIA), enzyme-linked immunosorbent assays (ELISA), BIACORE, or other assays known in the art. Binding molecules or fragments thereof that immunospecifically bind to an antigen may be cross-reactive with related antigens. Preferably, binding molecules or fragments thereof that immunospecifically bind to an antigen do not cross-react with other antigens.

Substitutions

A "substitution", as used herein, denotes the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

Therapeutically effective amount

The term "therapeutically effective amount" refers to an amount of the binding molecule as defined herein that is effective for preventing, ameliorating and/or treating a condition resulting from infection with SARS-CoV.

Treatment

The term "treatment" refers to therapeutic treatment as well as prophylactic or preventative measures to cure or halt or at least retard disease progress. Those in need of treatment include those already inflicted with a condition resulting from infection with SARS-CoV as well as those in which infection with SARS-CoV is to be prevented. Subjects partially or totally recovered form infection with SARS-CoV might also be in need of treatment. Prevention encompasses inhibiting or reducing the spread of SARS-CoV or inhibiting or reducing the onset, development or progression of one or more of the symptoms associated with infection with SARS-CoV.

Vector

The term "vector" denotes a nucleic acid molecule into which a second nucleic acid molecule can be inserted for introduction into a host where it will be replicated, and in some cases expressed. In other words, a vector is capable of transporting a nucleic acid molecule to which it has been linked. Cloning as well as expression vectors are contemplated by the term "vector", as used herein. Vectors include, but are not limited to, plasmids, cosmids, bacterial artificial chromosomes (BAC)

and yeast artificial chromosomes (YAC) and vectors derived from bacteriophages or plant or animal (including human) viruses. Vectors comprise an origin of replication recognised by the proposed host and in case of expression vectors, promoter and other regulatory regions recognised by the host. A vector containing a second nucleic acid molecule is introduced into a cell by transformation, transfection, or by making use of viral entry mechanisms. Certain vectors are capable of autonomous replication in a host into which they are introduced (*e.g.*, vectors having a bacterial origin of replication can replicate in bacteria). Other vectors can be integrated into the genome of a host upon introduction into the host, and thereby are replicated along with the host genome.

SUMMARY OF THE INVENTION

The invention provides binding molecules capable of specifically binding to SARS-CoV. In a preferred embodiment, said binding molecules are human binding molecules. Furthermore, the invention pertains to nucleic acid molecules encoding at least the binding region of the binding molecules. The invention further provides for the use of the binding molecules of the invention in the prophylaxis and/or treatment of a subject having, or at risk of developing, a condition resulting from SARS-CoV. Besides that, the invention pertains to the use of the binding molecules of the invention in the diagnosis/detection of SARS-CoV.

DETAILED DESCRIPTION OF THE INVENTION

In a first aspect the present invention encompasses binding molecule capable of specifically binding to SARS-CoV.

The binding molecules may be capable of specifically binding to SARS-CoV in activated or inactivated/attenuated form. Methods for inactivating/attenuating viruses are well known in the art and include, but are not limited to, heat inactivation, inactivation by UV irradiation, inactivation by gamma irradiation. The binding molecules may also be capable of specifically binding to one or more fragments of the SARS-CoV such as *inter alia* a preparation of one or more proteins and/or (poly)peptides derived from SARS-CoV. For methods of treatment and/or prevention of SARS the binding molecules are preferably capable of specifically binding to surface accessible proteins, which include, but are not limited to, inner and outer membrane proteins, proteins adhering to the cell wall, and potential secreted proteins. Surface accessible proteins of SARS-CoV include, but are not limited to, the spike protein, the membrane (matrix) protein, the (small) envelope protein, Orf 3, Orf 4, Orf 7, Orf 8, Orf 9, Orf 10 and Orf 14. For diagnostical purposes the binding molecules may also be capable of specifically binding to proteins not present on the surface of SARS-CoV. Therefore, proteins including, but not limited to, the nucleocapsid (N) protein, Orf 11 and Orf 13 may be used. The amino acid sequence of proteins and potential proteins of various known strains of SARS-CoV can be found in the EMBL-database and/or other databases. For instance the complete genome of the SARS coronavirus Urbani can be found in the EMBL-database under accession number AY278741, the complete genome of the SARS coronavirus HSR 1 can be found under accession number AY323977, the complete genome of the SARS coronavirus Frankfurt 1 can be found under accession number AY291315 and the complete genome of the SARS coronavirus TOR2 can be found under accession number AY274119. Preferably, the fragment at

least comprises an antigenic determinant recognised by the binding molecules of the invention. An "antigenic determinant" as used herein is a moiety, such as a SARS-CoV (poly)peptide, protein, glycoprotein, analog or fragment thereof, that is capable of binding to a binding molecule of the invention with sufficiently high affinity to form a detectable antigen-binding molecule complex.

The binding molecules according to the invention are preferably human binding molecules, preferably human monoclonal antibodies. They can be intact immunoglobulin molecules such as polyclonal or monoclonal antibodies, in particular human monoclonal antibodies, or the binding molecules can be antigen-binding fragments including, but not limited to, Fab, F(ab'), $F(ab')_2$, Fv, dAb, Fd, complementarity determining region (CDR) fragments, single-chain antibodies (scFv), bivalent single-chain antibodies, single-chain phage antibodies, diabodies, triabodies, tetrabodies, and (poly)peptides that contain at least a fragment of an immunoglobulin that is sufficient to confer specific antigen binding to the SARS-CoV or fragment thereof. The binding molecules of the invention can be used in non-isolated or isolated form. Furthermore, the binding molecules of the invention can be used alone or in a mixture comprising at least one binding molecule (or variant or fragment thereof). In other words, the binding molecules can be used in combination, *e.g.*, as a pharmaceutical composition comprising two or more binding molecules, variants or fragments thereof. For example, binding molecules having different, but complementary activities can be combined in a single therapy to achieve a desired prophylactic, therapeutic or diagnostic effect, but alternatively, binding molecules having identical activities can also be combined in a single therapy to achieve

a desired prophylactic, therapeutic or diagnostic effect. The mixture may further comprise at least one other therapeutic agent. Preferably, the therapeutic agent is useful in the prophylaxis and/or treatment of a condition resulting from SARS-CoV.

Typically, binding molecules according to the invention can bind to their binding partners, *i.e.* SARS-CoV or fragments thereof, with an affinity constant (K_d-value) that is lower than $0.2*10^{-4}$ M, $1.0*10^{-5}$ M, $1.0*10^{-6}$ M, $1.0*10^{-7}$ M, preferably lower than $1.0*10^{-8}$ M, more preferably lower than $1.0*10^{-9}$ M, more preferably lower than $1.0*10^{-10}$ M, even more preferably lower than $1.0*10^{-11}$ M, and in particular lower than $1.0*10^{-12}$ M. The affinity constants can vary for antibody isotypes. For example, affinity binding for an IgM isotype refers to a binding affinity of at least about $1.0*10^{-7}$ M. Affinity constants can for instance be measured using surface plasmon resonance, *i.e.* an optical phenomenon that allows for the analysis of real-time biospecific interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIACORE system (Pharmacia Biosensor AB, Uppsala, Sweden).

The binding molecules according to the invention may bind to SARS-CoV in soluble form such as for instance in a sample or may bind to SARS-CoV bound or attached to a carrier or substrate, *e.g.*, microtiter plates, membranes and beads, etc. Carriers or substrates may be made of glass, plastic (*e.g.*, polystyrene), polysaccharides, nylon, nitrocellulose, or teflon, etc. The surface of such supports may be solid or porous and of any convenient shape. Furthermore, the binding molecules may bind to SARS-CoV in purified/isolated or non-purified/non-isolated form.

In a preferred embodiment of the invention, the binding molecules of the invention neutralize SARS-CoV infectivity. This may be achieved by preventing the attachment of SARS-CoV to possible receptors on host cells or inhibition of the release of RNA into the cytoplasm of the cell or prevention of RNA transcription or translation. In a specific embodiment, the binding molecules of the invention prevent SARS-CoV from infecting host cells by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to infection of host cells by SARS-CoV in the absence of said binding molecules. Neutralization can for instance be measured as described herein.

Binding molecules of the invention which do not prevent SARS-CoV from binding its host cell receptor, but inhibit or downregulate SARS-CoV replication can also be administered to a mammal to treat, prevent or ameliorate one or more symptoms associated with a SARS-CoV infection. The ability of a binding molecule to inhibit or downregulate SARS-CoV replication may be determined by techniques known in the art, for example, the inhibition or downregulation of SARS-CoV replication can be determined by detecting the SARS-CoV titer in a biological sample of a mammal, preferably a human. A binding molecule of the present invention may inhibit or downregulate SARS-CoV replication by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to SARS-CoV replication in absence of said binding molecules. Furthermore, the binding molecules of the

invention may be complement fixing binding molecules capable of assisting in the lysis of enveloped SARS-CoV. The binding molecules of the invention might also act as opsonins and augment phagocytosis of SARS-CoV either by promoting its uptake via Fc or C3b receptors or by agglutinating SARS-CoV to make it more easily phagocytosed.

In a preferred embodiment, the binding molecules according to the invention comprise at least a CDR3 region, preferably a heavy chain CDR3 region, comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300 and SEQ ID NO:301.

In yet another embodiment, the binding molecules according to the invention comprise a variable heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:303, SEQ ID NO:307, SEQ ID NO:311, SEQ ID NO:315, SEQ ID NO:319, SEQ ID NO:323, SEQ ID NO:327, SEQ ID NO:331, SEQ ID NO:335, SEQ ID NO:339, SEQ ID NO:343, SEQ ID NO:347, SEQ ID NO:351, SEQ ID NO:355, SEQ ID NO:359, SEQ ID NO:363, SEQ ID NO:367, SEQ ID NO:371, SEQ ID NO:375, SEQ ID NO:379, SEQ ID NO:383, SEQ ID NO:387, SEQ ID NO:391, SEQ ID NO:395, SEQ ID NO:399, SEQ ID NO:403, SEQ ID NO:407, SEQ ID NO:411, SEQ ID NO:415, SEQ ID NO:419, SEQ ID NO:423, SEQ ID NO:427,

SEQ ID NO:431, SEQ ID NO:435, SEQ ID NO:439, SEQ ID NO:443, SEQ ID NO:447, SEQ ID NO:451, SEQ ID NO:455 and SEQ ID NO:459.

In a further embodiment, the binding molecules according to the invention comprise a variable heavy chain comprising the amino acid sequence of SEQ ID NO:15 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:17 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:19 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:21 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:23 and a variable light chain comprising the amino acid sequence of SEQ ID NO:43, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:25 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:27 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:29 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:31 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:33 and a variable light chain comprising the amino acid sequence of SEQ ID NO:45, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:35 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ

ID NO:37 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:39 and a variable light chain comprising the amino acid sequence of SEQ ID NO:45, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:80 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:82 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:84 and a variable light chain comprising the amino acid sequence of SEQ ID NO:88, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:86 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:303 and a variable light chain comprising the amino acid sequence of SEQ ID NO:305, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:307 and a variable light chain comprising the amino acid sequence of SEQ ID NO:309, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:311 and a variable light chain comprising the amino acid sequence of SEQ ID NO:313, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:315 and a variable light chain comprising the amino acid sequence of SEQ ID NO:317, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:319 and a variable light chain comprising the amino acid sequence of SEQ ID NO:321, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:323 and a variable light chain comprising the amino acid sequence of SEQ ID NO:325, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:327 and a variable light chain comprising the amino acid sequence of SEQ ID NO:329, a variable heavy chain comprising

the amino acid sequence of SEQ ID NO:331 and a variable light chain comprising the amino acid sequence of SEQ ID NO:333, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:335 and a variable light chain comprising the amino acid sequence of SEQ ID NO:337, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:339 and a variable light chain comprising the amino acid sequence of SEQ ID NO:341, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:343 and a variable light chain comprising the amino acid sequence of SEQ ID NO:345, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:347 and a variable light chain comprising the amino acid sequence of SEQ ID NO:349, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:351 and a variable light chain comprising the amino acid sequence of SEQ ID NO:353, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:355 and a variable light chain comprising the amino acid sequence of SEQ ID NO:357, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:359 and a variable light chain comprising the amino acid sequence of SEQ ID NO:361, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:363 and a variable light chain comprising the amino acid sequence of SEQ ID NO:365, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:367 and a variable light chain comprising the amino acid sequence of SEQ ID NO:369, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:371 and a variable light chain comprising the amino acid sequence of SEQ ID NO:373, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:375 and a variable light chain comprising the amino acid sequence of SEQ ID NO:377, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:379 and a variable light chain comprising the amino acid sequence of SEQ ID NO:381, a

variable heavy chain comprising the amino acid sequence of SEQ ID NO:383 and a variable light chain comprising the amino acid sequence of SEQ ID NO:385, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:387 and a variable light chain comprising the amino acid sequence of SEQ ID NO:389, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:391 and a variable light chain comprising the amino acid sequence of SEQ ID NO:393, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:395 and a variable light chain comprising the amino acid sequence of SEQ ID NO:397, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:399 and a variable light chain comprising the amino acid sequence of SEQ ID NO:401, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:403 and a variable light chain comprising the amino acid sequence of SEQ ID NO:405, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:407 and a variable light chain comprising the amino acid sequence of SEQ ID NO:409, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:411 and a variable light chain comprising the amino acid sequence of SEQ ID NO:413, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:415 and a variable light chain comprising the amino acid sequence of SEQ ID NO:417, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:419 and a variable light chain comprising the amino acid sequence of SEQ ID NO:421, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:423 and a variable light chain comprising the amino acid sequence of SEQ ID NO:425, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:427 and a variable light chain comprising the amino acid sequence of SEQ ID NO:429, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:431 and a variable light chain comprising the amino acid

sequence of SEQ ID NO:433, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:435 and a variable light chain comprising the amino acid sequence of SEQ ID NO:437, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:439 and a variable light chain comprising the amino acid sequence of SEQ ID NO:441, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:443 and a variable light chain comprising the amino acid sequence of SEQ ID NO:445, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:447 and a variable light chain comprising the amino acid sequence of SEQ ID NO:449, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:451 and a variable light chain comprising the amino acid sequence of SEQ ID NO:453, a variable heavy chain comprising the amino acid sequence of SEQ ID NO:455 and a variable light chain comprising the amino acid sequence of SEQ ID NO:457, or a variable heavy chain comprising the amino acid sequence of SEQ ID NO:459 and a variable light chain comprising the amino acid sequence of SEQ ID NO:461.

In an embodiment of the invention the binding molecules having SARS-CoV neutralising activity are the binding molecules comprising at least a CDR3 region, preferably a heavy chain CDR3 region, comprising the amino acid sequence selected from the group consisting of SEQ ID NO:11 and SEQ ID NO:12. In a further embodiment, the binding molecules having SARS-CoV neutralising activity are the binding molecules comprising a variable heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NO:35 and SEQ ID NO:37. In yet a further embodiment, the binding molecules having SARS-CoV neutralising activity are the binding molecules comprising a variable heavy chain comprising the amino acid sequence of SEQ ID NO:35 and a variable light

chain comprising the amino acid sequence of SEQ ID NO:41 or a variable heavy chain comprising the amino acid sequence of SEQ ID NO:37 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41. In a prefered embodiment the binding molecules having SARS-CoV neutralising activity of the invention are administered in IgG1 or IgA (for instance for mucosal administration) format.

Another aspect of the invention includes functional variants of binding molecules as defined herein. Molecules are considered to be functional variants of a binding molecule according to the invention, if the variants are capable of competing for specifically binding to SARS-CoV or a fragment thereof with the parent binding molecules. In other words, when the functional variants are still capable of binding to SARS-CoV or a fragment thereof. Functional variants include, but are not limited to, derivatives that are substantially similar in primary structural sequence, but which contain *e.g. in vitro or in vivo* modifications, chemical and/or biochemical, that are not found in the parent binding molecule. Such modifications include *inter alia* acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI-anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation,

sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, ubiquitination, and the like.

Alternatively, functional variants can be binding molecules as defined in the present invention comprising an amino acid sequence containing substitutions, insertions, deletions or combinations thereof of one or more amino acids compared to the amino acid sequences of the parent binding molecules. Furthermore, functional variants can comprise truncations of the amino acid sequence at either or both the amino or carboxy termini. Functional variants according to the invention may have the same or different, either higher or lower, binding affinities compared to the parent binding molecule but are still capable of binding to SARS-CoV or a fragment thereof. For instance, functional variants according to the invention may have increased or decreased binding affinities for SARS-CoV or a fragment thereof compared to the parent binding molecules. Preferably, the amino acid sequences of the variable regions, including, but not limited to, framework regions, hypervariable regions, in particular the CDR3 regions, are modified. Generally, the light chain and the heavy chain variable regions comprise three hypervariable regions, comprising three CDRs, and more conserved regions, the so-called framework regions (FRs). The hypervariable regions comprise amino acid residues from CDRs and amino acid residues from hypervariable loops. Functional variants intended to fall within the scope of the present invention have at least about 50% to about 99%, preferably at least about 60% to about 99%, more preferably at least about 70% to about 99%, even more preferably at least about 80% to about 99%, most preferably at least about 90% to about 99%, in particular at least about 95% to about 99%, and in particluar at least about 97% to about 99% amino acid sequence homology

with the parent binding molecules as defined herein. Computer algorithms such as *inter alia* Gap or Bestfit known to a person skilled in the art can be used to optimally align amino acid sequences to be compared and to define similar or identical amino acid residues. Functional variants can be obtained by altering the parent binding molecules or parts thereof by general molecular biology methods known in the art including, but not limited to, error-prone PCR, oligonucleotide-directed mutagenesis and site-directed mutagenesis. Preferably, the functional variants of the invention have SARS-CoV neutralizing activity. This neutralizing activity may either be higher or be lower compared to the parent binding molecules. Furthermore, the functional variants may inhibit or downregulate SARS-CoV replication, are complement fixing binding molecules capable of assisting in the lysis of enveloped SARS-CoV and/or act as opsonins and augment phagocytosis of SARS-CoV either by promoting its uptake via Fc or C3b receptors or by agglutinating SARS-CoV to make it more easily phagocytosed.

In yet a further aspect, the invention includes immunoconjugates, *i.e.* molecules comprising at least one binding molecule or functional variant thereof as defined herein and further comprising at least one tag, such as *inter alia* a detectable moiety/agent. Also contemplated in the present invention are mixtures of immunoconjugates according to the invention or mixtures of at least one immunoconjugates according to the invention and another molecule, such as a therapeutic agent or another binding molecule or immunoconjugate. In a further embodiment, the immunoconjugates of the invention may comprise more than one tag. These tags can be the same or distinct from each other and can be joined/conjugated non-covalently to the binding molecules. The

tag(s) can also be joined/conjugated directly to the binding molecules through covalent bonding, including, but not limited to, disulfide bonding, hydrogen bonding, electrostatic bonding, recombinant fusion and conformational bonding. Alternatively, the tag(s) can be joined/conjugated to the binding molecules by means of one or more linking compounds. Techniques for conjugating tags to binding molecules are well known to the skilled artisan.

The tags of the immunoconjugates of the present invention may be therapeutic agents, but preferably they are detectable moieties/agents. Immunoconjugates comprising a detectable agent can be used diagnostically to, for example, assess if a subject has been infected with SARS-CoV or monitor the development or progression of a SARS-CoV infection as part of a clinical testing procedure to, *e.g.*, determine the efficacy of a given treatment regimen. However, they may also be used for other detection and/or analytical and/or diagnostic purposes. Detectable moieties/agents include, but are not limited to, enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals, and nonradioactive paramagnetic metal ions.

The tags used to label the binding molecules for detection and/or analytical and/or diagnostic purposes depend on the specific detection/analysis/diagnosis techniques and/or methods used such as *inter alia* immunohistochemical staining of (tissue) samples, flow cytometric detection, scanning laser cytometric detection, fluorescent immunoassays, enzyme-linked immunosorbent assays (ELISA's), radioimmunoassays (RIA's), bioassays (*e.g.*, neutralisation assays), Western blotting applications, etc. For immunohistochemical staining of tissue samples preferred labels are enzymes that catalyze production

and local deposition of a detectable product. Enzymes typically conjugated to binding molecules to permit their immunohistochemical visualization are well-known and include, but are not limited to, acetylcholinesterase, alkaline phosphatase, beta-galactosidase, glucose oxidase, horseradish peroxidase, and urease. Typical substrates for production and deposition of visually detectable products include, but are not limited to, o-nitrophenyl-beta-D-galactopyranoside (ONPG), o-phenylenediamine dihydrochloride (OPD), p-nitrophenyl phosphate (PNPP), p-nitrophenyl-beta-D-galactopryanoside (PNPG), 3', 3'diaminobenzidine (DAB), 3-amino-9-ethylcarbazole (AEC), 4-chloro-1-naphthol (CN), 5-bromo-4-chloro-3-indolyl-phosphate (BCIP), ABTS, BluoGal, iodonitrotetrazolium (INT), nitroblue tetrazolium chloride (NBT), phenazine methosulfate (PMS), phenolphthalein monophosphate (PMP), tetramethyl benzidine (TMB), tetranitroblue tetrazolium (TNBT), X-Gal, X-Gluc, and X-glucoside. Other substrates that can be used to produce products for local deposition are luminescent substrates. For example, in the presence of hydrogen peroxide, horseradish peroxidase can catalyze the oxidation of cyclic diacylhydrazides such as luminol. Next to that, binding molecules of the immunoconjugate of the invention can also be labeled using colloidal gold or they can be labeled with radioisotopes, such as ^{33}p, ^{32}p, ^{35}S, ^{3}H, and ^{125}I. Binding molecules of the invention can be attached to radionuclides directly or indirectly via a chelating agent by methods well known in the art.

When the binding molecules of the present invention are used for flow cytometric detections, scanning laser cytometric detections, or fluorescent immunoassays, they can usefully be labeled with fluorophores. A wide variety of fluorophores useful for fluorescently labeling the binding molecules of the

present invention include, but are not limited to, Alexa Fluor and Alexa Fluor&commat dyes, BODIPY dyes, Cascade Blue, Cascade Yellow, Dansyl, lissamine rhodamine B, Marina Blue, Oregon Green 488, Oregon Green 514, Pacific Blue, rhodamine 6G, rhodamine green, rhodamine red, tetramethylrhodamine, Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, fluorescein isothiocyanate (FITC), allophycocyanin (APC), R-phycoerythrin (PE), peridinin chlorophyll protein (PerCP), Texas Red, fluorescence resonance energy tandem fluorophores such as PerCP-Cy5.5, PE-Cy5, PE-Cy5.5, PE-Cy7, PE-Texas Red, and APC-Cy7. When the binding molecules of the present invention are used for secondary detection using labeled avidin, streptavidin, captavidin or neutravidin, the binding molecules may be labeled with biotin to form suitable prosthetic group complexes.

When the immunoconjugates of the invention are used for *in vivo* diagnostic use, the binding molecules can also be made detectable by conjugation to *e.g.* magnetic resonance imaging (MRI) contrast agents, such as gadolinium diethylenetriaminepentaacetic acid, to ultrasound contrast agents or to X-ray contrast agents, or by radioisotopic labeling.

A suitable luminescent material includes, but is not limited to, luminol and suitable bioluminescent materials include, but are not limited to, luciferase, luciferin, and aequorin.

Furthermore, the binding molecules, functional variants or immunoconjugates of the invention can also be attached to solid supports, which are particularly useful for *in vitro* immunoassays or purification of SARS-CoV or a fragment thereof. Such solid supports might be porous or nonporous, planar or nonplanar and include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene,

polyvinyl chloride or polypropylene supports. The binding molecules can also for example usefully be conjugated to filtration media, such as NHS-activated Sepharose or CNBr-activated Sepharose for purposes of immunoaffinity chromatography. They can also usefully be attached to paramagnetic microspheres, typically by biotin-streptavidin interaction. The microspheres can be used for isolation of SARS-CoV or a fragment thereof from a sample containing SARS-CoV or a fragment thereof. As another example, the binding molecules of the present invention can usefully be attached to the surface of a microtiter plate for ELISA.

The binding molecules of the present invention or functional fragments thereof can be fused to marker sequences, such as a peptide to facilitate purification. Examples include, but are not limited to, the hexa-histidine tag, the hemagglutinin (HA) tag, the myc tag or the flag tag.

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate. In another aspect the binding molecules of the invention may be conjugated/attached to one or more antigens. Preferably, these antigens are antigens which are recognised by the immune system of a subject to which the binding molecule-antigen conjugate is administered. The antigens may be identical but may also differ from each other. Conjugation methods for attaching the antigens and binding molecules are well known in the art and include, but are not limited to, the use of cross-linking agents. The binding molecules will bind to SARS-CoV and the antigens attached to the binding molecules will initiate a powerful T-cell attack on the conjugate which will eventually lead to the destruction of the SARS-CoV.

Next to producing immunoconjugates chemically by conjugating, directly or indirectly via for instance a linker,

the immunoconjugates can be produced as fusion proteins comprising the binding molecules of the invention and a suitable tag. Fusion proteins can be produced by methods known in the art such as, *e.g.*, recombinantly by constructing nucleic acid molecules comprising nucleotide sequences encoding the binding molecules in frame with nucleotide sequences encoding the suitable tag(s) and then expressing the nucleic acid molecules.

It is another aspect of the present invention to provide a nucleic acid molecule encoding at least a binding molecule or functional fragment thereof according to the invention. Such nucleic acid molecules can be used as intermediates for cloning purposes, *e.g.* in the process of affinity maturation described above. In a preferred embodiment, the nucleic acid molecules are isolated or purified.

The skilled man will appreciate that functional variants of these nucleic acid molecules are also intended to be a part of the present invention. Functional variants are nucleic acid sequences that can be directly translated, using the standard genetic code, to provide an amino acid sequence identical to that translated from the parent nucleic acid molecules.

Preferably, the nucleic acid molecules encode binding molecules comprising a CDR3 region, preferably a heavy chain CDR3 region, comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300 and SEQ ID NO:301.

Even more preferably, the nucleic acid molecules encode binding molecules comprising a variable heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:303, SEQ ID NO:307, SEQ ID NO:311, SEQ ID NO:315, SEQ ID NO:319, SEQ ID NO:323, SEQ ID NO:327, SEQ ID NO:331, SEQ ID NO:335, SEQ ID NO:339, SEQ ID NO:343, SEQ ID NO:347, SEQ ID NO:351, SEQ ID NO:355, SEQ ID NO:359, SEQ ID NO:363, SEQ ID NO:367, SEQ ID NO:371, SEQ ID NO:375, SEQ ID NO:379, SEQ ID NO:383, SEQ ID NO:387, SEQ ID NO:391, SEQ ID NO:395, SEQ ID NO:399, SEQ ID NO:403, SEQ ID NO:407, SEQ ID NO:411, SEQ ID NO:415, SEQ ID NO:419, SEQ ID NO:423, SEQ ID NO:427, SEQ ID NO:431, SEQ ID NO:435, SEQ ID NO:439, SEQ ID NO:443, SEQ ID NO:447, SEQ ID NO:451, SEQ ID NO:455 and SEQ ID NO:459.

In yet another embodiment, the nucleic acid molecules encode binding molecules comprising a variable heavy chain comprising the amino acid sequence of SEQ ID NO:15 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:17 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:19 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:21 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:23 and a variable light chain comprising the amino acid sequence of SEQ

ID NO:43, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:25 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:27 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:29 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:31 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:33 and a variable light chain comprising the amino acid sequence of SEQ ID NO:45, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:35 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:37 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:39 and a variable light chain comprising the amino acid sequence of SEQ ID NO:45, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:80 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:82 and a variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:84 and a variable light chain comprising the amino acid sequence of SEQ ID NO:88, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:86 and a

variable light chain comprising the amino acid sequence of SEQ ID NO:41, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:303 and a variable light chain comprising the amino acid sequence of SEQ ID NO:305, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:307 and a variable light chain comprising the amino acid sequence of SEQ ID NO:309, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:311 and a variable light chain comprising the amino acid sequence of SEQ ID NO:313, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:315 and a variable light chain comprising the amino acid sequence of SEQ ID NO:317, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:319 and a variable light chain comprising the amino acid sequence of SEQ ID NO:321, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:323 and a variable light chain comprising the amino acid sequence of SEQ ID NO:325, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:327 and a variable light chain comprising the amino acid sequence of SEQ ID NO:329, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:331 and a variable light chain comprising the amino acid sequence of SEQ ID NO:333, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:335 and a variable light chain comprising the amino acid sequence of SEQ ID NO:337, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:339 and a variable light chain comprising the amino acid sequence of SEQ ID NO:341, or they encode a variable heavy chain comprising the amino acid

sequence of SEQ ID NO:343 and a variable light chain comprising the amino acid sequence of SEQ ID NO:345, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:347 and a variable light chain comprising the amino acid sequence of SEQ ID NO:349, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:351 and a variable light chain comprising the amino acid sequence of SEQ ID NO:353, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:355 and a variable light chain comprising the amino acid sequence of SEQ ID NO:357, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:359 and a variable light chain comprising the amino acid sequence of SEQ ID NO:361, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:363 and a variable light chain comprising the amino acid sequence of SEQ ID NO:365, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:367 and a variable light chain comprising the amino acid sequence of SEQ ID NO:369, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:371 and a variable light chain comprising the amino acid sequence of SEQ ID NO:373, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:375 and a variable light chain comprising the amino acid sequence of SEQ ID NO:377, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:379 and a variable light chain comprising the amino acid sequence of SEQ ID NO:381, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:383 and a variable light chain comprising the amino acid sequence of SEQ ID NO:385, or they

encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:387 and a variable light chain comprising the amino acid sequence of SEQ ID NO:389, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:391 and a variable light chain comprising the amino acid sequence of SEQ ID NO:393, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:395 and a variable light chain comprising the amino acid sequence of SEQ ID NO:397, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:399 and a variable light chain comprising the amino acid sequence of SEQ ID NO:401, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:403 and a variable light chain comprising the amino acid sequence of SEQ ID NO:405, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:407 and a variable light chain comprising the amino acid sequence of SEQ ID NO:409, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:411 and a variable light chain comprising the amino acid sequence of SEQ ID NO:413, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:415 and a variable light chain comprising the amino acid sequence of SEQ ID NO:417, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:419 and a variable light chain comprising the amino acid sequence of SEQ ID NO:421, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:423 and a variable light chain comprising the amino acid sequence of SEQ ID NO:425, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:427 and a variable light chain

comprising the amino acid sequence of SEQ ID NO:429, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:431 and a variable light chain comprising the amino acid sequence of SEQ ID NO:433, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:435 and a variable light chain comprising the amino acid sequence of SEQ ID NO:437, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:439 and a variable light chain comprising the amino acid sequence of SEQ ID NO:441, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:443 and a variable light chain comprising the amino acid sequence of SEQ ID NO:445, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:447 and a variable light chain comprising the amino acid sequence of SEQ ID NO:449, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:451 and a variable light chain comprising the amino acid sequence of SEQ ID NO:453, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:455 and a variable light chain comprising the amino acid sequence of SEQ ID NO:457, or they encode a variable heavy chain comprising the amino acid sequence of SEQ ID NO:459 and a variable light chain comprising the amino acid sequence of SEQ ID NO:461.

In a specific embodiment of the invention the nucleic acid molecules encoding the variable heavy chain of the binding molecules of the invention comprise a nucleotide sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:79, SEQ ID NO:81,

SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:302, SEQ ID NO:306, SEQ ID NO:310, SEQ ID NO:314, SEQ ID NO:318, SEQ ID NO:322, SEQ ID NO:326, SEQ ID NO:330, SEQ ID NO:334, SEQ ID NO:338, SEQ ID NO:342, SEQ ID NO:346, SEQ ID NO:350, SEQ ID NO:354, SEQ ID NO:358, SEQ ID NO:362, SEQ ID NO:366, SEQ ID NO:370, SEQ ID NO:374, SEQ ID NO:378, SEQ ID NO:382, SEQ ID NO:386, SEQ ID NO:390, SEQ ID NO:394, SEQ ID NO:398, SEQ ID NO:402, SEQ ID NO:406, SEQ ID NO:410, SEQ ID NO:414, SEQ ID NO:418, SEQ ID NO:422, SEQ ID NO:426, SEQ ID NO:430, SEQ ID NO:434, SEQ ID NO:438, SEQ ID NO:442, SEQ ID NO:446, SEQ ID NO:450, SEQ ID NO:454 and SEQ ID NO:458.

In yet another specific embodiment of the present invention, the nucleic acid molecules encoding the variable light chain of the binding molecules of the invention comprise a nucleotide sequence selected of the group consisting of SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:87, SEQ ID NO:304, SEQ ID NO:308, SEQ ID NO:312, SEQ ID NO:316, SEQ ID NO:320, SEQ ID NO:324, SEQ ID NO:328, SEQ ID NO:332, SEQ ID NO:336, SEQ ID NO:340, SEQ ID NO:344, SEQ ID NO:348, SEQ ID NO:352, SEQ ID NO:356, SEQ ID NO:360, SEQ ID NO:364, SEQ ID NO:368, SEQ ID NO:372, SEQ ID NO:376, SEQ ID NO:380, SEQ ID NO:384, SEQ ID NO:388, SEQ ID NO:392, SEQ ID NO:396, SEQ ID NO:400, SEQ ID NO:404, SEQ ID NO:408, SEQ ID NO:412, SEQ ID NO:416, SEQ ID NO:420, SEQ ID NO:424, SEQ ID NO:428, SEQ ID NO:432, SEQ ID NO:436, SEQ ID NO:440, SEQ ID NO:444, SEQ ID NO:448, SEQ ID NO:452, SEQ ID NO:456 and SEQ ID NO:460.

It is another aspect of the invention to provide vectors, *i.e.* nucleic acid constructs, comprising one or more nucleic acid molecules according to the present invention. Vectors can be derived from plasmids such as *inter alia* F, R1, RP1, Col, pBR322, TOL, Ti, etc; cosmids; phages such as lambda, lambdoid, M13, Mu, P1, P22, Q_{μ}, T-even, T-odd, T2, T4, T7, etc;

plant viruses such as *inter alia* alfalfa mosaic virus, bromovirus, capillovirus, carlavirus, carmovirus, caulivirus, clostervirus, comovirus, cryptovirus, cucumovirus, dianthovirus, fabavirus, fijivirus, furovirus, geminivirus, hordeivirus, ilarvirus, luteovirus, machlovirus, marafivirus, necrovirus, nepovirus, phytorepvirus, plant rhabdovirus, potexvirus, potyvirus, sobemovirus, tenuivirus, tobamovirus, tobravirus, tomato spotted wilt virus, tombusvirus, tymovirus, etc; or animal viruses such as *inter alia* adenovirus, arenaviridae, baculoviridae, birnaviridae, bunyaviridae, calciviridae, cardioviruses, coronaviridae, corticoviridae, cystoviridae, Epstein-Barr virus, enteroviruses, filoviridae, flaviviridae, Foot-and-Mouth disease virus, hepadnaviridae, hepatitis viruses, herpesviridae, immunodeficiency viruses, influenza virus, inoviridae, iridoviridae, orthomyxoviridae, papovaviruses, paramyxoviridae, parvoviridae, picornaviridae, poliovirus, polydnaviridae, poxviridae, reoviridae, retroviruses, rhabdoviridae, rhinoviruses, Semliki Forest virus, tetraviridae, togaviridae, toroviridae, vaccinia virus, vescular stomatitis virus, etc. Vectors can be used for cloning and/or for expression of the binding molecules of the invention and might even be used for gene therapy purposes. Vectors comprising one or more nucleic acid molecules according to the invention operably linked to one or more expression-regulating nucleic acid molecules are also covered by the present invention. The choice of the vector is dependent on the recombinant procedures followed and the host used. Introduction of vectors in host cells can be effected by *inter alia* calcium phosphate transfection, virus infection, DEAE-dextran mediated transfection, lipofectamin transfection or electroporation. Vectors may be autonomously replicating or may replicate together with the chromosome into which they

have been integrated. Preferably, the vectors contain one or more selection markers. The choice of the markers may depend on the host cells of choice, although this is not critical to the invention as is well known to persons skilled in the art. They include, but are not limited to, kanamycin, neomycin, puromycin, hygromycin, zeocin, thymidine kinase gene from Herpes simplex virus (HSV-TK), dihydrofolate reductase gene from mouse (dhfr). Vectors comprising one or more nucleic acid molecules encoding the binding molecules as described above operably linked to one or more nucleic acid molecules encoding proteins or peptides that can be used to isolate the binding molecules are also covered by the invention. These proteins or peptides include, but are not limited to, glutathione-S-transferase, maltose binding protein, metal-binding polyhistidine, green fluorescent protein, luciferase and beta-galactosidase.

Hosts containing one or more copies of the vectors mentioned above are an additional subject of the present invention. Preferably, the hosts are host cells. Host cells include, but are not limited to, cells of mammalian, plant, insect, fungal or bacterial origin. Bacterial cells include, but are not limited to, cells from Gram positive bacteria such as several species of the genera *Bacillus*, *Streptomyces* and *Staphylococcus* or cells of Gram negative bacteria such as several species of the genera Escherichia, such as *E. coli*, and *Pseudomonas*. In the group of fungal cells preferably yeast cells are used. Expression in yeast can be achieved by using yeast strains such as *inter alia Pichia pastoris*, *Saccharomyces cerevisiae* and *Hansenula polymorpha*. Furthermore, insect cells such as cells from Drosophila and Sf9 can be used as host cells. Besides that, the host cells can be plant cells such as *inter alia* cells from crop plants

such as forestry plants, or cells from plants providing food and raw materials such as cereal plants, or medicinal plants, or cells from ornamentals, or cells from flower bulb crops. Transformed (transgenic) plants or plant cells are produced by known methods, for example, Agrobacterium-mediated gene transfer, transformation of leaf discs, protoplast transformation by polyethylene glycol-induced DNA transfer, electroporation, sonication, microinjection or bolistic gene transfer. Additionally, a suitable expression system can be a baculovirus system. Expression systems using mammalian cells such as Chinese Hamster Ovary (CHO) cells, COS cells, BHK cells or Bowes melanoma cells are preferred in the present invention. Mammalian cells provide expressed proteins with posttranslational modifications that are most similar to natural molecules of mammalian origin. Since the present invention deals with molecules that may have to be administered to humans, a completely human expression system would be particularly preferred. Therefore, even more preferably, the host cells are human cells. Examples of human cells are *inter alia* HeLa, 911, AT1080, A549, 293 and HEK293T cells. Preferred mammalian cells are human retina cells such as 911 cells or the cell line deposited at the European Collection of Cell Cultures (ECACC), CAMR, Salisbury, Wiltshire SP4 OJG, Great Britain on 29 February 1996 under number 96022940 and marketed under the trademark PER.C6® (PER.C6 is a registered trademark of Crucell Holland B.V.). For the purposes of this application "PER.C6" refers to cells deposited under number 96022940 or ancestors, passages up-stream or downstream as well as descendants from ancestors of deposited cells, as well as derivatives of any of the foregoing.

In preferred embodiments, the human producer cells comprise at least a functional part of a nucleic acid sequence encoding an adenovirus E1 region in expressible format. In even more preferred embodiments, said host cells are derived from a human retina and immortalised with nucleic acids comprising adenoviral E1 sequences, such as the cell line deposited at the European Collection of Cell Cultures (ECACC), CAMR, Salisbury, Wiltshire SP4 OJG, Great Britain on 29 February 1996 under number 96022940 and marketed under the trademark PER.C6™, and derivatives thereof. Production of recombinant proteins in host cells can be performed according to methods well known in the art. The use of the cells marketed under the trademark PER.C6™ as a production platform for proteins of interest has been described in WO 00/63403 the disclosure of which is incorporated herein by reference in its entirety.

A method of producing a binding molecule or a functional variant according to the invention is an additional part of the invention. The method comprises the steps of a) culturing a host according to the invention under conditions conducive to the expression of the binding molecule or functional variant, and b) optionally, recovering the expressed binding molecule or functional variant. The expressed binding molecules or functional variants thereof can be recovered from the cell free extract, but preferably they are recovered from the culture medium. Methods to recover proteins, such as binding molecules, from cell free extracts or culture medium are well known to the man skilled in the art. Binding molecules or functional variants thereof as obtainable by the above described method are also a part of the present invention.

Alternatively, next to the expression in hosts, such as host cells, the binding molecules or functional variants thereof of the invention can be produced synthetically by conventional peptide synthesizers or in cell-free translation systems using RNA nucleic acid derived from DNA molecules according to the invention. Binding molecule or functional variants thereof as obtainable by the above described synthetic production methods or cell-free translation systems are also a part of the present invention.

In yet another embodiment, human binding molecules of the present invention can also be produced in transgenic, non-human, mammals such as *inter alia* rabbits, goats or cows, and secreted into for instance the milk thereof.

In yet another alternative embodiment, binding molecules according to the present invention, preferably human binding molecules specifically binding to SARS-CoV or a fragment thereof, may be generated by transgenic non-human mammals, such as for instance transgenic mice or rabbits, that express human immunoglobulin genes. Preferably, the transgenic non-human mammals have a genome comprising a human heavy chain transgene and a human light chain transgene encoding all or a portion of the human binding molecules as described above. The transgenic non-human mammals can be immunized with a purified or enriched preparation of SARS-CoV or a fragment thereof. Protocols for immunizing non-human mammals are well established in the art. See Using Antibodies: A Laboratory Manual, Edited by: E. Harlow, D. Lane (1998), Cold Spring Harbor Laboratory, Cold Spring Harbor, New York and Current Protocols in Immunology, Edited by: J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober (2001), John Wiley & Sons Inc., New York, the disclosures of which are incorporated herein by reference. Immunization protocols often

include multiple immunizations, either with or without adjuvants such as Freund's complete adjuvant and Freund's incomplete adjuvant, but may also include naked DNA immunizations. In another embodiment, the human binding molecules are produced by B cells or plasma cells derived from the transgenic animals. In yet another embodiment, the human binding molecules are produced by hybridomas which are prepared by fusion of B cells obtained from the above described transgenic non-human mammals to immortalized cells. B cells, plasma cells and hybridomas as obtainable from the above described transgenic non-human mammals and human binding molecules as obtainable from the above described transgenic non-human mammals, B cells, plasma cells and hybridomas are also a part of the present invention.

In a further aspect, the invention provides a method of identifying binding molecules, preferably human binding molecules such as human monoclonal antibodies or fragments thereof, according to the invention or nucleic acid molecules according to the invention and comprises the steps of a) contacting a phage library of binding molecules, preferably human binding molecules, with SARS-CoV or a fragment thereof, b) selecting at least once for a phage binding to the SARS-CoV or the fragment thereof, and c) separating and recovering the phage binding to the SARS-CoV or the fragment thereof. The selection step according to the present invention is preferably performed in the presence of SARS-CoV which is inactivated. The SARS-CoV may be isolated or non-isolated, *e.g.* present in serum and/or blood of an infected individual. Alternatively, the selection step may be performed in the presence of a fragment of SARS-CoV such as an extracellular part of the SARS-CoV, one or more proteins or (poly)peptides derived from SARS-CoV, fusion proteins comprising these

proteins or (poly)peptides, and the like. Phage display methods for identifying and obtaining binding molecules, *e.g.* antibodies, are by now well-established methods known by the person skilled in the art. They are *e.g.* described in US Patent Number 5,696,108; Burton and Barbas, 1994; de Kruif *et al.*, 1995b; and Phage Display: A Laboratory Manual. Edited by: CF Barbas, DR Burton, JK Scott and GJ Silverman (2001), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. All these references are herewith incorporated herein in their entirety. For the construction of phage display libraries, collections of human monoclonal antibody heavy and light chain variable region genes are expressed on the surface of bacteriophage, preferably filamentous bacteriophage, particles, in for example single-chain Fv (scFv) or in Fab format (see de Kruif *et al.*, 1995b). Large libraries of antibody fragment-expressing phages typically contain more than $1.0*10^9$ antibody specificities and may be assembled from the immunoglobulin V regions expressed in the B lymphocytes of immunized- or non-immunized individuals. In a specific embodiment of the invention the phage library of binding molecules, preferably scFv phage library, is prepared from RNA isolated from cells obtained from a subject that has been vaccinated or exposed to a SARS-CoV. RNA can be isolated from *inter alia* bone marrow or peripheral blood, preferably peripheral blood lymphocytes. The subject can be an animal vaccinated or exposed to SARS-CoV, but is preferably a human subject which has been vaccinated or has been exposed to SARS-CoV. Preferably the human subject has recovered from SARS-CoV.

Alternatively, phage display libraries may be constructed from immunoglobulin variable regions that have been partially assembled *in vitro* to introduce additional antibody diversity in the library (semi-synthetic libraries). For example, *in*

vitro assembled variable regions contain stretches of synthetically produced, randomized or partially randomized DNA in those regions of the molecules that are important for antibody specificity, *e.g.* CDR regions. SARS-CoV specific phage antibodies can be selected from the library by immobilising target antigens such as antigens from SARS-CoV on a solid phase and subsequently exposing the target antigens to a phage library to allow binding of phages expressing antibody fragments specific for the solid phase-bound antigen(s). Non-bound phages are removed by washing and bound phages eluted from the solid phase for infection of *Escherichia coli* (*E.coli*) bacteria and subsequent propagation. Multiple rounds of selection and propagation are usually required to sufficiently enrich for phages binding specifically to the target antigen(s). If desired, before exposing the phage library to target antigens the phage library can first be subtracted by exposing the phage library to non-target antigens bound to a solid phase. Phages may also be selected for binding to complex antigens such as complex mixtures of SARS-CoV proteins or (poly)peptides, host cells expressing one or more proteins or (poly)peptides of SARS-CoV, or SARS-CoV itself. Antigen specific phage antibodies can be selected from the library by incubating a solid phase with bound thereon a preparation of inactivated SARS-CoV with the phage antibody library to let for example the scFv or Fab part of the phage bind to the proteins/polypeptides of the SARS-CoV preparation. After incubation and several washes to remove unbound and loosely attached phages, the phages that have bound with their scFv or Fab part to the preparation are eluted and used to infect *Escherichia coli* to allow amplification of the new specificity. Generally, one or more selection rounds are required to separate the phages of interest from the large

excess of non-binding phages. Alternatively, known proteins or (poly)peptides of the SARS-CoV can be expressed in host cells and these cells can be used for selection of phage antibodies specific for the proteins or (poly)peptides. A phage display method using these host cells can be extended and improved by subtracting non-relevant binders during screening by addition of an excess of host cells comprising no target molecules or non-target molecules that are similar, but not identical, to the target, and thereby strongly enhance the chance of finding relevant binding molecules (This process is referred to as the Mabstract™ process. Mabstract™ is a pending trademark application of Crucell Holland B.V., see also US Patent Number 6,265,150 which is incorporated herein by reference).

In yet a further aspect, the invention provides a method of obtaining a binding molecule, preferably a human binding molecule or a nucleic acid molecule according to the invention, wherein the method comprises the steps of a) performing the above described method of identifying binding molecules, preferably human binding molecules such as human monoclonal antibodies or fragments thereof according to the invention, or nucleic acid molecules according to the invention, and b) isolating from the recovered phage the human binding molecule and/or the nucleic acid encoding the human binding molecule. Once a new monoclonal phage antibody has been established or identified with the above mentioned method of identifying binding molecules or nucleic acid molecules encoding the binding molecules, the DNA encoding the scFv or Fab can be isolated from the bacteria or phages and combined with standard molecular biological techniques to make constructs encoding bivalent scFv's or complete human immunoglobulins of a desired specificity (*e.g.* IgG, IgA or IgM). These constructs can be transfected into suitable cell

lines and complete human monoclonal antibodies can be produced (see Huls *et al.*, 1999; Boel *et al.*, 2000).

In a further aspect, the invention is directed to a phage library of binding molecules, preferably a scFv phage display library which is prepared from RNA isolated from cells obtained from a subject that has been vaccinated or exposed to a SARS-CoV. RNA can be isolated from *inter alia* bone marrow or peripheral blood, preferably peripheral blood lymphocytes. The subject can be an animal vaccinated or exposed to SARS-CoV, but is preferably a human subject which has been vaccinated or has been exposed to SARS-CoV. Preferably the human subject has recovered from SARS-CoV.

In yet a further aspect, the invention provides compositions comprising at least one binding molecule, at least one functional variant or fragment thereof, at least one immunoconjugate according to the invention or a combination thereof. In addition to that, the compositions may comprise *inter alia* stabilising molecules, such as albumin or polyethylene glycol, or salts. Preferably, the salts used are salts that retain the desired biological activity of the binding molecules and do not impart any undesired toxicological effects. Examples of such salts include, but are not limited to, acid addition salts and base addition salts. Acid addition salts include, but are not limited to, those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted alkanoic acids, hydroxy alkanoic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include, but are not limited to, those derived from alkaline earth metals, such as sodium, potassium,

magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chloroprocaine, choline, diethanolamine, ethylenediamine, procaine and the like. If necessary, the binding molecules of the invention may be coated in or on a material to protect them from the action of acids or other natural or non-natural conditions that may inactivate the binding molecules.

In yet a further aspect, the invention provides compositions comprising at least one nucleic acid molecule as defined in the present invention. The compositions may comprise aqueous solutions such as aqueous solutions containing salts (*e.g.*, NaCl or salsts as described above), detergents (*e.g.*, SDS) and/or other suitable components.

Furthermore, the present invention pertains to pharmaceutical compositions comprising at least one binding molecule according to the invention, at least one functional variant or fragment thereof, at least one immunoconjugate according to the invention, at least one composition according to the invention, or combinations thereof. The pharmaceutical composition of the invention further comprises at least one pharmaceutically acceptable excipient.

A pharmaceutical composition according to the invention can further comprise at least one other therapeutic, prophylactic and/or diagnostic agent. Preferably, the pharmaceutical composition comprises at least one other prophylactic and/or therapeutic agent. Preferably, said further therapeutic and/or prophylactic agents are agents capable of preventing and/or treating an infection and/or a condition resulting from SARS-CoV. Therapeutic and/or prophylactic agents include, but are not limited to, anti-viral agents. Such agents can be binding molecules, small

molecules, organic or inorganic compounds, enzymes, polynucleotide sequences etc.

Examples of anti-viral agents include, but are not limited to, abacavir, acyclovir, adefovir, afovirsen, amantadine, amprenavir, AZT, camptothecins, castanospermine, cidofovir, D4T, ddC, ddI, d4T, delavirdine, didanosine, efavirenz, famciclovir, fialuridine, foscarnet, FTC, ganciclovir, GG167, idoxuridine, indinavir, interferon alpha, lamivudine, lobucavir, loviride, nelfinavir, nevirapine, oseltamivir, penciclovir, pirodavir, ribavirin, rimantadine, ritonavir, saquinavir, sICAM-1, sorivudine, stavudine, trifluridine, 3TC, valacyclovir, vidarabine, zalcitabine, zanamivir, zidovudine, and pharmaceutically acceptable salts, acids or derivatives of any of the above. Other agents that are currently used to treat patients infected with SARS-CoV are interferon-alpha, steroids and potential replicase inhibitors. Furthermore, patients infected with SARS-CoV are currently treated by transfusion of serum produced from blood donated by recovering/recovered SARS patients who have produced antibodies after being exposed to the virus. Agents capable of preventing and/or treating an infection with SARS-CoV and/or a condition resulting from SARS-CoV that are in the experimental phase might also be used as other therapeutic and/or prophylactic agents useful in the present invention.

The binding molecules of the invention or pharmaceutical compositions of the invention can be tested in suitable animal model systems prior to use in humans. Such animal model systems include, but are not limited to, mice, rats, chicken, cows, monkeys, pigs, dogs, rabbits, etc. Any animal system well-known in the art may be used.

Typically, pharmaceutical compositions must be sterile and stable under the conditions of manufacture and storage. The

binding molecules, variant or fragments thereof, immunoconjugates, nucleic acid molecules or compositions of the present invention can be in powder form for reconstitution in the appropriate pharmaceutically acceptable excipient before or at the time of delivery. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Alternatively, the binding molecules, variant or fragments thereof, immunoconjugates, nucleic acid molecules or compositions of the present invention can be in solution and the appropriate pharmaceutically acceptable excipient can be added and/or mixed before or at the time of delivery to provide a unit dosage injectable form. Preferably, the pharmaceutically acceptable excipient used in the present invention is suitable to high drug concentration, can maintain proper fluidity and, if necessary, can delay absorption.

The choice of the optimal route of administration of the pharmaceutical compositions will be influenced by several factors including the physico-chemical properties of the active molecules within the compositions, the urgency of the clinical situation and the relationship of the plasma concentrations of the active molecules to the desired therapeutic effect. For instance, if necessary, the binding molecules of the invention can be prepared with carriers that will protect them against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can *inter alia* be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid,

collagen, polyorthoesters, and polylactic acid. Furthermore, it may be necessary to coat the binding molecules with, or co-administer the binding molecules with, a material or compound that prevents the inactivation of the binding molecules. For example, the binding molecules may be administered to a subject in an appropriate carrier, for example, liposomes, or a diluent.

The routes of administration can be divided into two main categories, oral and parenteral administration. These two categories include, but are not limited to, bolus, buccal, epidermal, epidural, inhalation, intra-abdominal, intra-arterial, intra-articular, intrabronchial, intracapsular, intracardiac, intracartilaginous, intracavitary, intracelial, intracelebellar, intracerebronventricular, intracolic, intracervical, intradermal, intragastric, intrahepatic, intramedullary, intramuscular, intramyocardial, intranasal, intra-ocular intra-orbital, intra-osteal, intrapelvic, intrapericardiac, intraperitoneal, intraplaque, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasternal, intrasynovial, intrathecal, intrathoracic, intratumoral, intra-uterine, intravenous, intraventricular, intravesical, rectal, spinal, subarachnoid, subcapsular, subcutaneous, subcuticular, sublingual, topical, transdermal, transmucosal, transtracheal, and vaginal administration. The preferred administration route is intravenous, particularly preferred is intramuscular.

Oral dosage forms can be formulated *inter alia* as tablets, troches, lozenges, aqueous or oily suspensions, dispersable powders or granules, emulsions, hard capsules, soft gelatin capsules, syrups or elixirs, pills, dragees, liquids, gels, or slurries. These formulations can contain pharmaceutically excipients including, but not limited to,

inert diluents such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents such as corn starch or alginic acid; binding agents such as starch, gelatin or acacia; lubricating agents such as calcium stearate, glyceryl behenate, hydrogenated vegatable oils, magnesium stearate, mineral oil, polyethylene glycol, sodium stearyl, fumarate, stearic acid, talc, zinc stearate; preservatives such as n-propyl-p-hydroxybenzoate; colouring, flavouring or sweetening agents such as sucrose, saccharine, glycerol, propylene glycol or sorbitol; vegetable oils such as arachis oil, olive oil, sesame oil or coconut oil; mineral oils such as liquid parrafin; wetting agents such as benzalkonium chloride, docusate sodium, lecithin, poloxamer, sodium lauryl sulfate, sorbitan esters; and thickening agents such as agar, alginic acid, beeswax, carboxymethyl cellulose calcium, carageenan, dextrin or gelatin.

The pharmaceutical compositions of the present invention can also be formulated for parenteral administration. Formulations for parenteral administration can be *inter alia* in the form of aqueous or non-aqueous isotonic sterile non-toxic injection or infusion solutions or suspensions. Preferred parenteral administration routes include intravenous, intraperitoneal, epidural, intramuscular and intratumoral injection or infusion. The solutions or suspensions may comprise agents that are non-toxic to recipients at the dosages and concentrations employed such as 1,3-butanediol, Ringer's solution, Hank's solution, isotonic sodium chloride solution, oils such as synthetic mono- or diglycerides or fatty acids such as oleic acid, local anaesthetic agents, preservatives, buffers, viscosity or solubility increasing agents, water-soluble antioxidants such

as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like, oil-soluble antioxidants such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like, and metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

In a further aspect, the binding molecules, functional variants, immunoconjugates, compositions, or pharmaceutical compositions of the invention can be used as a medicament. So, a method of treatment and/or prevention of a SARS-CoV infection using the binding molecules, functional variants, immunoconjugates, compositions, or pharmaceutical compositions of the invention is another part of the present invention. The above-mentioned molecules can *inter alia* be used in the diagnosis, prophylaxis, treatment, or combination thereof, of one or more conditions resulting from SARS-CoV. They are suitable for treatment of yet untreated patients suffering from a condition resulting from SARS-CoV and patients who have been or are treated from a condition resulting from SARS-CoV. They protect against further infection by SARS-CoV and/or will retard the onset or progress of the symptoms associated with SARS. They may even be used in the prophylaxis of SARS in for instance people exposed to the SARS-CoV such as hospital personnel taking care of suspected SARS patients.

The above mentioned molecules or compositions may be employed in conjunction with other molecules useful in diagnosis, prophylaxis and/or treatment. They can be used *in vitro*, *ex vivo* or *in vivo*. For instance, the binding molecules, functional variants, immunoconjugates or pharmaceutical compositions of the invention can be co-

administered with a vaccine against SARS-CoV. Alternatively, the vaccine may also be administered before or after administration of the molecules of the invention. Administration of the molecules of the invention with a vaccine might be suitable for postexposure prophylaxis and might also decrease possible side effects of a live-attenuated vaccine in immunocompromised recipients.

The molecules are typically formulated in the compositions and pharmaceutical compositions of the invention in a therapeutically or diagnostically effective amount. Dosage regimens can be adjusted to provide the optimum desired response (*e.g.*, a therapeutic response). A suitable dosage range may for instance be 0.1-100 mg/kg body weight, preferably 0.5-15 mg/kg body weight. Furthermore, for example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. The molecules and compositions according to the present invention are preferably sterile. Methods to render these molecules and compositions sterile are well known in the art. The other molecules useful in diagnosis, prophylaxis and/or treatment can be administered in a similar dosage regimen as proposed for the binding molecules of the invention. If the other molecules are administered separately, they may be adminstered to a patient prior to (*e.g.*, 2 minutes, 5 minutes, 10 minutes, 15 minutes, 30 minutes, 45 minutes, 60 minutes, 2 hours, 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 7 days, 2 weeks, 4 weeks or 6 weeks before), concomitantly with, or subsequent to (*e.g.*, 2 minutes, 5 minutes, 10 minutes, 15 minutes, 30 minutes, 45 minutes, 60 minutes, 2 hours, 4 hours,

6 hours, 8 hours, 10 hours, 12 hours, 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 7 days, 2 weeks, 4 weeks or 6 weeks after) the administration of one or more of the binding molecules or pharmaceutical compositions of the invention. The exact dosing regimen is usually sorted out during clinical trials in human patients.

Human binding molecules and pharmaceutical compositions comprising the human binding molecules are particularly useful, and often preferred, when to be administered to human beings as *in vivo* therapeutic agents, since recipient immune response to the administered antibody will often be substantially less than that occasioned by administration of a monoclonal murine, chimeric or humanised binding molecule.

In another aspect, the invention concerns the use of binding molecules, preferably human binding molecules, functional variants thereof, immunoconjugates according to the invention, nucleic acid molecules according to the invention, compositions or pharmaceutical compositions according to the invention in the preparation of a medicament for the diagnosis, prophylaxis, treatment, or combination thereof, of a condition resulting from SARS-CoV.

Next to that, kits comprising at least one binding molecule, preferably human binding molecule, according to the invention, at least one functional variant thereof according to the invention, at least one immunoconjugate according to the invention, at least one nucleic acid molecule according to the invention, at least one composition according to the invention, at least one pharmaceutical composition according to the invention, at least one vector according to the invention, at least one host according to the invention or a combination thereof are also a part of the present invention.

Optionally, the above described components of the kits of the invention are packed in suitable containers and labeled for diagnosis, prophylaxis and/or treatment of the indicated conditions. The above-mentioned components may be stored in unit or multi-dose containers, for example, sealed ampules, vials, bottles, syringes, and test tubes, as an aqueous, preferably sterile, solution or as a lyophilized, preferably sterile, formulation for reconstitution. The containers may be formed from a variety of materials such as glass or plastic and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The kit may further comprise more containers comprising a pharmaceutically acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, culture medium for one or more of the suitable hosts. Associated with the kits can be instructions customarily included in commercial packages of therapeutic, prophylactic or diagnostic products, that contain information about for example the indications, usage, dosage, manufacture, administration, contraindications and/or warnings concerning the use of such therapeutic, prophylactic or diagnostic products.

The invention further pertains to a method of detecting a SARS-CoV in a sample, wherein the method comprises the steps of a) contacting a sample with a diagnostically effective amount of a binding molecule, a functional variant or an immunoconjugate according to the invention, and b) determining whether the binding molecule, functional variant, or immunoconjugate specifically binds to a molecule of the

sample. The sample may be a biological sample including, but not limited to blood, serum, urine, tissue or other biological material from (potentially) infected subjects, or a nonbiological sample such as water, drink, etc. The (potentially) infected subjects may be human subjects, but also animals that are suspected as carriers of SARS-CoV might be tested for the presence of SARS-CoV using the binding molecules, functional variants or immunoconjugates of the invention. The sample may first be manipulated to make it more suitable for the method of detection. Manipulation mean *inter alia* treating the sample suspected to contain and/or containing SARS-CoV in such a way that the SARS-CoV will disintigrate into antigenic components such as proteins, (poly)peptides or other antigenic fragments. Preferably, the binding molecules, functional variants or immunoconjugates of the invention are contacted with the sample under conditions which allow the formation of an immunological complex between the binding molecules and SARS-CoV or antigenic components thereof that may be present in the sample. The formation of an immunological complex, if any, indicating the presence of SARS-CoV in the sample, is then detected and measured by suitable means. Such methods include, *inter alia*, homogeneous and heterogeneous binding immunoassays, such as radioimmunoassays (RIA), ELISA, immunofluorescence, immunohistochemistry, FACS, BIACORE and Western blot analyses.

Preferred assay techniques, especially for large-scale clinical screening of patient sera and blood and blood-derived products are ELISA and Western blot techniques. ELISA tests are particularly preferred. For use as reagents in these assays, the binding molecules, functional variants or immunoconjugates of the invention are conveniently bonded to the inside surface of microtiter wells. The binding molecules,

functional variants or immunoconjugates of the invention may be directly bonded to the microtiter well. However, maximum binding of the the binding molecules, functional variants or immunoconjugates of the invention to the wells might be accomplished by pretreating the wells with polylysine prior to the addition of the binding molecules, functional variants or immunoconjugates of the invention. Furthermore, the novel the binding molecules, functional variants or immunoconjugates of the invention may be covalently attached by known means to the wells. Generally the the binding molecules, functional variants or immunoconjugates of the invention are used in a concentration of between 0.01 to 100 µg/ml for coating, although higher as well as lower amounts may also be used. Samples are then added to the wells coated with the binding molecules, functional variants or immunoconjugates of the invention.

Furthemore, the binding molecules or functional variants of the invention can be used to identify epitopes of SARS-CoV. The epitopes can be linear, but also structural and/or conformational. In one embodiment, binding of binding molecules or functional variants of the invention to a series of overlapping peptides, such as 15-mer peptides, of a protein from SARS-CoV can be analyzed by means of PEPSCAN analysis (see *inter alia* WO 84/03564, WO 93/09872, Slootstra et al. 1996). The binding of binding molecules to each peptide can be tested in a PEPSCAN-based enzyme-linked immuno assay (ELISA). In another embodiment, a random peptide library comprising peptides from SARS-CoV can be screened for peptides capable of binding to the binding molecules or functional variants of the invention. In the above assays the use of neutralizing binding molecules may identify one or more neutralizing epitopes. The peptides/epitopes found can be used as vaccines and for the

diagnosis of SARS. In yet a further embodiment, the binding of (neutralizing) binding molecules of the invention to domains of a surface protein of SARS-CoV, such as the spike glycoprotein, may be analysed. Alternatively, the binding molecules of the invention may identify one or more epitopes of another protein of SARS-CoV including, but not limited to, the membrane protein (M protein), the small envelope protein (E protein) and the nucleocapsid protein (N protein). In a preferred embodiment binding molecule 018 recognised epitopes on the N protein. These epitopes might be useful in the treatment but also in the detection of SARS-CoV.

In a further aspect, the invention provides a method of screening a binding molecule or a functional variant of a binding molecule for specific binding to the same epitope of a SARS-CoV as the epitope bound by a binding molecule or functional variant of the invention, wherein the method comprises the steps of a) contacting a binding molecule or a functional variant to be screened, a binding molecule or functional variant of the invention and a SARS-CoV or fragment thereof, b) measure if the binding molecule or functional variant to be screened is capable of competing for specifically binding to the SARS-CoV or fragment thereof with the binding molecule or functional variant of the invention. In a further step it may be determined if the screened binding molecules that are capable of competing for specifically binding to the SARS-CoV or fragment thereof have neutralizing activity. A binding molecule or functional variant that is capable of competing for specifically binding to the SARS-CoV or fragment thereof with the binding molecule or functional variant of the invention is another part of the present invention. In the above-described screening method, "specifically binding to the same epitope" also contemplates

specific binding to substantially or essentially the same epitope as the epitope bound by the binding molecules of the invention. The capacity to block, or compete with, the binding of the binding molecules of the invention to SARS-CoV typically indicates that a binding molecule to be screened binds to an epitope or binding site on SARS-CoV that structurally overlaps with the binding site on SARS-CoV that is immunospecifically recognised by the binding molecules of the invention. Alternatively, this can indicate that a binding molecule to be screened binds to an epitope or binding site which is sufficiently proximal to the binding site immunospecifically recognised by the binding molecules of the invention to sterically or otherwise inhibit binding of the binding molecules of the invention to SARS-CoV.

In general, competitive inhibition is measured by means of an assay, wherein an antigen composition, *i.e.* a composition comprising SARS-CoV or fragments thereof, is admixed with reference binding molecules, *i.e.* the binding molecules of the invention, and binding molecules to be screened. Usually, the binding molecules to be screened are present in excess. Protocols based upon ELISAs and Western blotting are suitable for use in such simple competition studies. In certain embodiments, one may pre-mix the reference binding molecules with varying amounts of the binding molecules to be screened (*e.g.*, 1:10, 1:20, 1:30, 1:40, 1:50, 1:60, 1:70, 1:80, 1:90 or 1:100) for a period of time prior to applying to the antigen composition. In other embodiments, the reference binding molecules and varying amounts of binding molecules to be screened can simply be admixed during exposure to the antigen composition. In any event, by using species or isotype secondary antibodies one will be able to detect only the bound reference binding molecules, the binding of which

will be reduced by the presence of a binding molecule to be screened that recognizes substantially the same epitope. In conducting a binding molecule competition study between a reference binding molecule and any binding molecule to be screened (irrespective of species or isotype), one may first label the reference binding molecule with a detectable label, such as, *e.g.*, biotin, an enzymatic, a radioactive or other label to enable subsequent identification. In these cases, one would pre-mix or incubate the labeled reference binding molecules with the binding molecules to be screened at various ratios (*e.g.*, 1:10, 1:20, 1:30, 1:40, 1:50, 1:60, 1:70, 1:80, 1:90 or 1:100) and (optionally after a suitable period of time) then assay the reactivity of the labeled reference binding molecules and compare this with a control value in which no potentially competing binding molecule was included in the incubation. The assay may again be any one of a range of immunological assays based upon antibody hybridization, and the reference binding molecules would be detected by means of detecting their label, *e.g.*, using streptavidin in the case of biotinylated reference binding molecules or by using a chromogenic substrate in connection with an enzymatic label (such as 3,3'5,5'-tetramethylbenzidine (TMB) substrate with peroxidase enzyme) or by simply detecting a radioactive label. A binding molecule to be screened that binds to the same epitope as the reference binding molecule will be able to effectively compete for binding and thus will significantly reduce reference binding molecule binding, as evidenced by a reduction in bound label. The reactivity of the (labeled) reference binding molecule in the absence of a completely irrelevant binding molecule would be the control high value. The control low value would be obtained by incubating the labeled reference binding molecule with unlabelled reference

binding molecules of exactly the same type, when competition would occur and reduce binding of the labeled reference binding molecule. In a test assay, a significant reduction in labeled reference binding molecule reactivity in the presence of a binding molecule to be screened is indicative of a binding molecule that recognizes the same epitope, *i.e.*, one that "cross-reacts" with the labeled reference binding molecule.

Binding molecules identified by these competition assays ("competitive binding molecules" or "cross-reactive binding molecules") include, but are not limited to, antibodies, antibody fragments and other binding agents that bind to an epitope or binding site bound by the reference binding molecule, i.e. a binding molecule of the invention, as well as antibodies, antibody fragments and other binding agents that bind to an epitope or binding site sufficiently proximal to an epitope bound by the reference binding molecule for competitive binding between the binding molecules to be screened and the reference binding molecule to occur. Preferably, competitive binding molecules of the invention will, when present in excess, inhibit specific binding of a reference binding molecule to a selected target species by at least 10%, preferably by at least 25%, more preferably by at least 50%, and most preferably by at least 75%-90% or even greater. The identification of one or more competitive binding molecules that bind to about, substantially, essentially or at the same epitope as the binding molecules of the invention is a straightforward technical matter. As the identification of competitive binding molecules is determined in comparison to a reference binding molecule, i.e. a binding molecule of the invention, it will be understood that actually determining the epitope to which the reference binding molecule and the

competitive binding molecule bind is not in any way required in order to identify a competitive binding molecule that binds to the same or substantially the same epitope as the reference binding molecule.

In yet a further apect the invention relates to a method of identifying a binding molecule, preferably a human binding molecule, potentially having neutralizing activity against SARS-CoV, wherein the method comprises the steps of (a) contacting a collection of binding molecules on the surface of replicable genetic packages with the SARS-CoV under conditions conducive to binding, (b) separating and recovering binding molecules that bind to the SARS-CoV from binding molecules that do not bind, (c) isolating at least one recovered binding molecule, (d) verifying if the binding molecule isolated has neutralizing activity against the SARS-CoV, characterized in that the SARS-CoV in step a is inactivated. The inactivated SARS-CoV may be purified before being inactivated. Purification may be performed by means of well known purification methods suitable for viruses such as for instance centrifugation through a glycerol cushion. The inactivated SARS-CoV in step (a) may be immobilized to a suitable material before use.

A replicable genetic package as used herein can be prokaryotic or eukaryotic and includes cells, spores, bacteria, viruses, (bacterio)phage and polysomes. A preferred replicable genetic package is a phage. The binding molecules, such as for instance single chain Fv's, are displayed on the replicable genetic package, *i.e.* they are attached to a group or molecule located at an exterior surface of the replicable genetic package. The replicable genetic package is a screenable unit comprising a binding molecule to be screened linked to a nucleic acid molecule encoding the binding

molecule. The nucleic acid molecule should be replicable either *in vivo* (*e.g.*, as a vector) or *in vitro* (*e.g.*, by PCR, transcription and translation). *In vivo* replication can be autonomous (as for a cell), with the assistance of host factors (as for a virus) or with the assistance of both host and helper virus (as for a phagemid). Replicable genetic packages displaying a collection of binding molecules is formed by introducing nucleic acid molecules encoding exogenous binding molecules to be displayed into the genomes of the replicable genetic packages to form fusion proteins with endogenous proteins that are normally expressed from the outer surface of the replicable genetic packages. Expression of the fusion proteins, transport to the outer surface and assembly results in display of exogenous binding molecules from the outer surface of the replicable genetic packages.

The inactivation of the SARS-CoV may be performed by viral inactivation methods well known to the skilled artisan such as *inter alia* pasteurization (wet heat), *i.e.* heat treatment while still in aqueous solution, at 60°C for 10 hours; dry heat treatment, *i.e.* heat treatment in the lyophilized state, at 80°C for 72 hours; vapor heat treatment at 60°C for 10 hours and then 80°C for 1 hour; treatment with low pH, *i.e.* pH 4 for 6 hours to 21 days; treatment with organic solvent/detergent, *i.e.* addition of organic solvents and detergents (Triton X-100 or Tween-80) to the virus; treatment by means of cold ethanol fractionation; column chromatography; nanofiltration; UV/light irradiation; gamma-irradiation; and addition of iodine. Preferably, the inactivation is performed by gamma- or UV-irradiation. Methods to test if a virus is still infective or partly or completely inactivated are well known to the person skilled in the art.

In a further aspect the invention pertains to a binding molecule having neutralizing activity against the SARS-CoV and being obtainable by the identification method as descibed above. A pharmaceutical composition comprising the binding molecule, the pharmaceutical composition further comprising at least one pharmaceutically acceptable excipient is also an aspect of the present invention. Pharmaceutically acceptable excipient are described above. The pharmaceutical composition according to the invention may further comprise at least one other therapeutic agent. Suitable agents have been described above.

The invention further relates to the binding molecule or a pharmaceutical composition according to the invention for use as a medicament. They can be used in the diagnosis, prophylaxis, treatment, or combination thereof of a condition resulting from SARS-CoV.

EXAMPLES

To illustrate the invention, the following examples are provided. The examples are not intended to limit the scope of the invention in any way.

Example 1

Selection of phage carrying single-chain Fv fragments specifically recognizing SARS-CoV.

Antibody fragments were selected using antibody phage display libraries and technology, essentially as described in US patent 6,265,150 and in WO 98/15833, both of which are incorporated herein in their entirety. All procedures were performed at room temperature unless stated otherwise. An inactivated SARS-CoV preparation (Frankfurt 1 strain) was prepared as follows. Medium from Vero cells which were

infected with SARS-CoV strain Frankfurt 1 was harvested as soon as cyotopathic effect (CPE) was observed. Cell debris was removed by centrifugation of the harvested medium for 15 minutes at 3000 rpm. The obtained supernatant was collected, spun again for 15 minutes at 3000 rpm and transferred to a clean tube. Subsequently, ultracentrifuge tubes were filled with 10 ml sterile 25% glycerol in PBS. 20 ml of the cleared supernatant was gently applied on the glycerol cushion and the tubes were spun for 2 hours at 20,000 rpm at 4°C. The supernatant was discarded and the virus pellets were resuspended in 1 ml TNE buffer (10 mM Tris-HCl pH 7.4, 1 mM EDTA, 200 mM NaCl) and stored at -80°C. Next, the resuspended virus pellets were gamma-irradiated at 45kGy on dry ice. Subsequently, they were tested for the absence of infectivity in cell culture. If absence of infectivity was established, the thus obtained inactivated SARS-CoV preparation was used for selection of single-chain phage antibodies specifically binding to SARS-CoV.

The inactivated virus preparation and heat-inactivated fetal bovine serum (FBS) were coated overnight at 4°C onto the surface of separate Maxisorp™ plastic tubes (Nunc). The tubes were blocked for two hours in 3 ml PBS containing 2% FBS and 2% fat free milk powder (2% PBS-FM). After two hours the FBS-coated tube was emptied and washed three times with PBS. To this tube, 500 µl (approximately 10^{13} cfu) of a phage display library expressing single-chain Fv fragments (scFv's) essentially prepared as described by De Kruif *et al.* (1995a) and references therein (which are incorporated herein in their entirety), 500 µl 4% PBS-FM and 2 ml 2% PBS-FM were added. The tube was sealed and rotated slowly at room temperature for two hours. Subsequently, the obtained blocked phage library (3 ml) was transferred to a SARS-CoV preparation-coated tube that had

been washed three times with PBS. Tween-20 was added to a final concentration of 0.05% and binding was allowed to proceed for two hours on a slowly rotating wheel at room temperature or at 37°C. The tube was emptied and washed ten times with PBS containing 0.05% Tween-20, followed by washing ten times with PBS. 1 ml glycine-HCL (0.05 M, pH 2.2) was added to elute bound phages, and the tube was rotated slowly for ten minutes. For neutralisation purposes, the eluted phages were added to 500 µl 1 M Tris-HCl pH 7.4. To this mixture, 5 ml of exponentially growing XL-1 blue bacterial culture was added. The obtained culture was incubated for thirty minutes at 37°C without shaking. Then, the bacteria were plated on TYE agar plates containing ampicillin, tetracycline and glucose. After overnight incubation of the plates at 37°C, the colonies were scraped from the plates and used to prepare an enriched phage library, essentially as described by De Kruif *et al.* (1995a) and WO 02/103012 (both are incorporated by reference herein). Briefly, scraped bacteria were used to inoculate 2TY medium containing ampicillin, tetracycline and glucose and grown at a temperature of 37°C to an OD600nm of ~0.3. CT or VCSM13 helper phages were added and allowed to infect the bacteria after which the medium was changed to 2TY containing ampicillin, tetracycline and kanamycin. Incubation was continued overnight at 30°C. The next day, the bacteria were removed from the 2TY medium by centrifugation after which the phages in the obtained supernatant were precipitated using polyethylene glycol 6000/NaCl. Finally, the phages were dissolved in a small volume of PBS containing 1% BSA, filter-sterilized and used for a next round of selection. The selection/re-infection procedure was performed two or three times. After each round of selection, individual *E.coli*

colonies were used to prepare monoclonal phage antibodies. Essentially, individual colonies were grown to log-phase and infected with VCSM13 helper phages after which phage antibody production was allowed to proceed overnight. Phage antibody containing supernatants were tested in ELISA for binding activity to the SARS-CoV preparation which was coated to 96-well plates. In the above described selection, the phage antibodies called SC03-001, SC03-002, SC03-003, SC03-004, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 were obtained.

To overcome selection of previously identified phage antibodies, alternative selections in the presence of scFv's corresponding to the previous selected phage antibodies were performed as follows. ScFv's of the phage antibodies SC03-001, SC03-002, SC03-003, SC03-004, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 were produced as described before in De Kruif *et al.* (1995b). The buffer of the scFv's was adjusted to 1 x PBS. Then the scFv's were mixed with 500 µl (approximately 10^{13} cfu) of a phage display library expressing single-chain Fv fragments essentially prepared as described by De Kruif *et al.* (1995a) and references therein (which are incorporated herein in their entirety). Next, the obtained mixture was blocked in an FBS-coated tube as described above and subsequently selection was carried out with the obtained blocked mixture essentially as described above for the blocked phage library. In this alternative selection, the phage antibodies called SC03-016, SC03-017 and SC03-018 were obtained.

Example 2

Validation of the SARS-CoV specific single-chain phage antibodies.

Selected single-chain phage antibodies that were obtained in the screens described above, were validated in ELISA for specificity, *i.e.* binding to the SARS-CoV preparation prepared as described *supra*. Additionally, the single-chain phage antibodies were also tested for binding to 10% FBS. For this purpose, the SARS-CoV preparation or 10% FBS preparation was coated to Maxisorp™ ELISA plates. After coating, the plates were blocked in 2% PBS-FM. The selected single-chain phage antibodies were incubated in an equal volume of 4% PBS-FM to obtain blocked phage antibodies. The plates were emptied, washed three times with PBS, after which the blocked phage antibodies were added. Incubation was allowed to proceed for one hour, the plates were washed in PBS containing 0.05% Tween-20 and bound phage antibodies were detected (using OD 492 nm measurement) using an anti-M13 antibody conjugated to peroxidase. As a control, the procedure was performed simultaneously using no single-chain phage antibody or control single-chain phage antibody directed against thyroglobulin (SC02-006) (see De Kruif *et al.* 1995a and 1995b) or control single-chain phage antibody directed against CD46 (SC02-300). Both controls served as a negative control. As shown in Table 1 and Figure 1, the selected phage antibodies called SC03-001, SC03-002, SC03-003, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 displayed significant binding to the immobilized SARS-CoV preparation, while no binding to FBS was observed.

As shown in Table 2 and Figure 2, the selected phage antibody called SC03-018 displayed significant binding to the immobilized SARS-CoV preparation, while no binding to FBS was observed. The selected phage antibody called SC03-016 and SC03-017 displayed binding to the immobilized SARS-CoV

preparation compared to binding to FBS, although in a lesser amount than SC03-018.

Example 3

Characterization of the scFv's specific for SARS-CoV.

From the selected specific single chain phage antibody (scFv) clones plasmid DNA was obtained and nucleotide sequences were determined according to standard techniques. The nucleotide sequences of the scFv's (including restriction sites for cloning) called SC03-001, SC03-002, SC03-003, SC03-004, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 are shown in SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:89, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and SEQ ID NO:70, respectively. The amino acid sequences of the scFv's called SC03-001, SC03-002, SC03-003, SC03-004, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 are shown in SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:90, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, respectively. Furthermore, the nucleotide sequences of the scFv's (including restriction sites for cloning) called SC03-016, SC03-017 and SC03-018 are shown in SEQ ID NO:91, SEQ ID NO:93 and SEQ ID NO:95, respectively. The amino acid sequences of the scFv's called SC03-016, SC03-017 and SC03-018 are shown in SEQ ID NO:92, SEQ ID NO:94 and SEQ ID NO:96, respectively.

The VH and VL gene identity (see Tomlinson IM, Williams SC, Ignatovitch O, Corbett SJ, Winter G. V-BASE Sequence Directory. Cambridge United Kingdom: MRC Centre for Protein Engineering (1997)) and heavy chain CDR3 compositions of the

scFv's specifically binding the SARS-CoV preparation are depicted in Table 3.

Example 4

Production of human SARS-CoV specific bivalent scFv's in Pichia Pastoris.

Methods for the cloning and expression of bivalent scFv fragments in the Pichia pastoris system were based on protocols provided by the supplier (Invitrogen) in "A Manual of Methods for Expression of Recombinant Proteins Using pPICZ and pPICZα in Pichia pastoris (Version F)". The bivalent scFv expression vector pPicZbiFVH (see figure 3B) was constructed from the vector pPICZμB (see figure 3A)(Invitrogen) following standard molecular biology techniques known to a person skilled in the art. Three modifications were introduced in the pPICZμB (see figure 3C):

1. A restriction site (NcoI) was introduced by PCR-generated point mutation directly after the KEK2 cleavage site of the signal peptide to facilitate cloning into the vector.
2. A second NcoI restriction site was removed by PCR generated point mutation inside the coding region of the sh ble gene.
3. A synthetic fragment comprising the hinge region of murine IgG3 and a linker fragment was introduced between the restriction sites NotI and XbaI.

All modifications were confirmed by sequencing. ScFv's were cloned into pPicZbiFVH from the phage display expression vector by directional cloning using the restriction sites NcoI and NotI. The Pichia pastoris strain SMD1168 kek1:suc1 (ATCC # 204414) was transformed with 5-10 μg of linearized construct cDNA by electroporation according to the manufacturer's protocols (supra). The transformed cells were plated on YPDS

agar containing 250 µg/ml Zeocin and incubated at 30°C for 3-4 days. High producing clones were selected by colony lift immunoblot screening, as follows. Pre-wet nitrocellulose membranes were layered over the transformation plates and a fraction of each colony was lifted onto the membrane. The membrane was then placed colony side up on YPD agar containing 0.5% methanol and incubated overnight at 30°C. The membranes were then washed repeatedly with Tris buffered saline containing 0.5% Tween-20 (TBST) to remove colonies, then blocked for 30 minutes with TBST and 4% non-fat milk powder. The membranes were then placed in TBST containing 4% non-fat milk powder and horseradish peroxidase conjugated anti-c-myc antibody (Roche) for one hour. Finally, the membranes were washed extensively in TBST followed by a PBS washing step and scFv-secreting colonies were revealed by a chemofluorescence detection system (Apbiochem). Selected high producers were purified by streaking on YPD plates and were subsequently used for bivalent scFv expression. Small-scale expression cultures were carried out in shaker flasks essentially as described by the manufacturer's protocols (*supra*). BMGY medium was used for the cell expansion phase, while BMMY medium was used during the bivalent scFv expression phase. After 48 hours of induction supernatants were clarified by repeated centrifugation. The supernatant was conditioned for purification by the addition of 1 M Na_2HPO_4 pH 8 to a concentration of 20 mM, 0.5 M Imidazole to a concentration of 10 mM, 5 M NaCl to a concentration of 500 mM. Hereafter, the samples were purified by immobilized metal affinity chromatography followed by anion exchange chromatography on an AKTAprime FPLC-system (Pharmacia). A 5 ml HiTrap chelating column (Pharmacia) was charged with $NiSO_4$ and equilibrated according to the manufacturers instructions. Conditioned

supernatant was loaded directly onto the column and washed extensively in equilibration buffer (20 mM Na_2PO_4 pH 8, 10 mM imidazole). Bivalent scFv were eluted directly off the column on to a 1 ml sepharose Q HP column (Pharmacia) in the presence of 250 mM imidazole pH 8.5. The column was then washed in 20 mM Tris-HCl pH 8, then briefly in 20 mM Na_2PO_4 pH 7.3, and bivalent scFv's were eluted off the column over a gradient of 0-0.5 M NaCl in 7 column volumes. Fractions were then measured for protein content and were analyzed for activity and purity. The bivalent scFv's of the selected scFv's called SC03-001, SC03-002, SC03-003, SC03-005, SC03-006, SC03-007, SC03-008, SC03-009, SC03-0010, SC03-012, SC03-013, SC03-014 and SC03-015 were called pyBi03-001C02, pyBi03-002C02, pyBi03-003C02, pyBi03-005C02, pyBi03-006C02, pyBi03-007C02, pyBi03-008C02, pyBi03-009C02, pyBi03-010C02, pyBi03-012C02, pyBi03-013C02, pyBi03-014C02, pyBi03-015C02, respectively.

Example 5

Construction of fully human immunoglobulin molecules (human monoclonal anti-SARS-CoV antibodies) from the selected anti-SARS-CoV single chain Fv's

Heavy and light chain variable regions of the scFv's called SC03-001, SC03-002, SC03-009, SC03-013, SC03-014 and SC03-018 were PCR-amplified using oligonucleotides to append restriction sites and/or sequences for expression in the IgG expression vectors pSyn-C03-HCμ1 (see SEQ ID No:110) and pSyn-C05-Cμ (see SEQ ID No:111), respectively. The V_L gene shared between scFv's was amplified using oligonucleotides 5K-I (SEQ ID NO:112) and sy3K-C (SEQ ID NO:113) (see below) and the PCR products cloned into vector pSyn-C05-Cμ. Nucleotide sequences for all constructs were verified according to standard techniques known to the skilled artisan. V_H genes were

amplified using the following oligonucleotide set: 5H-B (SEQ ID NO:114) and sy3H-A (SEQ ID NO:115). Thereafter, the PCR products were cloned into vector pSyn-C03-HCμ1 and nucleotide sequences were verified according to standard techniques known to the skilled person in the art.

5H-B
acctgtcttgaattctccatggccgaggtgcagctggtggagtctg

sy3H-A
gcccttggtgctagcgctggagacggtcaccagggtgccctggcccc

5K-I
acctgtctcgagttttccatggctgacatccagatgacccagtctccatcctcc

sy3K-C
gggaccaaggtggagatcaaacggaccgtggccgcccccagc

The resulting expression constructs pgG103-001C03, pgG103-002C03, pgG103-009C03, pgG103-013C03, pgG103-014C03 and pgG103-018C03 encoding the anti-SARS-CoV human IgG1 heavy chains were transiently expressed in combination with the pSyn-C05-VkI construct encoding the common light chain in 293T cells and supernatants containing IgG1 antibodies were obtained. The nucleotide sequences of the heavy chains of the antibodies called 03-001, 03-002, 03-009, 03-013, 03-014 and 03-018 are shown in SEQ ID NOs 116, 118, 120, 122, 124 and 126, respectively. The amino acid sequences of the heavy chains of the antibodies called 03-001, 03-002, 03-009, 03-013, 03-014 and 03-018 are shown in SEQ ID NOs 117, 119, 121, 123, 125 and 127, respectively.

The nucleotide sequences of the light chain of antibodies 003-001, 03-002, 03-009, 03-013, 03-014 and 03-018 is shown in SEQ ID NO:128. The amino acid sequences of the light chain of antibodies 03-001, 03-002, 03-009, 03-013, 03-014 and 03-018 is shown in SEQ ID NO:129. Essentially as described above the antibodies called 03-006 and 03-015 were generated. The nucleotide sequences of the heavy chains of the antibodies called 03-006 and 03-015 are shown in SEQ ID NO:471 and SEQ ID NO:473, respectively. The amino acid sequences of the heavy chains of the antibodies called 03-006 and 03-015 are shown in SEQ ID NO:472 and SEQ ID NO:474, respectively. The nucleotide sequences of the light chain of antibodies called 03-006 and 03-015 are shown in SEQ ID NO:475 and SEQ ID NO:477, respectively. The amino acid sequences of the light chain of antibodies called 03-006 and 03-015 are shown in SEQ ID NO:476 and SEQ ID NO:478, respectively. Subsequently, the recombinant human monoclonal antibodies were purified over protein-A columns and size-exclusion columns using standard purification methods used generally for immunoglobulins (see for instance WO 00/63403 which is incorporated by reference herein).

Example 6

Competition ELISA of human monoclonal anti-SARS-CoV antibodies and single chain phage antibodies specific for SARS-CoV.

To determine whether the above selected single-chain phage antibodies bind to similar or overlapping epitopes which are recognised by the recombinant human monoclonal anti-SARS-CoV antibodies of the invention a competition ELISA was performed. Briefly, an gamma-irradiated SARS-CoV preparation was immobilized as described *supra*. The immobilized SARS-CoV preparation and the selected single-chain phage antibodies were blocked in an equal volume of 4% ELK in PBS.

Subsequently, the blocked immobilized SARS-CoV preparation was incubated with a blocked single-chain phage antibody in the presence or absence of 1 µg/ml of an anti-SARS-CoV IgG for one hour at room temperature. Binding of the single-chain phage antibody was monitored as described *supra*. A reduction of binding of the single-chain phage antibody to the SARS-CoV preparation in the presence of anti-SARS-CoV IgG compared to binding of single-chain phage antibody alone indicated that similar or overlapping epitopes were recognized by the single-chain phage antibody and the anti-SARS-CoV IgG. As shown in Figure 4, the anti-SARS-CoV IgG called 03-001 was capable of significantly reduce binding of the single-chain phage antibodies SC03-001, SC03-005, and SC03-0010. The anti-SARS-CoV IgG called 03-002 reduced binding of both SC03-002 and SC03-012, whereas the anti-SARS-CoV IgGs called 03-009 and 03-018 reduced binding of the single-chain phage antibodies called SC03-009 and SC03-018, respectively. The anti-SARS-CoV IgGs called 03-013 and 03-014 reduced binding of SC03-013, SC03-014 and SC03-006. In addition, IgG pGg03-013 slightly reduced binding of SC03-015.

Example 7

Screening assay for SARS-CoV neutralizing activity of recombinant human anti-SARS-CoV bivalent scFv's and recombinant human anti-SARS-CoV antibodies

The SARS-CoV neutralization assay was performed on Vero cells (ATCC CCL 81). The SARS-CoV strains used in the neutralisation assay were the Frankfurt 1 strain (for the complete genome of this strain see EMBL-database accession # AY291315) and the Frankfurt 2 strain, derived from a patient who acquired the infection from the Frankfurt 1 - index case (Rickerts *et al.* 2003). This latter SARS-isolate has not yet

been sequenced. Virus stocks of the strains were used in a titer of 4x 10^3 $TCID_{50}$/ml (50% tissue culture infective dose per ml), with the titer calculated according to the well known method of Spearman and Kaerber. Recombinant human anti-SARS-CoV bivalent scFv's and recombinant human anti-SARS-CoV antibodies produced as described above were prescreened by serially 2-fold-dilution of the undiluted material in PBS starting from 1:10 (dilution range 1:10 - 1:320). A neutralization titer of ≥ 1:10 was regarded as specific evidence of reactivity of the bivalent scFv's or the antibodies against SARS-CoV in the prescreening assay. To determine the antibody-concentration dependent neutralizing activity the bivalent scFv's or the antibodies against SARS-CoV were then adjusted to a protein concentration of 10 µg/ml and serially 2-fold diluted in PBS (dilution range 1:2 to 1:512). In general, the neutralisation assay worked as follows. 25 µl of the respective bivalent scFv or antibody dilutions were mixed with 25 µl of virus suspension (= approx. 100 $TCID_{50}$/25 µl) and incubated for one hour at 37°C. The suspension was then pipetted two times in triplicate into 96-well plates. Next, 50 µl of a freshly trypsinized and homogenized suspension of Vero cells (1:3 split of the confluent cell monolayer of a T75-flask), resuspended in DMEM containing 10% w/v fetal calf serum and antibiotics, were added. The inoculated cells were cultured for 3-4 days at 37°C and observed daily for the development of cytopathic effect (CPE). CPE was compared to the positive control (virus inoculated cells) and negative controls (mock-inoculated cells or cells incubated with bivalent scFv or antibody only). The complete absence of CPE in an individual cell culture was defined as protection (= 100% titer reduction). The serum dilution giving protection in 66% percent of wells was defined

as the neutralizing antibody titer. Serum from one of the two well characterised SARS-patients was used as a positive control for the neutralization assay; the clinical history of these two patients has been published (see Rickerts *et al.* 2003).

As shown in Table 4, the bivalent scFv's called pyBi03-001C02, pyBi03-002C02, pyBi03-003C02, pyBi03-005C02, pyBi03-006C02, pyBi03-007C02, pyBi03-008C02, pyBi03-009C02, pyBi03-010C02, pyBi03-012C02, pyBi03-013C02, pyBi03-014C02, pyBi03-015C02 were tested for SARS-CoV neutralizing activity. Furthermore, two negative controls, *i.e.* pyBi02-148C02 (bivalent scFv binding to antigen L6) and pyBi02-006C02 (bivalent scFv binding to thyroglobulin) and one positive control, *i.e.* serum from a SARS-patient, were tested for neutralizing activity. It is clear from Table 4 that the bivalent scFv's pyBi03-013C02 and pyBi03-014C02 displayed significant neutralizing activity. The bivalents neutralize the Frankfurt 1 or Frankfurt 2 strain at a dilution factor of 80 or 160 in the above described prescreening assay. In the light of the OD values and the neutralization titer, the neutralizing antibodies are useful in the prophylaxis and/or treatment of a condition resulting from SARS infection. Neutralisation data obtained with human monoclonal anti-SARS-CoV antibodies indicated that the antibodies called 03-013 and 03-014 displayed neutralizing activity (data not shown). This confirmed the above results for the bivalent single chain Fv's.

In an alternative embodiment the SARS-CoV neutralization assay is performed on Vero cells (ATCC CCL 81). The SARS-CoV strain used in the assay is the Frankfurt 1 strain (for the complete genome of this strain see EMBL-database accession # AY291315). The strain is used in a titer of 1.6×10^6 $TCID_{50}$/ml

(50% tissue culture infective dose per ml). Recombinant antibodies (in phage antibody, scFv, bivalent or IgG1 format) are adjusted to a concentration of 10 µg/ml and then serially 10-fold or 2-fold diluted in PBS to determine optimal inhibitory concentrations. 25 µl of the recombinant antibody are mixed with 25 µl of virus suspension (=150 $TCID_{50}$/25 µl) and incubated for one hour at 37°C. The suspension is then inoculated in triplicate onto sub-confluent Vero cells (approx. 80% density) grown in 96-well cell-culture plates. The inoculated cells are cultured for 3-4 days at 37°C and observed daily for the development of cytopathic effect (CPE). CPE is compared to the positive control (virus inoculated cells) and negative controls (mock-inoculated cells or cells incubated with recombinant antibody only).

In yet another embodiment the SARS-CoV neutralization assay was performed on Vero cells (ATCC CCL 81) as follows. The SARS-CoV strain SCV-P4(5688) used in this assay was obtained from patient 5688 (who died from SARS) and then passaged four times on Vero cells (see Fouchier *et al.* (2003), Kuiken *et al.* (2003); strain is also called HK-39849 (GenBank accession number AY278491)). The virus strain was used in a titer of $2x10^3$ $TCID_{50}$/ml (50% tissue culture infective dose per ml), with the titer calculated according to the method of Spearman and Kaerber which is well known to the average skilled person. Recombinant expressed human anti-SARS-CoV antibodies were screened by serially 2-fold-dilution in PBS starting at a concentration of 50 µg/ml (dilution range 50 - 0.025 µg/ml). 50 µl of virus suspension (10, 30 or 100 $TCID_{50}$/50 µl) was mixed with 50 µl of the respective recombinant human anti-SARS-CoV antibody dilution and incubated for one hour at 37°C. The suspension was then pipetted two times in triplicate into 96-well plates

containing an 80% confluent monolayer of Vero cells (seeded 16-20 hrs in advance at a density of $1x10^4$ cells per well in DMEM containing 5% FBS). The Vero cells were cultured for 4 days at 37°C and observed daily for the development of cytopathic effect (CPE). CPE was compared to the positive control (virus inoculated cells) and negative controls (mock-inoculated cells or cells incubated with recombinant antibody only). The complete absence of CPE in an individual cell culture was defined as protection (= 100% titer reduction). The dilution giving protection in 66% percent of wells was defined as the neutralizing antibody titer. The results are shown in Table 7. On the upper row the concentration of the antibody in µg/ml is shown. In the left column of Table 7 the $TCID_{50}$ and name of the antibody used are shown. From table 7 can be clearly deducted that the human anti-SARS-CoV antibodies called 03-013 and 03-014 contain SARS-CoV neutralizing activity. Complete protection from infectivity of 100TCID50 was reached at 170 nM for 03-013 and 42 nM for 03-014. In comparison the control antibody 02-027, a human monoclonal anti-EpCAM antibody, contained no neutralizing activity at all. The antibody called 03-006 did not show neutralizing capacity at the normal IgG dilution range, however subsequent neutralization assays revealed that 03-006 was capable of neutralizing SARS-CoV, but only at concentrations in the µM range (data not shown).

Example 8

Screening assay for binding of recombinant human anti-SARS-antibodies to SARS-infected cells in an indirect immunofluorescence staining assay (IIF).

Vero cells (ATCC CCL 81), which were grown to sub-confluency, were inoculated with a multiplicity of infection

(moi) of 0.1 with the Franfurt-1 strain of SARS-CoV. The cells were observed daily for any cyotopathic effect (CPE), which usually became first visible on day two. As soon as CPE appeared, cells were gently harvested using a cell scraper, washed once in PBS and spread in a thin layer onto microscopic slides coated with Teflon grids. The cell suspensions were allowed to dry for 30 minutes and the slides were then fixed in ice-cold aceton for 15 minutes and stored at -80°C until further use. Recombinant human antibodies against SARS-CoV were brought to a concentration of 10 µg/ml and were then further diluted 2-fold in PBS. The microscopic slides were brought to room temperature and 20 µl of the recombinant antibody suspension were spotted per field (the microscopic slides contain 10 or 12 fields). Sera from patients which have been infected with SARS-CoV were used as positive controls and serum of uninfected subjects as negative controls (see Rickerts *et al.* 2003). Slides were incubated in a humid chamber at 37°C for one hour and washed two times in PBS at room temperature. Working solutions of fluorescein-isothiocyanate-labelled secondary antibodies, *i.e.* anti-huIgG-FITC, were prepared as is known in the art. 20 µl of the secondary antibody was applied to each spot on the slides. After a further incubation of 30 minutes at 37°C, slides were washed again twice and coverslips were mounted on the slides. Slides were read using a fluorescent microscope, comparing the specific fluorescence (number of fluorescent cells and morphology) of the slides contacted with the recombinant antibodies with the slides contacted with the positive and negative controls. In Table 5 the data of the IIF assay are presented. The recombinant human monoclonal anti-SARS-CoV antibodies called 03-014 and 03-018 showed clear cytoplasmic staining of the cells infected with SARS-CoV. Clear staining

was also observed with the recombinant human monoclonal anti-SARS-CoV antibody called 03-009 (data not shown).

Example 9

Characterization of SARS-CoV preparations inactivated by gamma -or UV-irradiation

All procedures were performed at room temperature unless stated otherwise. An inactivated SARS-CoV preparation (Frankfurt 1 strain) was prepared as follows. Medium from Vero cells which were infected with O.I. moi SARS-CoV strain Frankfurt 1 was harvested as soon as cyotopathic effect (CPE) was observed. Cells were once frozen at -20°C and thawed. Cell debris was removed by centrifugation of the harvested medium for 15 minutes at 3000 rpm. The obtained supernatant was collected, spun again for 15 minutes at 3000 rpm and transferred to a clean tube. Subsequently, ultracentrifuge tubes were filled with 10 ml sterile 25% v/v glycerol in PBS. 20 ml of the cleared supernatant was gently applied on the glycerol cushion and the tubes were spun for 2 hours at 20,000 rpm at 4°C in a Beckman SW28 rotor. The supernatant was discarded and the virus pellets were resuspended in 1 ml TNE buffer (10 mM Tris-HCl pH 7.4, 1 mM EDTA, 200 mM NaCl) and stored at -80°C. Next, the resuspended virus pellets were either gamma-irradiated with a dose at 45kGy on dry ice, or UV-irradiated at 4°C for 15 minutes (UV-B radiation 280-350 nm; μmax 306 nm). Subsequently, they were tested for the absence of infectivity in cell culture. If absence of infectivity was established, the thus obtained inactivated SARS-CoV preparations were used for further experiments. To determine whether the isolated anti-SARS-CoV human IgG antibodies were capable of binding SARS preparations that were inactivated as described *supra* ELISA experiments were

performed. The SARS-CoV preparations were diluted 1:250 in coating buffer (50 mM carbonate buffer, pH 9.6) and immobilized over night at 4°C on Maxisorp™ ELISA plates. The ELISA plates were washed three times with PBS and incubated with human anti-SARS-CoV and control IgG (called 02-027) at concentrations of 1 and 5 µg/ml in PBS containing 1% BSA for one hour at room temperature. Subsequently, the plates were washed two times with PBS containing 0.05% Tween-20 and IgG bound was detected using an anti-human-IgG-HRP-conjugate (Pharmingen) at 492 nm.

As shown in Figure 5, the anti-SARS-CoV antibody called 03-001 and 03-002 were capable of binding both the UV- and gamma-irradiated SARS-CoV preparation to a similar extent. In contrast, the antibodies called 03-009 and 03-018 preferably bound to the gamma-irradiated SARS-CoV preparation, whereas the antibodies called 03-013 and 03-014 preferably bound to the UV-irradiated SARS-CoV preparation. The above might indicate that the antibodies called 03-009 and 03-018 bind a viral antigen that becomes more exposed upon the vigorous gamma-irradiation of the virus. The above might also indicate that the gamma-irradiation might damage the antigen recognized by the antibodies 03-013 and 03-014.

Example 10

Characterization of anti-SARS-CoV IgG antibodies in sandwich ELISA.

To determine if upon denaturation of a SARS-CoV preparation more antigen becomes accessible for the isolated recombinant human monoclonal anti-SARS-CoV antibodies and to determine which antigens are detected by the human monoclonal anti-SARS-CoV antibodies, the following sandwich ELISA was performed. For the detection of bound antigens different anti-

SARS-CoV rabbit antisera were used. The sandwich ELISA was performed as follows. Human anti-SARS-CoV antibodies or the control antibody called 02-300 (an antibody against CD46) were immobilized over night at 4°C to Maxisorp™ ELISA plates at a concentration of 5 µg/ml in coating buffer (50 mM carbonate buffer, pH 9.6). The plates were washed three times with PBS and blocked with PBS containing 1% BSA. Next, a gamma-irradiated SARS-CoV preparation prepared as described herein was denatured by diluting the preparation 1:10 in RIPA buffer (150 mM NaCl, 1% Nonidet P-40, 0.5% deoxycholate, 0.1% sodium dodecyl sulphate, 50 mM Tris, pH 8.0) followed by an incubation of 1 hour at room temperature. Subsequently, the denatured virus preparation was diluted 1:10 in PBS containing 1% BSA and the immobilized human IgGs were incubated with the denatured virus preparation for one hour at room temperature. To recognize which proteins of the SARS-CoV were detected by the immobilized recombinant human monoclonal anti-SARS-CoV antibodies polyclonal rabbit antibodies recognizing the complete SARS-CoV, the spike protein of SARS-CoV (Imgenex IMG-542 or IMG-557) or the nucleocapsid protein of SARS-CoV (Imgenex IMG-543). Finally, bound rabbit IgG was detected (using OD 492 nm measurement) using an anti-rabbit-IgG-HRP-conjugate (Dako).

As shown in Figure 6A (detection by means of a polyclonal serum against complete SARS-CoV), the recombinant human monoclonal anti-SARS-CoV antibodies called 03-009, 03-013, 03-014 and 03-018 were all capable of binding both a native and a denatured SARS-CoV preparation. The increased signal after denaturation might have been caused by the exposure of more antigenic sites upon denaturation. When detection was perfomed by means of two polyclonal rabbit antibodies against the SARS-CoV spike protein (Figures 6B and 6D for the antibodies called

IMG-542 and IMG-557, respectively), the values for the antibodies called 03-013 and 03-014 were higher compared to those for 03-009 and 03-018, which indicated that the antibodies called 03-013 and 03-014 are directed to the spike protein of SARS-CoV. When detection was performed using polyclonal antibodies against the SARS-CoV nucleocapsid protein (Figure 6C for the antibody called IMG-543), the values for the antibodies called 03-009 and 03-018 were higher compared to the values of the antibodies called 03-013 and 03-014, especially when the virus was denatured, indicating that 03-009 and 03-018 are directed to the nucleocapsid (N) protein of SARS-CoV. Based on the above it might be concluded that the recombinant human monoclonal anti-SARS-CoV antibodies called 03-009 and 03-018 are directed to the nucleocapsid protein of SARS-CoV, while the recombinant human monoclonal anti-SARS-CoV antibodies called 03-013 and 03-014 are directed to the spike protein of SARS-CoV.

Example 11

Identification of epitopes recognized by recombinant human anti-SARS-CoV antibodies by PEPSCAN-ELISA

15-mer linear and looped/cyclic peptides were synthesized from proteins of SARS-CoV and screened using credit-card format mini-PEPSCAN cards (455 peptide formats/card) as described previously (see inter alia WO 84/03564, WO 93/09872, Slootstra *et al.* 1996). All peptides were acetylated at the amino terminus. In short, series of overlapping peptides, which were either in linear form or in looped/cyclic form, of all the (potential) proteins of SARS-CoV Urbani, these proteins being called spike protein (the protein-id of the surface spike glycoprotein in the EMBL-database is AAP13441), protein X1 (the protein-id of protein X1 is AAP13446), protein

X2 (the protein-id of protein X1 is AAP13447), E protein (the protein-id of the small envelope protein, E protein, is AAP13443), M protein (the protein-id of the membrane protein, M protein, is AAP13444), protein X3 (the protein-id of protein X3 is AAP13448), protein X4 (the protein-id of protein X4 is AAP13449), protein X5 (the protein-id of protein X5 is AAP13450), and N protein (the protein-id of the nucleocapsid protein, N protein, is AAP13445), were produced and tested for binding to the recombinant human anti-SARS-CoV antibodies of the invention by means of PEPSCAN analysis.

Because the Urbani proteins indicated above are also found in identical or highly homologous form in other SARS-CoV strains, the antigenic peptides found in the analysis method may not only be used for detection of the SARS-CoV strain Urbani and the prevention and/or treatment of a condition resulting from the SARS-CoV strain Urbani, but may also be useful in detecting SARS-CoV in general and preventing and/or treating a condition resulting from SARS-CoV in general. The protein-id of the surface spike glycoprotein of for instance the SARS-CoV strains TOR2, Frankfurt 1 and HSR 1 in the EMBL-database is AAP41037, AAP33697 and AAP72986. The accession number in the EMBL-database of the complete genome of the strains TOR2, Frankfurt 1 and HSR 1 is AY274119, AY291315 and AY323977, respectively. Under these accession numbers the amino acid sequence of the other (potential) proteins of these strains can be found.

As indicated above, several proteins of SARS-CoV, such as *inter alia* the spike protein and the N protein, are shared by all SARS-CoV strains. However, the strains TOR2, Frankfurt 1 and HSR 1 contain open reading frames encoding (potential) proteins that are not present in the SARS-CoV strain Urbani. In the SARS-CoV strain called TOR2 these (potential) proteins

are called Orf9, Orf10, Orf13 and Orf14. The first three of these (potential) proteins are also found in the SARS-CoV strains called Frankfurt 1 and HSR 1. In these strains the (potential) proteins are called Orf7b, Orf8a and Orf9b, respectively. The coding sequence (CDS) of the (potential) proteins of SARS-CoV TOR2 is shown under EMBL-database accession number AY274119, the coding sequence (CDS) of the (potential) proteins of SARS-CoV HSR 1 can be found under accession number AY323977, the coding sequence (CDS) of the (potential) proteins of SARS-CoV Frankfurt 1 can be found under accession number AY291315. Series of overlapping peptides, which were either in linear form or in looped/cyclic form, of all the (potential) proteins of SARS-CoV TOR2 were also produced and tested for binding to the recombinant human anti-SARS-CoV antibodies of the invention by means of PEPSCAN analysis. Because the TOR2 proteins indicated above are also found in identical or highly homologous form in several other SARS-CoV strains, such as for instance the strains called Frankfurt 1 and HSR 1, the peptides found in the analysis method may not only be used for detection of the SARS-CoV strain TOR2 and the prevention and/or treatment of a condition resulting from the SARS-CoV strain TOR2, but may also be useful in detecting SARS-CoV strains which express these (potential) proteins and preventing and/or treating a condition resulting from SARS-CoV which express these (potential) proteins.

In all looped peptides position-2 and position-14 were replaced by a cysteine (acetyl-XCXXXXXXXXXXXCX-minicard). If other cysteines besides the cysteines at position-2 and position-14 were present in a prepared peptide, the other cysteines were replaced by an alanine. The looped peptides were synthesized using standard Fmoc-chemistry and deprotected

using trifluoric acid with scavengers. Subsequently, the deprotected peptides were reacted on the cards with an 0.5 mM solution of 1,3-bis(bromomethyl)benzene in ammonium bicarbonate (20 mM, pH 7.9/acetonitril (1:1 (v/v)). The cards were gently shaken in the solution for 30-60 minutes, while completely covered in the solution. Finally, the cards were washed extensively with excess of H_2O and sonicated in disrupt-buffer containing 1% SDS/0.1% beta-mercaptoethanol in PBS (pH 7.2) at 70°C for 30 minutes, followed by sonication in H_2O for another 45 minutes.

Recombinant human anti-SARS-CoV antibodies were tested for binding to each linear and looped peptide in a PEPSCAN-based enzyme-linked immuno assay (ELISA). The 455-well creditcard-format polypropylene cards, containing the covalently linked peptides, were incubated with the antibodies (1 µg/ml; diluted in blocking solution which contains 5% horse-serum (v/v) and 5% ovalbumin (w/v)) (4°C, overnight). After washing, the peptides were incubated with anti-human antibody peroxidase (dilution 1/1000) (1 hour, 25°C), and subsequently, after washing the peroxidase substrate 2,2'-azino-di-3-ethylbenzthiazoline sulfonate (ABTS) and 2 µl/ml 3% H_2O_2 were added. Controls (for linear and looped) were incubated with anti-human antibody peroxidase only. After 1 hour the color development was measured. The color development of the ELISA was quantified with a CCD-camera and an image processing system. The setup consisted of a CCD-camera and a 55 mm lens (Sony CCD Video Camera XC-77RR, Nikon micro-nikkor 55 mm f/2.8 lens), a camera adaptor (Sony Camera adaptor DC-77RR) and the Image Processing Software package Optimas, version 6.5 (Media Cybernetics, Silver Spring, MD 20910, U.S.A.). Optimas runs on a pentium II computer system.

The recombinant human anti-SARS-CoV-antibodies were tested for binding to the 15-mer linear and looped/cyclic peptides synthesized as described *supra*. Relevant binding of a peptide to a recombinant human anti-SARS-CoV antibody was calculated as follows. The average OD-value for each antibody was calculated for the respective proteins (sum of OD-values of all peptides/total number of peptides). Next, the standard deviation of this average was calculated. The standard deviation was multiplied by 2 and the obtained value was added to the average value to obtain the correction factor. The OD-value of each peptide was then divided by this correction factor. If a value of 0.9 or higher was found, then relevant binding was considered to be present between the specific peptide and the respective antibody. Particularly interesting appear to be domains comprising several relevant peptides. These domains are indicated (coloured grey) in Table 6. The recombinant human anti-SARS-CoV antibody called 03-018 reacted with peptides of the nucleocapsid (N) protein. The peptides recognized include NGPQSNQRSAPRITF (SEQ ID NO:97), GPQSNQRSAPRITFG (SEQ ID NO:98), PQSNQRSAPRITFGG (SEQ ID NO:99), QSNQRSAPRITFGGP (SEQ ID NO:100), SNQRSAPRITFGGPT (SEQ ID NO:101), NQRSAPRITFGGPTD (SEQ ID NO:102), QRSAPRITFGGPTDS (SEQ ID NO:103), RSAPRITFGGPTDST (SEQ ID NO:104), SAPRITFGGPTDSTD (SEQ ID NO:105), APRITFGGPTDSTDN (SEQ ID NO:106), PRITFGGPTDSTDNN (SEQ ID NO:107), RITFGGPTDSTDNNQ (SEQ ID NO:108) and ITFGGPTDSTDNNQN (SEQ ID NO:109). The highest binding of the recombinant human anti-SARS-CoV antibody called 03-018 was with a continuous series of linear and looped peptides starting with the sequence GPQSNQRSAPRITFG (SEQ ID NO:98) and ending with the sequence RSAPRITFGGPTDST (SEQ ID NO:104), thereby mapping the minimal binding site of 03-018 to the sequence RSAPRITFG (SEQ ID NO:468), which corresponds with

residues 11 - 19 of the N protein. Strinkingly, this linear epitope is conserved in the N protein sequence of all published human SARS-CoV and animal SARS-CoV-like isolates, but is absent in other members of the family of *Coronaviridae*. The PEPSCAN analysis further revealed that the recombinant human N protein specific anti-SARS-CoV antibody called 03-009 did not recognize a stretch of linear or looped amino acids on the N protein suggesting that this antibody recognizes a non-linear/conformational epitope of the N protein. All of the above peptides or parts thereof are useful in the detection of SARS-CoV in general.

Example 12

Selection of single-chain phage antibodies specifically recognizing proteins derived from SARS-CoV using transfected HEK293T-cells.

In another assay the single-chain phage antibodies are analyzed for their ability to bind HEK293T cells that recombinantly express proteins of the SARS-CoV. To this purpose HEK293T cells are transfected with a plasmid carrying a cDNA sequence encoding the envelope (E) protein, membrane (M) protein or spike (S) protein from SARS-CoV strain Frankfurt 1 or with the empty vector. Stable transfectants are selected using standard techniques known to a person skilled in the art (see Coligan JE, Dunn BM, Ploegh HL, Speicher DW and Wingfield PT (eds.) (2001) Current protocols in protein science, volume I. John Wiley & Sons, Inc., New York). For flow cytometry analysis, single-chain phage antibodies are first blocked in an equal volume of 4% PBS-M for 15 minutes at 4°C prior to the staining of the transfected HEK293T cells. The blocked phage antibodies are added to control transfected HEK293T cells and HEK293T cells transfected with the SARS-CoV

proteins mentioned above. The binding of the single chain phage antibodies to the cells is visualized using a biotinylated anti-M13 antibody (Santa Cruz Biotechnology) followed by streptavidin-phycoerythrin (Caltag).

In yet another assay scFv antibodies were analyzed for their ability to bind to portions of the spike (S) protein and the complete nucleocapsid (N) protein of SARS-CoV. The cDNA encoding the S protein of the SARS-CoV strain Frankfurt 1 was adapted to the codon-bias of *Homo sapiens* genes and gene-optimized for optimal expression by Geneart (Regensburg, Germany). The codon-optimized nucleotide sequence of the S protein is shown in SEQ ID NO:462. The amino acid sequence encoded by this codon-optimized nucleotide sequence is shown in SEQ ID NO:463.

DNA encoding for the N-terminal 565 amino acids (portion called S565) was cloned as a *Kpn*I-*Bam*HI fragment in pAdapt (Havenga *et al.*, 2001) that was modified by insertion of the polylinker of the vector called pcDNA3.1/myc-His C (Invitrogen) (vector called pAdapt/myc-His C).

DNA encoding for the N-terminal 826 amino acids (portion called S826) was cloned as *Kpn*I-*Eco*RV fragment in pAdapt that was modified by insertion of the polylinker of the vector called pcDNA3.1/myc-His B (Invitrogen) (vector called pAdapt/myc-His B).

DNA encoding for the N-terminal 1195 amino acids (portion called S1195) is constructed as follows. A DNA fragment is amplified from codon-optimized S protein cDNA using the oligonucleotide primers: *Xho*ISpikeRevCOG 5′-gttcctcgaggggccacttgatgtactgc-3′ (SEQ ID NO:464) and SpikeCOG seq 1 5′-ccaggtgaagcagatgta-3′ (SEQ ID NO:465). The resulting fragment is cloned as *Bst*EII-*Xho*I fragment together with a *Kpn*I-*Bst*EII fragment derived from the codon-optimized S

protein cDNA (alternatively, a restriction site other than *Bst*EII, which is unique in the amplified fragment can be used) in pAdapt that is modified by insertion of the polylinker of the vector called pcDNA3.1/myc-His A (Invitrogen) (vector called pAdapt/myc-His A).

A fragment corresponding to amino acid residues 318-510 of the S protein (portion called S318-510) was amplified on S gene cDNA using the oligonucleotide primers: *Eco*RIspikeFor318 5′-cctggaattctccatggccaacatcaccaacc-3′ (SEQ ID NO:469) and *Xba*IspikeRev510 5′-gaagggccctctagacacggtggcagg-3′ (SEQ ID NO:470). The resulting fragment was digested with *Eco*RI-*Xba*I and cloned into pHAVT20/myc His A to yield pHAVT20/myc-His A S318-510. In this vector expression of fragment S318-510 fused to the HAVT20 leader sequence was under control of the human, full-length, immediate-early CMV promoter.

DNA encoding for the nucleocapsid protein was amplified from total random hexamer cDNA from the SARS-CoV strain Frankfurt 1 using the oligonucleotide primers *Kpn*INCFor 5′-cttggtaccgccaccatgtctgataatggacc-3′ (SEQ ID NO:466) and *Xba*INCRev 5′-gttctctagatgcctgagttgaatcagc-3′ (SEQ ID NO:467) and cloned as *Kpn*I-*Xba*I fragment in pAdapt/myc-His A. DNA transfections were performed in HEK293T cells for transient expression using standard techniques. The S protein derived fragments and nucleocapsid (N) protein were used directly from culture supernatant or cell lysates. Alternatively, the fragments and nucleocapsid (N) protein were purified from culture supernatant using Ni-NTA (Qiagen).

The ELISA for the detection of scFv antibodies to the S protein derived fragments or the nucleocapsid (N) protein was performed as follows. Wells of ELISA plates were coated overnight with 5 µg/ml anti-myc antibody in 50 mM bicarbonate buffer pH 9.6. In case of the UV-inactivated SARS-CoV

preparation, the wells were coated with the preparation as described above. The wells of the plates were washed three times with PBS containing 0.05% Tween and blocked for 2 hours at 37°C with PBS containing 1% BSA. The wells coated with anti-myc antibody were incubated with culture supernatant or cell lysate containing the myc-tagged fragment S565 or nucleocapsid (N) protein diluted in PBS containing 1% BSA for 1 hour at room temperature. The wells were washed three times with PBS containing 0.05% Tween. Next, the scFv's SC03-014 and SC03-009 were diluted in PBS containing 0.05% Tween and were incubated for 1 hour at room temperature. The wells were washed three times with PBS containing 0.05% Tween and incubated for 1 hour at room temperature using an anti-VSV-HRP conjugate (for scFv). As shown in Figure 8, SC03-009 and SC03-014 were both capable of binding an inactivated SARS-CoV preparation in ELISA in contrast to the control scFv SC02-006 (Anti-thyroglobulin scFv). Testing the reactivity of the scFv's with SARS-CoV derived proteins or portions captured through their myc-tag revealed that SC03-009 was capable of binding to the nucleocapsid (N) protein, but not the spike fragment S565 and an irrelevant control myc-tagged protein (the bivalent scFv called 02-300). In contrast, SC03-014 only reacted with the S565 fragment and not with the nucleocapsid (N) protein and the control protein 02-300. For ELISA experiments with IgG's (see below) a murine anti-Hu-IgG HRP conjugate instead of an anti-VSV-HRP conjugate was used. Development was done with O-phenylenediamine substrate, the reaction was stopped by the addition of 1M H_2SO_4 and the absorbance was measured at 492 nm. Similar results were obtained in ELISA experiments when the wells coated with anti-myc antibody were incubated with myc-tagged fragment S565 or

nucleocapsid (N) protein which was first purified from culture supernatant or cell lysate using Ni-NTA (data not shown).

To further investigate binding to the SARS coronavirus fragments and proteins, the following experiments were performed with the monoclonal antibodies 03-001, 03-002, 03-006, 03-009, 03-013, 03-014, 03-015 and 03-018. Full length N protein from transfected HEK293T cell lysates was captured on an ELISA plate by means of an anti-myc antibody as described above and incubated with the above mentioned IgG molecules. Figure 9 shows that the monoclonal antibodies 03-009 and 03-018 bound specifically to the N protein, while not binding the control protein, *i.e.* bivalent scFv 02-300.

In order to rank the affinities of the monoclonal antibodies binding the N protein, a titration of IgG concentration (by diluting the antibodies in PBS containing 1% ELK) followed by ELISA as described above was performed. Titration of the monoclonal antibodies showed that 03-009 bound better to the N protein than 03-018 (see Figure 10). This may reflect a difference in affinity.

To further explore the antibody binding sites within the N protein, a competition ELISA on immobilized N protein was performed. Captured N protein was incubated with 1 µg/ml (non-saturating) biotinylated antibody 03-009 without competing antibody or in the presence of a 25 or 50-fold excess of competing antibody (antibody 03-009 or 03-018). Bound biotinylated antibody 03-009 was detected with streptavidin-conjugated-HRP (BD Pharmingen) and developed as described above. Results (see Figure 11) show that binding of monoclonal antibody 03-009 is unaffected in the presence of a 25 or 50-fold excess of unlabeled monoclonal antibody 03-018. This demonstrated that the antibodies 03-009 and 03-018 do not

compete with each other for binding to the N protein and recognize different epitopes.

Subsequently, the interaction of the above antibodies with the S protein was evaluated. Binding of the antibodies to the full length S protein expressed on HEK293T cells was first investigated by flow cytometry. The transfected cells were incubated with human IgGs at a concentration of 10 µg/ml for 1 h on ice. Cell were washed three times, incubated for 45 minutes with biotinylated goat anti-human IgG followed by a 10 minute incubation with streptavidin-conjugated phycoerythin. The analysis showed that the monoclonal antibodies 03-006, 03-013, 03-014 and 03-015 specifically bound S protein transfected HEK293T cells (see Figure 12).

To further localize the binding site of these antibodies within the S protein, binding to a recombinant soluble fragment encompassing S protein residues 1-565 (S565) was tested by means of ELISA as described above. Within the antibody panel binding the full length S protein on the HEK293T cells, all antibodies except 03-015 bound to fragment S565 (see Figure 12).

To further narrow the binding site of the antibodies, binding to a recombinant fragment comprising residues 318-510 of the S protein (S318-510) was evaluated. Figure 12 shows that only 03-006, 03-013 and 03-014 were capable of binding the S318-510 fragment.

As shown in a titration experiment performed similarly as the titration experiment described above, antibody 03-014 appeared to bind S565 with a higher affinity than the antibodies 03-006 and 03-013 (see Figure 13).

Using a similar set-up as described above, a competition ELISA was performed. Captured S565 was incubated with 1 µg/ml (nonsaturating) biotinylated antibody 03-014 without competing

antibody or in the presence of a 25 or 50-fold excess of competing IgG (antibody 03-006 or 03-014). Bound biotinylated antibody 03-014 was detected with streptavidin-conjugated-HRP (BD Pharmingen) and developed as described above. The competition ELISA revealed that binding of antibody 03-014 was unaffected in the presence of a 25 or 50 fold excess of unlabeled 03-006 and it was concluded that their binding sites do not overlap (see Figure 14).

Flow cytometry analysis was used to assay binding of the fragments of the S protein to angiotensin-converting enzyme 2 (ACE2), the natural receptor for SARS-CoV infectivity (Li *et al.*, 2003). Vero cells expressing ACE2 (measured by means of a polyclonal anti-ACE2 antibody (R&D systems)) were incubated for 1 hour at 4°C with saturating concentrations of the myc-tagged S565 fragment. As a control the Vero cells were incubated with a myc-tagged bivalent scFv 02-006. Alternatively, the S565 fragment was incubated with the IgG antibodies 03-014 (anti-SARS-CoV S protein antibody), 03-018 (anti-SARS-CoV N protein antibody) or 02-027 (anti-EPCAM control antibody) prior to incubation with the Vero cells. After three washes, bound fragment and the control protein were detected by flow cytometry analysis by using biotinylated anti-myc antibody (Santa Cruz Biotechnology Inc.) and streptavidin-conjugated phycoerythrin (Caltag). All incubations and washes were performed at 4°C in PBS, supplemented with 0.5% bovine serum albumin (BSA). As shown in Figure 15, preincubation of fragment S565 in the presence of 0.5 µM antibody 03-014 resulted in complete loss of S565 binding to Vero cells, whereas in the presence of antibody 0.5 µM antibody 03-018 (see Figure 16) or 0.5 µM antibody 02-027 (see Figure 17), S565 binding to Vero cells remained unaffected. In conclusion, monoclonal antibody 03-014 blocked

binding of S565 to Vero cells, whereas the antibodies 03-018 and 02-027 did not. In an identical experiment it was shown that antibody 03-006 was capable of partially blocking binding of the S565 fragment to Vero cells (data not shown). Together, these data suggest that antibody 03-014 neutralizes SARS-CoV, by preventing the interaction of the S protein to cellular receptors such as ACE2.

Example 13

Construction of a ScFv phage display library using peripheral blood lymphocytes of a patient having been exposed to SARS-CoV

Lymphocytes were obtained from a patient recovered from SARS-CoV (see Rickerts *et al.* 2003) and frozen in liquid nitrogen. The lymphocytes were quickly thawed in a 37°C water bath and transferred to wet-ice. The lymphocytes were diluted with cold DMEM culture medium to a final volume of 50 ml in a 50 ml tube and centrifuged for 5 minutes at 350xg. The obtained cell pellet was suspended in 5 ml DMEM and cell density was determined microscopically using trypan-blue exclusion to visualize dead cells. All cells (~$5x10^6$) were spun again for 5 minutes at 350xg, decanted and suspended in residual fluid (DMEM). Total RNA was prepared from these cells using organic phase separation (TRIZOL™) and subsequent ethanol precipitation. The obtained RNA was dissolved in DEPC treated ultrapure water and the concentration was determined by OD 260nm measurement. Thereafter, the RNA was diluted to a concentration of 100 ng/µl. Next, 1 µg of RNA was converted into cDNA as follows: To 10 µl total RNA, 13 µl DEPC treated ultrapure water and 1 µl random hexamers (500 ng/µl) were added and the obtained mixture was heated at 65°C for 5 minutes and quickly cooled on wet-ice. Then, 8 µl 5X First-Strand buffer, 2 µl dNTP (10 mM each), 2 µl DTT (0.1 M), 2 µl

Rnase-inhibitor (40 U/µl) and 2 µl Superscript™III MMLV reverse transcriptase (200 U/µl) were added to the mixture, incubated at room temperature for 5 minutes and incubated for 1 hour at 50°C. The reaction was terminated by heat inactivation, *i.e.* by incubating the mixture for 15 minutes at 75°C.

The obtained cDNA products were diluted to a final volume of 200 µl with DEPC treated ultrapure water. The OD260nm of a 50 times diluted solution (in 10 mM Tris buffer) of the dilution of the obtained cDNA products gave a value of 0.1.

5 to 10 µl of the diluted cDNA products were used as template for PCR amplification of the immunoglobulin gamma heavy chain family and kappa or lambda light chain sequences using specific oligonucleotide primers (see Tables 8-15). PCR reaction mixtures contained, besides the diluted cDNA products, 25 pmol sense primer and 25 pmol anti-sense primer in a final volume of 50 µl of 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 2.5 mM $MgCl_2$, 250 µM dNTPs and 1.25 units Taq polymerase. In a heated-lid thermal cycler having a temperature of 96°C, the mixtures obtained were quickly melted for 2 minutes, followed by 30 amplification cycles of: 30 seconds at 96°C, 30 seconds at 60°C and 60 seconds at 72°C. In a first round amplification, each of nine sense directed primers (see Table 8; covering all families of heavy chain variable regions) was combined with an IgG specific constant region anti-sense primer called HuCIgG 5′-GTC CAC CTT GGT GTT GCT GGG CTT-3′ (SEQ ID NO:131) yielding nine products of about 650 basepairs. These products were purified on a 2% agarose gel and isolated from the gel using Qiagen gel-extraction columns. 1/10 of each of the isolated products was used in an identical PCR reaction as described above using the same nine sense primers (covering all families of heavy chain variable regions), whereby each

sense primer was combined with one of the four J-region specific anti-sense primers (see Table 9). This resulted in 36 products of approximately 350 basepairs. The products obtained were purified on a 2% agarose gel and isolated from the gel using Qiagen gel-extraction columns. In a third round, 1/10 of each of the isolated products was subjected to re-amplification with the same set of primers as in the second round with the proviso that the primers used were extended with restriction sites (see Table 10) to enable directed cloning in the phage display vector pDV-C05 (see Figure 7 and SEQ ID NO:130). This resulted again in 36 products. These products were pooled per used (VH) sense primer into nine fractions. In the next step, 2.5 µg of pooled fraction and 100 µg pDV-C05 vector were digested with NcoI and XhoI and purified by gel. Thereafter, a ligation was performed overnight at 16°C as follows. To 500 ng pDV-C05 vector 70 ng pooled fraction was added in a total volume of 50 µl ligation mix containing 50 mM Tris-HCl (pH 7.5), 10 mM $MgCl_2$, 10 mM DTT, 1 mM ATP, 25 µg/ml BSA and 2.5 µl T4 DNA Ligase (400 u/µl). This procedure was followed for each pooled fraction. The ligation mixes were purified by phenol/chloroform, followed by a chloroform extraction and ethanol precipitation, methods well known to the skilled artisan. The DNA obtained was dissolved in 50 µl ultrapure water and per ligation mix two times 2.5 µl aliquots were electroporated into 40 µl of TG1 competent *E. coli* bacteria according to the manufacturer's protocol (Stratagene). Transformants were grown overnight at 37°C in a total of 27 dishes (three dishes per pooled fraction; dimension of dish: 240 mm x 240 mm) containing 2TY agar supplemented with 50 µg/ml ampicillin and 4.5% glucose. A (sub)library of variable heavy chain regions was obtained by scraping the transformants from the agar plates. This

(sub)library was directly used for plasmid DNA preparation using a Qiagen™ kit.

The light chain immunoglobulin sequences were amplified from the same cDNA preparation in a similar three round PCR procedure and identical reaction parameters as described above for the heavy chain regions with the proviso that the primers depicted in Tables 11-15 were used. The first amplification was performed using a set of seventeen light chain variable region sense primers (eleven for the lambda light chain (see Table 11) and six for the kappa light chain (see Table 12)) each combined with an anti-sense primer recognizing the C-kappa called HuCk 5′-ACACTCTCCCCTGTTGAAGCT CTT-3′ (see SEQ ID NO:158) or C-lambda constant region HuCμ2 5′-TGAACATTCTGTAGGGGCCACTG-3′ (see SEQ ID NO:159) or HuCμ7 5′-AGAGCATTCTGCAGGGGCCACTG-3′ (see SEQ ID NO:160) (the HuCμ2 and HuCμ7 anti-sense primers were mixed to equimolarity before use), yielding 17 products of about 600 basepairs. These products were purified on a 2% agarose gel and isolated from the gel using Qiagen gel-extraction columns. 1/10 of each of the isolated products was used in an identical PCR reaction as described above using the same seventeen sense primers, whereby each lambda light chain sense primer was combined with one of the three Jlambda-region specific anti-sense primers (see Table 13) and each kappa light chain sense primer was combined with one of the five Jkappa-region specific anti-sense primers (see Table 14). This resulted in 63 products of approximately 350 basepairs. The products obtained were purified on a 2% agarose gel and isolated from the gel using Qiagen gel-extraction columns. In a third round, 1/10 of each of the isolated products was subjected to re-amplification with the same set of primers as in the second round with the proviso that the primers used were extended with restriction

sites (see Table 15) to enable directed cloning in the heavy chain (sub)library vector. This resulted again in 63 products. These products were pooled to a total of 10 fractions. This number of fractions was chosen to maintain the natural distribution of the different light chain families within the library and to over or under represent certain families. The number of alleles within a family was used to determine the percentage of representation within a library (see Table 16). Next, the fractions were digested with SalI and NotI and ligated in the heavy chain (sub)library vector, which was cut with the same restriction enzymes, using the same ligation procedure and volumes as described above for the heavy chain (sub)library. Ligation purification and subsequent transformation of the resulting definitive library was also performed as described above for the heavy chain (sub)library. The transformants were grown in 30 dishes (three dishes per pooled fraction; dimension of dish: 240 mm x 240 mm) containing 2TY agar supplemented with 50 µg/ml ampicillin and 4.5% glucose. All bacteria were harvested in 2TY culture medium containing 50 µg/ml ampicillin and 4.5% glucose, mixed with glycerol to 15% (v/v) and frozen in 1.5 ml aliquots at -80°C. Rescue and selection of the library were performed as described supra for the non-immune libraries.

Additionally, a naïve phage display library of scFv's was prepared. For that purpose, healthy donor peripheral blood lymphocytes were used as source of immuno globulin transcripts. Using the protocols described above, immunoglobulin gamma VH regions were amplified and cloned into a PDV-C05 vector already containing a VkIII light chain fragment. This resulted in a non-immunized, naïve library expressing scFv with a fixed VkIII light chain variable region and having a size of approximately $10x10^6$.

Example 14

Selection of phage carrying single chain Fv fragments specifically recognizing SARS-CoV from naïve and immune phage display libraries

Antibody fragments were selected essentially as described previously (see Example 1). For the selections described below an UV-inactivated SARS-CoV preparation was used (for preparation thereof see Example 9). In contrast to the selections described in Example 1, no pre-subtraction using heat-inactivated fetal bovine serum coated Maxisorp™ tubes (Nunc) was performed. To the SARS-CoV coated tubes, 500 µl (approximately 10^{13} cfu) of a naïve or an immune phage display library expressing single chain Fv fragments (scFv's) (see Example 13 for the construction of these libraries), one volume of 4% PBS-FM and Tween-20 to a final concentration of 0.05% was added.

For the naïve phage display library selections, binding was allowed to proceed for 1 hour on a slowly rotating wheel at 37°C followed by an incubation of 30 minutes without agitation. The tubes were emptied and washed as follows: first round, 10 times with PBS containing 0.05% Tween-20 (PBST) and 10 times with PBS; second round, 15 times with PBST and 10 times with PBS; third round 15 times with PBST and 15 times with PBS.

For the immune phage display library selections which consisted of a single round only, binding was allowed to proceed at 37°C or room temperature as described above. The following selections and washes were performed: incubation at 37°C, washing 5 times with PBST and 5 times with PBS; incubation at 37°C, washing 10 times with PBST and 10 times with PBS; incubation at room temperature, washing 10 times

with PBST and 10 times with PBS. Bound phages were eluted and processed as described in Example 1. Phages derived from individual colonies were tested in ELISA for binding activity to SARS-CoV coated to 96-well plates.

In the selections from the naïve phage display library the phage antibodies called SC03-019 and SC03-059 were obtained. In the selections from the immune phage display library the phage antibodies called SC03-020, SC03-021, SC03-022, SC03-023, SC03-024, SC03-025, SC03-026, SC03-027, SC03-029, SC03-030, SC03-031, SC03-032, SC03-033, SC03-034, SC03-035, SC03-036, SC03-037, SC03-038, SC03-039, SC03-040, SC03-041, SC03-042, SC03-043, SC03-044, SC03-045, SC03-046, SC03-047, SC03-048, SC03-049, SC03-050, SC03-051, SC03-052, SC03-053, SC03-054, SC03-055, SC03-056, SC03-057 and SC03-058 were obtained.

Example 15

Validation of the SARS-CoV specific single-chain phage antibodies derived from the naïve and immune phage display library

Selected single-chain phage antibodies that were obtained in the screens described in Example 14 were validated in ELISA for specificity, *i.e.* binding to the SARS-CoV preparation mentioned in Example 14, essentially as described in Example 2. In contrast to Example 2, the single-chain phage antibodies were not tested for binding to 10% FBS.

As shown in Table 17, the selected phage antibodies called SC03-019, SC03-020, SC03-021, SC03-022, SC03-023, SC03-024, SC03-025, SC03-026, SC03-027, SC03-029, SC03-030, SC03-031, SC03-032, SC03-033, SC03-034, SC03-035, SC03-036, SC03-037, SC03-038, SC03-039, SC03-040, SC03-041, SC03-042, SC03-043, SC03-044, SC03-045, SC03-046, SC03-047, SC03-048, SC03-

049, SC03-050, SC03-051, SC03-052, SC03-053, SC03-054, SC03-055, SC03-056, SC03-057, SC03-058 and SC03-059 displayed significant binding to the immobilized SARS-CoV preparation. As a control, the procedure was performed simultaneously using no single-chain phage antibody.

Example 16

Characterization of the scFv's specific for SARS-CoV derived from the naïve and immune phage display library

From the selected specific single chain phage antibody (scFv) clones (see Example 14) plasmid DNA was obtained and nucleotide sequences were determined according to standard techniques. The nucleotide sequences of the scFv's (including restriction sites for cloning) called SC03-019, SC03-020, SC03-021, SC03-022, SC03-023, SC03-024, SC03-025, SC03-026, SC03-027, SC03-029, SC03-030, SC03-031, SC03-032, SC03-033, SC03-034, SC03-035, SC03-036, SC03-037, SC03-038, SC03-039, SC03-040, SC03-041, SC03-042, SC03-043, SC03-044, SC03-045, SC03-046, SC03-047, SC03-048, SC03-049, SC03-050, SC03-051, SC03-052, SC03-053, SC03-054, SC03-055, SC03-056, SC03-057, SC03-058 and SC03-059 are shown in SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287 and SEQ ID NO:289, respectively.

The amino acid sequences of the scFv's called SC03-019, SC03-020, SC03-021, SC03-022, SC03-023, SC03-024, SC03-025, SC03-026, SC03-027, SC03-029, SC03-030, SC03-031, SC03-032, SC03-033, SC03-034, SC03-035, SC03-036, SC03-037, SC03-038, SC03-039, SC03-040, SC03-041, SC03-042, SC03-043, SC03-044, SC03-045, SC03-046, SC03-047, SC03-048, SC03-049, SC03-050, SC03-051, SC03-052, SC03-053, SC03-054, SC03-055, SC03-056, SC03-057, SC03-058 and SC03-059 are shown in SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288 and SEQ ID NO:290, respectively.

The VH and VL gene identity (see Tomlinson IM, Williams SC, Ignatovitch O, Corbett SJ, Winter G. V-BASE Sequence Directory. Cambridge United Kingdom: MRC Centre for Protein Engineering (1997)) and heavy chain CDR3 compositions of the scFv's specifically binding the SARS-CoV preparation are depicted in Table 18.

Example 17

In vivo experiment in ferrets with recombinant human anti-SARS-CoV antibodies having neutralizing activity

The experiment was performed to investigate the neutralizing capacity of the anti-SARS-CoV monoclonal antibodies of the invention *in vivo* essentially as described by Emini *et al.* (1990). Briefly, the human monoclonal anti-

SARS-CoV antibody 03-014 and the control anti-Epcam antibody 02-027 were pre-incubated *in vitro* with two different titres (10^3 and 10^4 $TCID_{50}$) of the SARS-CoV strain SCV-P4(5688) (obtained from patient 5688, see above). Antibody concentrations used were extrapolated from the concentration of antibody needed to neutralize $100TCID_{50}$ of virus in a volume of 100 µl (*i.e.* 6.25 µg/ml; see *in vitro* neutralization data in Example 7) and multiplied by twenty (*i.e.* 0.13 mg/ml for $1000TCID_{50}$, 1.3 mg/ml for $10,000TCID_{50}$). The virus/antibody mixtures obtained were used to infect ferrets via the intratracheal route (Fouchier *et al.* 2003). Cell cultures of Vero 118 cells were inoculated in parallel to verify the *in vitro* neutralizing activity of the monoclonal antibody 03-014 and the expected infectivity of the virus in case of pre-incubation with the control antibody. Ferrets were monitored for signs of disease and shedding of virus (RT-PCR) and ultimately sacrificed and examined by histopathology.

High dose and low dose solutions of the monoclonal antibody 03-014 and the control antibody were prepared as follows. The working solution of the monoclonal antibody 03-014 had a concentration of 1.44 mg/ml. 4.87 ml of this working solution was brought into a 15 ml tube (high dose solution, 1.44 mg/ml final concentration). To obtain the low dose solution, 541 µl of the working solution was added to 2.46 ml PBS (low dose solution, 0.26 mg/ml final concentration) and mixed well. 2.7 ml of this low dose solution was brought into a 15 ml tube.

The starting solution of the control antibody had a concentration of 3.90 mg/ml. 2.10 ml of this starting solution was added to 3.58 ml PBS to obtain a working solution with a final concentration of 1.44 mg/ml. 4.87 ml of this working solution was brought into a 15 ml tube (high dose solution,

1.44 mg/ml final concentration). To obtain the low dose solution, 541 µl of the working solution was added to 2.46 ml PBS (low dose solution, 0.26 mg/ml final concentration) and mixed well. 2.7 ml of this low dose solution was brought into a 15 ml tube.

After preparation of the high dose and low dose solutions of the monoclonal antibodies, the high dose and low dose solution of the SARS-CoV were prepared. The starting solution of the SARS-CoV had a concentration of 10^7 $TCID_{50}$/ml. The starting solution was thawed at 37°C and 100 µl of this solution was added to 900 µl PBS and mixed well. The working solution thus obtained had a concentration of 10^6 $TCID_{50}$/ml.

To obtain a high dose SARS-CoV solution 200 µl working solution was added to 1.8 ml PBS and mixed well (high dose SARS-CoV solution, 100,000 $TCID_{50}$/ml). To obtain a low dose SARS-CoV solution 200 µl high dose solution was added to 1.8 ml PBS and mixed well. After that, the thus obtained diluted high dose solution was further diluted by adding 1.2 ml of this diluted high dose solution to 4.8 ml PBS and mixing (low dose SARS-CoV solution, 2,000 $TCID_{50}$/ml).

Next, the high dose and low dose solutions of the monoclonal antibodies were mixed with the high and low dose SARS-CoV solutions at 37°C for 1 hour. The following groups were prepared.

Group 1: 2.7 ml low dose SARS-CoV solution was added to 2.7 ml low dose solution of the monoclonal antibody 03-014 and mixed well (final concentration of SARS-CoV was 1,000 $TCID_{50}$/ml; final concentration of monoclonal antibody 03-014 0.13 mg/ml; total volume 5.4 ml).

Group 2: 0.54 ml high dose SARS-CoV solution was added to 4.87 ml high dose solution of the monoclonal antibody 03-014 and mixed well (final concentration of SARS-CoV was 10,000

$TCID_{50}$/ml; final concentration of monoclonal antibody 03-014 1.3 mg/ml; total volume 5.4 ml).

Group 3: 2.7 ml low dose SARS-CoV solution was added to 2.7 ml low dose solution of the monoclonal control antibody and mixed well (final concentration of SARS-CoV was 1,000 $TCID_{50}$/ml; final concentration of monoclonal control antibody 0.13 mg/ml; total volume 5.4 ml).

Group 4: 0.54 ml high dose SARS-CoV solution was added to 4.87 ml high dose solution of the monoclonal control antibody and mixed well (final concentration of SARS-CoV was 10,000 $TCID_{50}$/ml; final concentration of monoclonal control antibody 1.3 mg/ml; total volume 5.4 ml).

1.1 ml of the solution of each of the 4 groups was removed for inoculation of Vero 118 cell cultures. 1.0 ml of the solution of each of the 4 groups was added to a separate well of substrate plates (each plate containing 6 wells). Each well contained an 80% monolayer of Vero 118 cells. The monolayers were prepared by trypsinizing Vero 118 cells, diluting them in DMEM with 5% FBS, seeding $2*10^6$ Vero 118 cells per separate well and incubating the cells for 16-20 hours at 37°C with 2 ml DMEM containing sodium bicarbonate 0.75%, L-glutamine 2mM and penicillin/streptomycin (10 U/ml). The plates with the above solutions were incubated overnight at 37°C. The medium was replaced by fresh medium and the plates were incubated for a further 3-5 days at 37°C and monitored for CPE.

To each of the remaining amounts (4.3 ml) of each of the 4 groups 8.6 ml PBS was added. Prior to any handling or sampling, the animals were anaesthesized by means of light ketamine (2.5 mg/kg) and domitor (0.1 ml/kg), followed by antisedan (0.05 ml/kg). Before inoculation, from each ferret a nasal swab was taken (day 0). Each ferret was intratrachealy

inoculated with 3 ml of the respective solutions as indicated in the scheme shown in Table 19. Nasal swabs alone were taken from each ferret as indicated in the scheme shown in Table 19 (day 2). Animals were checked every day for clinical symptoms such as respiratory problems, erythema and lethargy. Animals were weighed every other day. From each ferret nasal and pharyngeal swabs were taken as indicated in the scheme shown in Table 19 (day 4 or 7). Swabs were preserved in standard virus transport medium and stored at -80°C. Ferrets were euthanised by means of total exsanguination under full anaesthesia by means of ketamine (5 mg/kg) and domitor (0.1 ml/kg) as indicated in the scheme shown in Table 19 (day 4 or 7). Next, the samples were analysed by RT-PCR with primers and probes specific for the nucleoprotein (NP) gene of SARS-CoV to quantify SARS-CoV in lung tissues as described in Kuiken *et al.* 2003.

As shown in Figure 18, ferrets inoculated with the virus-control antibody mixture displayed dose dependent SARS-CoV excretion at 2, 4 and 7 days after inoculum administration. In contrast, in the animals inoculated with the virus-03-014 antibody mixture no SARS-CoV could be detected at any time point, indicating that no virus had disseminated from the site of inoculation.

SARS-CoV titres in the lung were obtained using an in vitro virus titration assay. Lung samples were collected and weighed and transferred to a 5 ml tubes containing 1 ml RPMI1640 medium. The samples were transferred to ice, homogenized and cellular debris was pelleted by centrifugation. From the supernatant ten-fold serial dilutions were prepared starting with a dilution of 1:10. 100 µl of the homogenate dilutions were added to 80% confluent monolayers of Vero 118 cells in a 96 well plate. The cells were incubated

for five days and the occurrence cytopathogenic effect (CPE) was scored. SARS-CoV lung titers were expressed as TCID50/ml and were calculated according to the Reed and Muench method.

As shown in Figure 19, ferrets inoculated with the virus-control antibody mixture displayed equal high SARS-CoV titers (10E6.5/ml lung homogenate) at day 4 independent of the virus challenge dose. At day seven, the virus load in the lungs of both control groups was significantly lower (10E4/ml lung homogenate), suggesting that the animals are capable of clearing the virus. Strikingly, very low amounts of SARS-CoV were detected in both the high and low dose groups inoculated with the virus-03-014 antibody mixture(10E1.5/ml lung homogenate is the detection limit of the assay used).

The analysis of the pathology in the ferret lungs was performed according to the following procedure. Necropsies were done according to a standard protocol; one lung of each ferret was inflated with 10% neutral-buffered formalin by intrabronchial intubation and suspended in 10% neutral-buffered formalin overnight. Samples were collected in a standard manner (one from the cranial part of the lung, one from the medial and two from the caudal part), embedded in paraffin, cut at 5 µm and stained with haematoxylin and eosin (HE). For semi-quantitative assessment of SARS-CoV-infection-associated inflammation in the lung, each HE-stained section was examined for inflammatory foci by light microscopy using a 2.5× objective. If any suspect lesions were seen, they were examined at higher power to determine whether typical characteristics are present (intra-alveolar oedema, neutrophils and macrophages in alveolar lumina, type 2 pneumocyte hyperplasia). Lung sections were scored as followed: -, no SARS lesions; +, mild SARS lesions; ++, moderate SARS lesions; +++, marked SARS lesions. The final

score for each animal is the cumulative score of two lung sections. Sections were examined in a blinded manner.

As shown in Figure 20, ferrets inoculated with the virus-control antibody mixture displayed significant lung pathology at day 4 independent of the virus challenge dose. At day seven, the pathological signs in the lungs of the low dose control group had disappeared, demonstrating that these animals had the capacity to recover from the disease. In both high and low dose groups inoculated with the virus-03-014 antibody mixture no signs of pathology were observed at both 4 and 7 days post treatment indicating that the very low amount of virus present in the lungs did not induce tissue damage.

Example 18

Efficacy of the human anti-SARS-CoV monoclonal antibodies upon passive transfer and SARS-CoV challenge in ferrets

To address whether the human anti-SARS-CoV monoclonal antibodies can be efficacious in a prophylactic setting a SARS-CoV challenge experiment has been performed in ferrets. One day prior to the SARS-CoV challenge ferrets were administered 10 mg/kg of monoclonal 03-014 IgG1 antibody intraperitoneally (i.p.). Prior to all experimental procedures the animals were anaesthesized as described *supra*. Two groups of four animals were treated with either a human monoclonal control IgG1 antibody (02-027, anti-Epcam antibody) or with the monoclonal anti-SARS-CoV 03-014 IgG1 antibody. The anti-SARS-CoV 03-014 antibody (concentration 1.23 mg/ml) was used undiluted for i.p. administration. The 02-027 control IgG1 antibody (concentration 3.9 mg/ml) was diluted 1:2 in PBS to achieve a final concentration of 1.3 mg/ml. The volume needed for the injection of the 10 mg/kg dose was based on the weight of the individual ferrets and varied between 6.5 and 8 ml. The

antibodies were injected at ambient temperature. Prior to the antibody transfer and prior to the SARS-CoV challenge, serum samples were obtained from each animal to assess the SARS-CoV neutralization titer as described before. All animals were challenged with 10^4 TCID50 of the SARS-CoV strain SCV-P4 (5688). To this purpose the 5866 SARS-CoV virus stock (concentration: 10^7 TCID50/ml) was thawed and 100 µl of the virus stock was added to 900 µl PBS (at room temperature) to obtain a working virus stock of 10^6 TCID50/ml. To obtain the final solution containing the challenge dose of 10^4 TCID50 per 3 ml challenge dose, 100 µl virus working stock was added to 30 ml PBS (at room temperature). Each ferret was inoculated intratracheally with 3 ml of virus mixture as described *supra*. Serum, pharyngeal swab and tissue samples were obtained according to Table 20. SARS-CoV excretion in pharyngeal swabs, SARS-CoV titers in lung tissue and lung pathology were analyzed as described *supra*.

Figure 21 shows that all control animals had high pulmonary SCV titers with a mean TCID50 in lung homogenates of 6.0 logs (SD 0.3), as compared to 2.7 logs (SD 0.5) in the 03-014 group, *i.e.* a difference in TCID50 of 3.3 logs (95%CI: 2.5-4.1 logs; $p <= 0.001$). The data were compared using the Students's T-test, differences were considered significant at p-value less than 0.05.

In the control group, shedding of SARS-CoV in the throat was apparent 2 and 4 days after challenge. By contrast, pharyngeal excretion was completely abolished in three of the 03-014-treated animals (see Figure 22). However, in one animal SARS-CoV excretion was comparable to the levels observed in the control group. Determination of the human IgG1 serum level of this ferret prior to challenge, revealed that this animal had acquired a 03-014 serum concentration below 5 µg/ml,

whereas in the other three animals serum IgG1 levels ranged from 65-84 µg/ml, suggesting inappropriate antibody administration. This finding was considered an artifact of the intraperitoneal antibody application procedure. In agreement with this, a declined serum neutralizing titer could be demonstrated in this animal compared to the three animals that did not display pharyngeal SARS-CoV excretion. Neutralising serum titers in this animal were less than half of those in the other animals on day 0 (titre of 5 against 100 TCID50), and were not detectable on day 2 after injection, compared with a titre of 5-10 against 100 TCID50 in the other animals on day 2.

Importantly, the differences in both pharyngeal and pulmonary viral titers between the control group and the 03-014 group were accompanied by a complete protection from macroscopic lung pathology in the group treated with 03-014 compared to the control group, who all showed multifocal lesions ($p=0.029$). Upon microscopic analysis, these lesions showed alveolar changes resembling diffuse alveolar damage as well as peribronchial, peribrochiolar, and perivascular lymphocytic cuffing.

Taken together, these results demonstrate that passive transfer of the 03-014 anti-SARS-CoV antibody was able to abolish SARS-CoV induced pulmonary lesions as well as SARS-CoV excretion in animals that had obtained sufficient 03-014 IgG serum titers (see Ter Meulen *et al.* 2004).

Example 19

Characterization of anti-SARS-CoV IgG antibodies by electron microscopy.

Supernatants of SARS-CoV producing Vero cells were harvested 24 hours p.i. and used directly for indirect, two-

step immuno-gold-labelling. SARS-CoV was adsorbed to carbon- and Pioloform-coated copper grids. After two washing steps with blocking buffer (PBS comprising 0.1% bovine serum albumin), the grids were incubated with the human monoclonal control IgG1 antibody (02-027, anti-Epcam antibody) or with the monoclonal anti-SARS-CoV 03-014 IgG1 antibody by floating on respective droplets for 30 minutes at room temperature. Next, surplus antibody was removed using a strip of filter paper and two washing steps on blocking buffer. Bound monoclonal antibodies were detected by incubation on droplets of anti-hu-IgG-gold-5 nm conjugates (British Biocell Corp). The grids were negative contrasted with 1% uranyl acetate and evaluated at a ZEISS EM 10 A transmission electron microscope. Incubation with the monoclonal anti-SARS-CoV 03-014 IgG1 antibody lead to a dense gold-label of the outer peplomer region of the SARS-CoV (see Figure 23, section a), while incubation with the human monoclonal control IgG1 antibody did not induce any label (see Figure 23, section b).

In a similar way, ultra-thin sections of Vero cells infected with SARS-CoV were analyzed by electron microscopy. In Figure 24A unstained ultra-thin sections of Vero cells infected with SARS-CoV are shown. In Figure 24B the sections were stained with the human monoclonal control IgG1 antibody (02-027, anti-Epcam antibody), while in Figure 24C and 24D the sections were stained with the monoclonal anti-SARS-CoV IgG1 antibodies 03-009 and 03-018, respectively. The localization of the gold label clearly indicates that the nucleocapsid protein is retained within the virion.

Example 20

Construction and evaluation of binding of the monoclonal anti-SARS-CoV antibodies to variant S318-510 fragments.

The diversity within the region 318-510 of the S protein was determined as follows. A list containing more than 146 genomes or genes encoding complete human SARS-CoV or fragments thereof was compiled. In 114 cases, an open reading frame encoding for full-length spike (S) protein was identified. Alignment of the spike amino acid residues 318-510 revealed 30 spike proteins, in which the region 318-510 was not identical to that of the spike protein of strain Frankfurt 1 (see Genbank accession number AY291315), which was used herein. The mutations, strains and Genbank numbers are depicted in Table 21. To investigate if 03-014 bound the S protein of all currently known human SARS-CoV isolates, eight recombinant spike fragments harboring the different amino acid substitutions as shown in Table 21 were generated. To this end, the above substitutions were introduced in the pHAVT20/myc-His A S318-510 vector using the Stratagene's QuikChange II site-directed mutagenesis kit according to the manufacturer's instructions. In case a sequence contained multiple amino acid substitutions, the process of mutagenesis, sequence analysis and confirmation was repeated for every single substitution. To rule out the introduction of additional mutations in the plasmid outside the gene of interest, the mutated (592 bp *Eco*RI-*Xba*I) fragment was recloned in *Eco*RI-*Xba*I cut pHAVT20/myc-His A. The resulting plasmids were transfected into 293T cells, and binding of 03-014 was evaluated by means of ELISA as described in Example 12. In addition, binding of HRP-conjugated monoclonal anti-His6 antibody (Roche) to each mutant was evaluated essentially as described above. Binding of anti-His6 and 03-014 to the wild-type S318-510 fragment derived from the Frankfurt 1 strain was set at 100%. Binding of the monoclonal anti-His6 antibody and 03-014 to the mutated S318-510 fragments was

expressed as percentage of binding compared to the wild-type S318-510 fragment.

As shown in Figure 25, the monoclonal anti-His 6 antibody and 03-014 were capable of binding all variant S318-510 fragments to a similar extent as the wild-type (non-mutated) S318-510 fragment, with the exception that the binding of monoclonal antibody 03-014 to variant F (N479S substitution) was approximately 50% of the binding to the other variant fragments and the wild-type S318-510 fragment. This indicates that residue N479 is involved in binding of 03-014, either directly by being part of the binding site of 03-014 or indirectly by being important for the correct conformation of the binding site of 03-014 within the spike protein. In conclusion, 03-014 is capable of binding the S318-510 region of the Frankfurt 1 strain and also of recombinant S318-510 fragments harboring mutations that can be found in the S318-510 region of the human SARS-CoV isolates described in Table 21. This suggests that 03-014 can be used to neutralize all currently known human SARS-CoV isolates.

Example 21

Screening assay for breadth of protection of the monoclonal anti-SARS-CoV antibodies

Different SARS-CoV strains were used to evaluate the potency and breadth of protection of the anti-SARS-CoV antibodies. The SARS-CoV strains HKU-36, HKU-39849, HKU-66, and HKU-61567 were passaged on FRhK-4 cells for two or three times before testing (see Table 22). Strain HKU-61644 was passaged on Vero cells and tested after passage 1 and 15. The SARS-CoV neutralization assay was performed on FRhK-4 cells as follows. A 500 µl 100 µg/ml stock solution of antibody was prepared in maintenance medium (MM, MEM supplemented with 1%

fetal calf serum). From this stock solution 2-fold-serially dilutions were prepared. 220 µl 100 µg/ml stock solution was added in duplo in a 96-well plate from which 110 µl was taken and mixed with 110 µl MM in each of the nine subsequent wells. 110 µl of the tenth well was discarded, which resulted in ten wells containing 110 µl 0.2-100 µg/ml antibody. 110 µl of the antibody dilution was mixed with 110 µl of the different SARS-CoV isolates at a concentration of 2000 TCID50/ml with the titer calculated according to the method of Reed and Muench. At this stage, in a 220 µl volume, antibody concentrations varied from 0.1 to 50 µg/ml in the presence of 1000 TCID50/ml SARS-CoV. The 96-well plate containing the antibody virus mixtures was preincubated for 1-2 hours at 37°C. 100 µl of the virus-antibody mixtures were added in quadruplicate to wells from a second 96-well tissue culture plate containing confluent FRhK-4 cells in 100 µl MM and incubated at 37°C. During this final incubation step, 100 TCID50 of SARS-CoV was present in the presence of antibody concentrations varying from 0.05 to 25 µg/ml. The cells were cultured at 37°C and observed for the development of CPE at 72 and 96 hours. CPE is compared to a positive control (SARS-CoV inoculated cells) and a negative control (cells incubated with MM only). The antibody neutralization titer was determined as the concentration of antibody which gives 100% protection of the quadruplicate cell cultures. The monoclonal anti-SARS-CoV antibody 03-014 completely neutralized 100 TCID50 of all tested SARS-CoV isolates at a concentration of 12.5 µg/ml (see Table 22). This indicates that antibody 03-014 is able to neutralize a variety of SARS-CoV isolates.

Table 1: Binding of single-chain (scFv) phage antibodies to a SARS-CoV preparation (Frankfurt 1 strain) and to FBS as measured by ELISA.

Name phage antibody	SARS-CoV preparation (OD492nm)	FBS (OD492nm)
SC03-001	0.979	0.142
SC03-002	0.841	0.091
SC03-003	0.192	0.092
SC03-005	0.869	0.098
SC03-006	1.056	0.086
SC03-007	0.876	0.096
SC03-008	0.358	0.114
SC03-009	0.760	0.087
SC03-010	0.327	0.082
SC03-012	0.495	0.100
SC03-013	0.979	0.101
SC03-014	0.917	0.089
SC03-015	0.796	0.077
Anti-thyroglobulin (SC02-006)	0.108	0.090
No phage antibody	0.072	0.083

Table 2: Binding of alternatively selected single-chain (scFv) phage antibodies to a SARS-CoV preparation (Frankfurt 1 strain) and to FBS as measured by ELISA.

Name phage antibody	SARS-CoV preparation (OD492nm)	FBS (OD492nm)
SC03-016	0.313	0.205
SC03-017	0.106	0.059
SC03-018	1.523	0.072
Anti-CD46 (SC02-300)	0.171	0.070
No phage antibody	0.081	0.045

Table 3: Data of the single-chain Fv's capable of binding SARS-CoV.

Name scFv	SEQ ID NO of nucleo-tide sequence	SEQ ID NO of amino acid sequence	HCDR3	V_H-germline	V_L-germline
SC03-001	46	47	HRFRHVFDY	V_H3 V_H3-38	V_kI DPK9 (02/012)
SC03-002	48	49	YYSRSLKAFDY	V_H3 DP29 (V_H3-72)	V_kI DPK9 (02/012)
SC03-003	50	51	RSYFRRFDY	V_H3 DP47 (V_H3-23)	V_kI DPK9 (02/012)
SC03-004	89	90	DGSRFPARFDY	V_H3 (V_H3-73)	V_kI DPK9 (02/012)
SC03-005	52	53	GGGRPYNPFDY	V_H3 V_H3-38	V_kI DPK9 (02/012)
SC03-006	54	55	DGSPRTPSFDY	V_H3 DP49 (V_H3-30)	V_kI DPK4 (A20)
SC03-007	56	57	GYWTSLTGFDY	V_H3 DP49 (V_H3-30)	V_kI DPK9 (02/012)
SC03-008	58	59	RVRPRRFDY	V_H3 DP47 (V_H3-23)	V_kI DPK9 (02/012)
SC03-009	60	61	GLFMVTTYAFDY	V_H3 DP47 (V_H3-23)	V_kI DPK9 (02/012)
SC03-010	62	63	GGGLPYLSFDY	V_H3 V_H3-38	V_kI DPK9 (02/012)
SC03-012	64	65	MFRKSSFDS	V_H1 DP14 (V_H1-18)	V_LIII DPL16 (2-13, 31)
SC03-013	66	67	GLTPLYFDY	V_H3 DP29 (V_H3-72)	V_kI DPK9 (02/012)
SC03-014	68	69	GISPFYFDY	V_H3 DP29 (V_H3-72)	V_kI DPK9 (02/012)
SC03-015	70	71	GLSLRP	V_H3 DP32 (V_H3-20)	V_LIII DPL16 (2-13, 31)
SC03-016	91	92	YGSAYRPPFDY	V_H3 (V_H3-49)	V_kI DPK9 (02/012)
SC03-017	93	94	SRSAGFFDY	V_H4 DP66 (V_H4-61)	V_kIII (L6)
SC03-018	95	96	FNPFTSFDY	V_H3 DP47 (V_H3-23)	V_kI DPK9 (02/012)

Table 4: Data of assay for SARS-CoV (strains Frankfurt 1 and Frankfurt 2) neutralising activity of bivalent scFv's.

Name bivalent scFv	OD 280 (mg/ml)	Neutralisation titer for Frankfurt 1 strain	Neutralisation titer for Frankfurt 2 strain
pyBi03-001C02	0.0238	<20	<20
pyBi03-002C02	0.0518	<20	<20
pyBi03-003C02	0.0406	<20	<20
pyBi03-005C02	0.0658	<20	<20
pyBi03-006C02	0.0343	<20	<20
pyBi03-007C02	0.0280	<20	<20
pyBi03-008C02	0.0210	<20	<20
pyBi03-009C02	0.0434	<20	<20
pyBi03-010C02	0.0567	<20	<20
pyBi03-012C02	0.0168	<20	<20
pyBi03-013C02	0.1743	160	80
pyBi03-014C02	0.1561	80	80
pyBi03-015C02	0.4816	<20	<20
pyBi02-148C02	0.0763	<20	<20
pyBi02-006C02	0.0791	<20	<20
Serum of SARS-patient		320	160

Table 5: Binding of recombinant human anti-SARS-antibodies to SARS-infected cells as measured by indirect immunofluorescence staining

Antibody	Staining
Negative control	-
Positive control	+
03-014	+
03-018	+

- indicates no staining of SARS-CoV transfected cells

+ indicates staining of SARS-CoV transfected cells

Table 6: Binding of antibody 03-018 to linear and looped/cyclic peptides of the N protein of SARS-CoV Urbani.

Peptides of N protein	Antibody 03-018 linear peptides	Antibody 03-018 looped peptides
MSDNGPQSNQRSAPR	0.1	0.3
SDNGPQSNQRSAPRI	0.0	0.2
DNGPQSNQRSAPRIT	0.2	0.3
NGPQSNQRSAPRITF	1.6	0.3
GPQSNQRSAPRITFG	3.2	0.3
PQSNQRSAPRITFGG	3.3	4.7
QSNQRSAPRITFGGP	2.9	4.1
SNQRSAPRITFGGPT	3.3	2.2
NQRSAPRITFGGPTD	2.9	1.4
QRSAPRITFGGPTDS	2.6	3.9
RSAPRITFGGPTDST	2.5	1.6
SAPRITFGGPTDSTD	1.4	0.6
APRITFGGPTDSTDN	2.3	0.5
PRITFGGPTDSTDNN	1.6	0.3
RITFGGPTDSTDNNQ	0.5	0.2
ITFGGPTDSTDNNQN	1.2	0.3
TFGGPTDSTDNNQNG	0.1	0.2
FGGPTDSTDNNQNGG	0.1	0.2
GGPTDSTDNNQNGGR	0.1	0.2
GPTDSTDNNQNGGRN	0.2	0.2
PTDSTDNNQNGGRNG	0.1	0.2
TDSTDNNQNGGRNGA	0.2	0.2
DSTDNNQNGGRNGAR	0.2	0.3
STDNNQNGGRNGARP	0.2	0.2
TDNNQNGGRNGARPK	0.2	0.2
DNNQNGGRNGARPKQ	0.2	0.3
NNQNGGRNGARPKQR	0.2	0.2
NQNGGRNGARPKQRR	0.2	0.2
QNGGRNGARPKQRRP	0.2	0.3
NGGRNGARPKQRRPQ	0.2	0.3
GGRNGARPKQRRPQG	0.2	0.2
GRNGARPKQRRPQGL	0.1	0.2
RNGARPKQRRPQGLP	0.1	0.3
NGARPKQRRPQGLPN	0.1	0.3
GARPKQRRPQGLPNN	0.1	0.2
ARPKQRRPQGLPNNT	0.1	0.2
RPKQRRPQGLPNNTA	0.1	0.2
PKQRRPQGLPNNTAS	0.2	0.3
KQRRPQGLPNNTASW	0.1	0.2
QRRPQGLPNNTASWF	0.1	0.2
RRPQGLPNNTASWFT	0.1	0.2

RPQGLPNNTASWFTA	0.1	0.2
PQGLPNNTASWFTAL	0.1	0.3
QGLPNNTASWFTALT	0.1	0.3
GLPNNTASWFTALTQ	0.1	0.3
LPNNTASWFTALTQH	0.1	0.3
PNNTASWFTALTQHG	0.1	0.3
NNTASWFTALTQHGK	0.1	0.2
NTASWFTALTQHGKE	0.1	0.2
TASWFTALTQHGKEE	0.1	0.2
ASWFTALTQHGKEEL	0.1	0.2
SWFTALTQHGKEELR	0.1	0.2
WFTALTQHGKEELRF	0.1	0.2
FTALTQHGKEELRFP	0.1	0.2
TALTQHGKEELRFPR	0.1	0.3
ALTQHGKEELRFPRG	0.2	0.2
LTQHGKEELRFPRGQ	0.1	0.2
TQHGKEELRFPRGQG	0.1	0.2
QHGKEELRFPRGQGV	0.1	0.2
HGKEELRFPRGQGVP	0.1	0.2
GKEELRFPRGQGVPI	0.1	0.3
KEELRFPRGQGVPIN	0.1	0.3
EELRFPRGQGVPINT	0.1	0.3
ELRFPRGQGVPINTN	0.1	0.2
LRFPRGQGVPINTNS	0.1	0.2
RFPRGQGVPINTNSG	0.1	0.2
FPRGQGVPINTNSGP	0.1	0.2
PRGQGVPINTNSGPD	0.1	0.2
RGQGVPINTNSGPDD	0.1	0.2
GQGVPINTNSGPDDQ	0.1	0.2
QGVPINTNSGPDDQI	0.1	0.1
GVPINTNSGPDDQIG	0.1	0.2
VPINTNSGPDDQIGY	0.1	0.2
PINTNSGPDDQIGYY	0.1	0.2
INTNSGPDDQIGYYR	0.1	0.2
NTNSGPDDQIGYYRR	0.1	0.3
TNSGPDDQIGYYRRA	0.1	0.2
NSGPDDQIGYYRRAT	0.1	0.2
SGPDDQIGYYRRATR	0.1	0.3
GPDDQIGYYRRATRR	0.1	0.3
PDDQIGYYRRATRRV	0.1	0.3
DDQIGYYRRATRRVR	0.1	0.3
DQIGYYRRATRRVRG	0.1	0.3
QIGYYRRATRRVRGG	0.1	0.2
IGYYRRATRRVRGGD	0.1	0.2
GYYRRATRRVRGGDG	0.1	0.2
YYRRATRRVRGGDGK	0.1	0.2

YRRATRRVRGGDGKM	0.1	0.2
RRATRRVRGGDGKMK	0.1	0.2
RATRRVRGGDGKMKE	0.1	0.2
ATRRVRGGDGKMKEL	0.1	0.2
TRRVRGGDGKMKELS	0.1	0.2
RRVRGGDGKMKELSP	0.1	0.2
RVRGGDGKMKELSPR	0.1	0.2
VRGGDGKMKELSPRW	0.1	0.2
RGGDGKMKELSPRWY	0.1	0.2
GGDGKMKELSPRWYF	0.1	0.2
GDGKMKELSPRWYFY	0.1	0.2
DGKMKELSPRWYFYY	0.1	0.2
GKMKELSPRWYFYYL	0.1	0.3
KMKELSPRWYFYYLG	0.1	0.2
MKELSPRWYFYYLGT	0.1	0.2
KELSPRWYFYYLGTG	0.1	0.3
ELSPRWYFYYLGTGP	0.1	0.2
LSPRWYFYYLGTGPE	0.1	0.2
SPRWYFYYLGTGPEA	0.1	0.2
PRWYFYYLGTGPEAS	0.1	0.2
RWYFYYLGTGPEASL	0.1	0.2
WYFYYLGTGPEASLP	0.1	0.2
YFYYLGTGPEASLPY	0.1	0.2
FYYLGTGPEASLPYG	0.1	0.2
YYLGTGPEASLPYGA	0.1	0.2
YLGTGPEASLPYGAN	0.1	0.2
LGTGPEASLPYGANK	0.1	0.2
GTGPEASLPYGANKE	0.1	0.2
TGPEASLPYGANKEG	0.1	0.2
GPEASLPYGANKEGI	0.1	0.2
PEASLPYGANKEGIV	0.1	0.2
EASLPYGANKEGIVW	0.1	0.2
ASLPYGANKEGIVWV	0.1	0.3
SLPYGANKEGIVWVA	0.1	0.2
LPYGANKEGIVWVAT	0.1	0.2
PYGANKEGIVWVATE	0.1	0.2
YGANKEGIVWVATEG	0.1	0.2
GANKEGIVWVATEGA	0.1	0.2
ANKEGIVWVATEGAL	0.1	0.2
NKEGIVWVATEGALN	0.1	0.2
KEGIVWVATEGALNT	0.1	0.2
EGIVWVATEGALNTP	0.1	0.2
GIVWVATEGALNTPK	0.1	0.2
IVWVATEGALNTPKD	0.1	0.2
VWVATEGALNTPKDH	0.1	0.3
WVATEGALNTPKDHI	0.1	0.2

VATEGALNTPKDHIG	0.2	0.2
ATEGALNTPKDHIGT	0.1	0.2
TEGALNTPKDHIGTR	0.2	0.3
EGALNTPKDHIGTRN	0.1	0.3
GALNTPKDHIGTRNP	0.1	0.2
ALNTPKDHIGTRNPN	0.1	0.2
LNTPKDHIGTRNPNN	0.1	0.2
NTPKDHIGTRNPNNN	0.1	0.2
TPKDHIGTRNPNNNA	0.1	0.2
PKDHIGTRNPNNNAA	0.1	0.2
KDHIGTRNPNNNAAT	0.1	0.2
DHIGTRNPNNNAATV	0.1	0.3
HIGTRNPNNNAATVL	0.1	0.3
IGTRNPNNNAATVLQ	0.1	0.3
GTRNPNNNAATVLQL	0.1	0.3
TRNPNNNAATVLQLP	0.1	0.2
RNPNNNAATVLQLPQ	0.1	0.2
NPNNNAATVLQLPQG	0.1	0.3
PNNNAATVLQLPQGT	0.1	0.3
NNNAATVLQLPQGTT	0.1	0.3
NNAATVLQLPQGTTL	0.1	0.3
NAATVLQLPQGTTLP	0.1	0.2
AATVLQLPQGTTLPK	0.1	0.2
ATVLQLPQGTTLPKG	0.1	0.2
TVLQLPQGTTLPKGF	0.1	0.3
VLQLPQGTTLPKGFY	0.1	0.3
LQLPQGTTLPKGFYA	0.1	0.2
QLPQGTTLPKGFYAE	0.1	0.2
LPQGTTLPKGFYAEG	0.1	0.3
PQGTTLPKGFYAEGS	0.1	0.2
QGTTLPKGFYAEGSR	0.1	0.2
GTTLPKGFYAEGSRG	0.1	0.2
TTLPKGFYAEGSRGG	0.1	0.2
TLPKGFYAEGSRGGS	0.1	0.2
LPKGFYAEGSRGGSQ	0.1	0.2
PKGFYAEGSRGGSQA	0.1	0.2
KGFYAEGSRGGSQAS	0.1	0.2
GFYAEGSRGGSQASS	0.1	0.2
FYAEGSRGGSQASSR	0.1	0.1
YAEGSRGGSQASSRS	0.1	0.2
AEGSRGGSQASSRSS	0.1	0.2
EGSRGGSQASSRSSS	0.1	0.2
GSRGGSQASSRSSSR	0.1	0.2
SRGGSQASSRSSSRS	0.1	0.2
RGGSQASSRSSSRSR	0.1	0.1
GGSQASSRSSSRSRG	0.1	0.2

GSQASSRSSSRSRGN	0.1	0.2
SQASSRSSSRSRGNS	0.1	0.2
QASSRSSSRSRGNSR	0.1	0.2
ASSRSSSRSRGNSRN	0.1	0.2
SSRSSSRSRGNSRNS	0.1	0.2
SRSSSRSRGNSRNST	0.1	0.2
RSSSRSRGNSRNSTP	0.1	0.2
SSSRSRGNSRNSTPG	0.1	0.2
SSRSRGNSRNSTPGS	0.1	0.2
SRSRGNSRNSTPGSS	0.1	0.2
RSRGNSRNSTPGSSR	0.1	0.2
SRGNSRNSTPGSSRG	0.1	0.2
RGNSRNSTPGSSRGN	0.1	0.2
GNSRNSTPGSSRGNS	0.1	0.2
NSRNSTPGSSRGNSP	0.1	0.2
SRNSTPGSSRGNSPA	0.1	0.2
RNSTPGSSRGNSPAR	0.1	0.2
NSTPGSSRGNSPARM	0.2	0.3
STPGSSRGNSPARMA	0.1	0.2
TPGSSRGNSPARMAS	0.1	0.3
PGSSRGNSPARMASG	0.1	0.3
GSSRGNSPARMASGG	0.1	0.2
SSRGNSPARMASGGG	0.1	0.2
SRGNSPARMASGGGE	0.1	0.2
RGNSPARMASGGGET	0.1	0.2
GNSPARMASGGGETA	0.2	0.2
NSPARMASGGGETAL	0.1	0.2
SPARMASGGGETALA	0.1	0.1
PARMASGGGETALAL	0.1	0.3
ARMASGGGETALALL	0.1	0.3
RMASGGGETALALLL	0.1	0.3
MASGGGETALALLLL	0.1	0.3
ASGGGETALALLLLD	0.1	0.2
SGGGETALALLLLDR	0.1	0.2
GGGETALALLLLDRL	0.1	0.2
GGETALALLLLDRLN	0.1	0.2
GETALALLLLDRLNQ	0.1	0.3
ETALALLLLDRLNQL	0.1	0.3
TALALLLLDRLNQLE	0.1	0.2
ALALLLLDRLNQLES	0.1	0.3
LALLLLDRLNQLESK	0.1	0.2
ALLLLDRLNQLESKV	0.1	0.3
LLLLDRLNQLESKVS	0.2	0.2
LLLDRLNQLESKVSG	0.1	0.2
LLDRLNQLESKVSGK	0.1	0.2
LDRLNQLESKVSGKG	0.1	0.2

DRLNQLESKVSGKGQ	0.1	0.3
RLNQLESKVSGKGQQ	0.1	0.2
LNQLESKVSGKGQQQ	0.1	0.3
NQLESKVSGKGQQQQ	0.1	0.3
QLESKVSGKGQQQQG	0.1	0.3
LESKVSGKGQQQQGQ	0.1	0.3
ESKVSGKGQQQQGQT	0.1	0.2
SKVSGKGQQQQGQTV	0.1	0.2
KVSGKGQQQQGQTVT	0.1	0.2
VSGKGQQQQGQTVTK	0.1	0.3
SGKGQQQQGQTVTKK	0.1	0.2
GKGQQQQGQTVTKKS	0.1	0.2
KGQQQQGQTVTKKSA	0.1	0.2
GQQQQGQTVTKKSAA	0.1	0.2
QQQQGQTVTKKSAAE	0.1	0.2
QQQGQTVTKKSAAEA	0.1	0.2
QQGQTVTKKSAAEAS	0.1	0.2
QGQTVTKKSAAEASK	0.1	0.2
GQTVTKKSAAEASKK	0.1	0.2
QTVTKKSAAEASKKP	0.1	0.2
TVTKKSAAEASKKPR	0.1	0.2
VTKKSAAEASKKPRQ	0.1	0.2
TKKSAAEASKKPRQK	0.1	0.2
KKSAAEASKKPRQKR	0.1	0.2
KSAAEASKKPRQKRT	0.1	0.1
SAAEASKKPRQKRTA	0.1	0.2
AAEASKKPRQKRTAT	0.1	0.2
AEASKKPRQKRTATK	0.1	0.2
EASKKPRQKRTATKQ	0.1	0.3
ASKKPRQKRTATKQY	0.1	0.2
SKKPRQKRTATKQYN	0.1	0.2
KKPRQKRTATKQYNV	0.1	0.2
KPRQKRTATKQYNVT	0.1	0.2
PRQKRTATKQYNVTQ	0.1	0.2
RQKRTATKQYNVTQA	0.1	0.2
QKRTATKQYNVTQAF	0.1	0.2
KRTATKQYNVTQAFG	0.1	0.2
RTATKQYNVTQAFGR	0.1	0.2
TATKQYNVTQAFGRR	0.1	0.3
ATKQYNVTQAFGRRG	0.1	0.3
TKQYNVTQAFGRRGP	0.1	0.3
KQYNVTQAFGRRGPE	0.1	0.1
QYNVTQAFGRRGPEQ	0.1	0.3
YNVTQAFGRRGPEQT	0.1	0.2
NVTQAFGRRGPEQTQ	0.1	0.2
VTQAFGRRGPEQTQG	0.1	0.2

TQAFGRRGPEQTQGN	0.1	0.2
QAFGRRGPEQTQGNF	0.1	0.2
AFGRRGPEQTQGNFG	0.1	0.2
FGRRGPEQTQGNFGD	0.1	0.1
GRRGPEQTQGNFGDQ	0.1	0.2
RRGPEQTQGNFGDQD	0.1	0.2
RGPEQTQGNFGDQDL	0.1	0.2
GPEQTQGNFGDQDLI	0.1	0.2
PEQTQGNFGDQDLIR	0.1	0.2
EQTQGNFGDQDLIRQ	0.1	0.0
QTQGNFGDQDLIRQG	0.1	0.2
TQGNFGDQDLIRQGT	0.1	0.2
QGNFGDQDLIRQGTD	0.1	0.2
GNFGDQDLIRQGTDY	0.1	0.2
NFGDQDLIRQGTDYK	0.1	0.2
FGDQDLIRQGTDYKH	0.1	0.2
GDQDLIRQGTDYKHW	0.1	0.2
DQDLIRQGTDYKHWP	0.1	0.2
QDLIRQGTDYKHWPQ	0.1	0.2
DLIRQGTDYKHWPQI	0.1	0.2
LIRQGTDYKHWPQIA	0.1	0.1
IRQGTDYKHWPQIAQ	0.1	0.2
RQGTDYKHWPQIAQF	0.1	0.2
QGTDYKHWPQIAQFA	0.1	0.2
GTDYKHWPQIAQFAP	0.1	0.2
TDYKHWPQIAQFAPS	0.1	0.2
DYKHWPQIAQFAPSA	0.1	0.2
YKHWPQIAQFAPSAS	0.1	0.2
KHWPQIAQFAPSASA	0.1	0.2
HWPQIAQFAPSASAF	0.1	0.2
WPQIAQFAPSASAFF	0.1	0.3
PQIAQFAPSASAFFG	0.1	0.2
QIAQFAPSASAFFGM	0.1	0.3
IAQFAPSASAFFGMS	0.1	0.3
AQFAPSASAFFGMSR	0.1	0.3
QFAPSASAFFGMSRI	0.1	0.3
FAPSASAFFGMSRIG	0.1	0.2
APSASAFFGMSRIGM	0.1	0.2
PSASAFFGMSRIGME	0.1	0.2
SASAFFGMSRIGMEV	0.1	0.2
ASAFFGMSRIGMEVT	0.1	0.2
SAFFGMSRIGMEVTP	0.1	0.2
AFFGMSRIGMEVTPS	0.1	0.2
FFGMSRIGMEVTPSG	0.1	0.2
FGMSRIGMEVTPSGT	0.1	0.2
GMSRIGMEVTPSGTW	0.1	0.2

MSRIGMEVTPSGTWL	0.1	0.2
SRIGMEVTPSGTWLT	0.1	0.2
RIGMEVTPSGTWLTY	0.1	0.2
IGMEVTPSGTWLTYH	0.1	0.2
GMEVTPSGTWLTYHG	0.1	0.2
MEVTPSGTWLTYHGA	0.1	0.2
EVTPSGTWLTYHGAI	0.1	0.2
VTPSGTWLTYHGAIK	0.1	0.2
TPSGTWLTYHGAIKL	0.1	0.2
PSGTWLTYHGAIKLD	0.1	0.2
SGTWLTYHGAIKLDD	0.1	0.2
GTWLTYHGAIKLDDK	0.1	0.2
TWLTYHGAIKLDDKD	0.1	0.2
WLTYHGAIKLDDKDP	0.1	0.2
LTYHGAIKLDDKDPQ	0.1	0.2
TYHGAIKLDDKDPQF	0.1	0.1
YHGAIKLDDKDPQFK	0.1	0.2
HGAIKLDDKDPQFKD	0.1	0.2
GAIKLDDKDPQFKDN	0.1	0.2
AIKLDDKDPQFKDNV	0.1	0.2
IKLDDKDPQFKDNVI	0.1	0.2
KLDDKDPQFKDNVIL	0.1	0.2
LDDKDPQFKDNVILL	0.1	0.3
DDKDPQFKDNVILLN	0.1	0.3
DKDPQFKDNVILLNK	0.1	0.4
KDPQFKDNVILLNKH	0.1	0.2
DPQFKDNVILLNKHI	0.1	0.3
PQFKDNVILLNKHID	0.1	0.2
QFKDNVILLNKHIDA	0.1	0.3
FKDNVILLNKHIDAY	0.1	0.2
KDNVILLNKHIDAYK	0.1	0.2
DNVILLNKHIDAYKT	0.1	0.2
NVILLNKHIDAYKTF	0.1	0.2
VILLNKHIDAYKTFP	0.1	0.2
ILLNKHIDAYKTFPP	0.1	0.2
LLNKHIDAYKTFPPT	0.1	0.2
LNKHIDAYKTFPPTE	0.1	0.2
NKHIDAYKTFPPTEP	0.1	0.2
KHIDAYKTFPPTEPK	0.1	0.2
HIDAYKTFPPTEPKK	0.1	0.2
IDAYKTFPPTEPKKD	0.1	0.2
DAYKTFPPTEPKKDK	0.1	0.2
AYKTFPPTEPKKDKK	0.1	0.1
YKTFPPTEPKKDKKK	0.1	0.2
KTFPPTEPKKDKKKK	0.1	0.2
TFPPTEPKKDKKKKT	0.1	0.2

FPPTEPKKDKKKKTD	0.1	0.2
PPTEPKKDKKKKTDE	0.1	0.2
PTEPKKDKKKKTDEA	0.1	0.2
TEPKKDKKKKTDEAQ	0.1	0.2
EPKKDKKKKTDEAQP	0.1	0.2
PKKDKKKKTDEAQPL	0.1	0.2
KKDKKKKTDEAQPLP	0.1	0.2
KDKKKKTDEAQPLPQ	0.1	0.2
DKKKKTDEAQPLPQR	0.1	0.2
KKKKTDEAQPLPQRQ	0.1	0.2
KKKTDEAQPLPQRQK	0.1	0.2
KKTDEAQPLPQRQKK	0.1	0.2
KTDEAQPLPQRQKKQ	0.1	0.2
TDEAQPLPQRQKKQP	0.1	0.1
DEAQPLPQRQKKQPT	0.1	0.2
EAQPLPQRQKKQPTV	0.1	0.2
AQPLPQRQKKQPTVT	0.1	0.1
QPLPQRQKKQPTVTL	0.1	0.3
PLPQRQKKQPTVTLL	0.1	0.3
LPQRQKKQPTVTLLP	0.1	0.3
PQRQKKQPTVTLLPA	0.1	0.3
QRQKKQPTVTLLPAA	0.1	0.3
RQKKQPTVTLLPAAD	0.1	0.2
QKKQPTVTLLPAADM	0.1	0.3
KKQPTVTLLPAADMD	0.1	0.2
KQPTVTLLPAADMDD	0.1	0.2
QPTVTLLPAADMDDF	0.1	0.2
PTVTLLPAADMDDFS	0.1	0.2
TVTLLPAADMDDFSR	0.1	0.2
VTLLPAADMDDFSRQ	0.1	0.2
TLLPAADMDDFSRQL	0.1	0.1
LLPAADMDDFSRQLQ	0.1	0.2
LPAADMDDFSRQLQN	0.1	0.2
PAADMDDFSRQLQNS	0.1	0.2
AADMDDFSRQLQNSM	0.2	0.2
ADMDDFSRQLQNSMS	0.1	0.1
DMDDFSRQLQNSMSG	0.1	0.2
MDDFSRQLQNSMSGA	0.2	0.2
DDFSRQLQNSMSGAS	0.2	0.2
DFSRQLQNSMSGASA	0.1	0.2
FSRQLQNSMSGASAD	0.1	0.2
SRQLQNSMSGASADS	0.1	0.2
RQLQNSMSGASADST	0.1	0.2
QLQNSMSGASADSTQ	0.1	0.2
LQNSMSGASADSTQA	0.2	0.2

Table 7: Data of assay for SARS-CoV (Hong Kong strain obtained from patient 5688) neutralizing activity of human monoclonal anti-SARS-CoV antibodies.

Conc. (µg/ml)	50.00	25.00	12.50	6.25	3.12	1.56	0.78	0.39	0.20	0.10	0.05	0.02
$TCID_{50}$/ Antibody												
10/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
10/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
10/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
10/ 03-013	-	-	+	-	+	+	+	3+	3+	3+	3+	3+
10/ 03-013	-	-	-	-	-	-	-	2+	2+	3+	3+	3+
10/ 03-013	-	-	-	-	+	-	2+	2+	3+	3+	3+	3+
10/ 03-014	-	-	-	-	-	-	-	-	2+	3+	3+	3+
10/ 03-014	-	-	-	-	-	-	-	+	+	2+	3+	3+
10/ 03-014	-	-	-	-	-	-	-	+	2+	3+	3+	3+
30/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
30/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
30/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
30/ 03-013	-	-	-	-	-	-	2+	2+	3+	3+	3+	3+
30/ 03-013	-	-	-	-	+	+	2+	3+	3+	3+	3+	3+
30/ 03-013	-	-	-	+	+	2+	2+	3+	3+	3+	3+	3+
30/ 03-014	-	-	-	-	-	+	+	3+	3+	3+	3+	3+
30/ 03-014	-	-	+	-	-	-	-	+	2+	3+	3+	3+
30/ 03-014	-	-	-	-	-	-	+	+	2+	3+	3+	3+
100/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
100/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
100/ 02-027	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+	3+
100/ 03-013	-	-	-	+	+	+	2+	3+	3+	3+	3+	3+
100/ 03-013	-	-	+	+	+	2+	3+	3+	3+	3+	3+	3+
100/ 03-013	-	-	+	+	+	2+	3+	3+	3+	3+	3+	3+
100/ 03-014	-	-	-	-	-	+	2+	2+	3+	3+	3+	3+
100/ 03-014	-	-	-	-	+	+	2+	2+	3+	3+	3+	3+

100/ 03-014	-	-	-	-	+	+	2+	2+	3+	3+	3+	3+

-: No CPE

+: CPE ≤ 50%

2+: CPE 50-90%

3+: CPE 100%

Table 8: Human IgG heavy chain variable region primers (sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuVH1B/7A	5′-CAGRTGCAGCTGGTG CARTCTGG-3′	SEQ ID NO:132
HuVH1C	5′-SAGGTCCAGCTGGTR CAGTCTGG-3′	SEQ ID NO:133
HuVH2B	5′-SAGGTGCAGCTGGTG GAGTCTGG-3′	SEQ ID NO:134
HuVH3B	5′-SAGGTGCAGCTGGTG GAGTCTGG-3'	SEQ ID NO:135
HuVH3C	5′-GAGGTGCAGCTGGTG GAGWCYGG-3′	SEQ ID NO:136
HuVH4B	5′-CAGGTGCAGCTACAG CAGTGGGG-3′	SEQ ID NO:137
HuVH4C	5′-CAGSTGCAGCTGCAG GAGTCSGG-3′	SEQ ID NO:138
HuVH5B	5′-GARGTGCAGCTGGTG CAGTCTGG-3′	SEQ ID NO:139
HuVH6A	5′-CAGGTACAGCTGCAG CAGTCAGG-3′	SEQ ID NO:140

Table 9: Human IgG heavy chain J-region primers (anti-sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuJH1/2	5′-TGAGGAGACGGTGAC CAGGGTGCC-3′	SEQ ID NO:141
HuJH3	5′-TGAAGAGACGGTGAC CATTGTCCC-3′	SEQ ID NO:142
HuJH4/5	5′-TGAGGAGACGGTGAC CAGGGTTCC-3′	SEQ ID NO:143
HuJH6	5′-TGAGGAGACGGTGAC CGTGGTCCC-3′	SEQ ID NO:144

Table 10: Human IgG heavy chain variable region primers extended with SfiI/NcoI restriction sites (sense) and human IgG heavy chain J-region primers extended with XhoI/BstEII restriction sites (anti-sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuVH1B/7A-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC CAGRTGCAGCTGGTGCAR TCTGG-3'	SEQ ID NO:145
HuVH1C-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC SAGGTCCAGCTGGTRCAG TCTGG-3'	SEQ ID NO:146
HuVH2B-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC CAGRTCACCTTGAAGGAG TCTGG-3'	SEQ ID NO:147

HuVH3B-NcoI	5'-GTCCTCGCAACTGCGGCC CAGCCGGCCATGGCCSAGGTG CAGCTGGTGGAGTCTGG-3'	SEQ ID NO:148
HuVH3C-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC GAGGTGCAGCTGGTGGAG WCYGG-3'	SEQ ID NO:149
HuVH4B-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC CAGGTGCAGCTACAGCAG TGGGG-3'	SEQ ID NO:150
HuVH4C-NcoI	5'-GTCCTCGCAACTGCGGCC CAGCCGGCCATGGCCCAGSTG CAGCTGCAGGAGTCSGG-3'	SEQ ID NO:151
HuVH5B-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC GARGTGCAGCTGGTGCAG TCTGG-3'	SEQ ID NO:152
HuVH6A-NcoI	5'-GTCCTCGCAACTGCG GCCCAGCCGGCCATGGCC CAGGTACAGCTGCAGCAG TCAGG-3'	SEQ ID NO:153
HuJH1/2-XhoI	5′-GAGTCATTCTCGACTCGA GACGGTGACCAGGGTGCC-3′	SEQ ID NO:154
HuJH3-XhoI	5′-GAGTCATTCTCGACT CGAGACGGTGACCATTGT CCC-3′	SEQ ID NO:155
HuJH4/5-XhoI	5′-GAGTCATTCTCGACT CGAGACGGTGACCAGGGT TCC-3′	SEQ ID NO:156
HuJH6-XhoI	5′-GAGTCATTCTCGACTCGA	SEQ ID NO:157

	GACGGTGACCGTGGTCCC-3′	

Table 11: Human lambda chain variable region primers (sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuVμ1A	5′-CAGTCTGTGCTGACT CAGCCACC-3′	SEQ ID NO:161
HuVμ1B	5′-CAGTCTGTGYTGACG CAGCCGCC-3′	SEQ ID NO:162
HuVμ1C	5′-CAGTCTGTCGTGACG CAGCCGCC-3′	SEQ ID NO:163
HuVμ2	5′-CARTCTGCCCTGACT CAGCCT-3′	SEQ ID NO:164
HuVμ3A	5′-TCCTATGWGCTGACT CAGCCACC-3′	SEQ ID NO:165
HuVμ3B	5′-TCTTCTGAGCTGACT CAGGACCC-3′	SEQ ID NO:166
HuVμ4	5′-CACGTTATACTGACT CAACCGCC-3′	SEQ ID NO:167
HuVμ5	5′-CAGGCTGTGCTGACT CAGCCGTC-3′	SEQ ID NO:168
HuVμ6	5′-AATTTTATGCTGACT CAGCCCCA-3′	SEQ ID NO:169
HuVμ7/8	5′-CAGRCTGTGGTGACY CAGGAGCC-3′	SEQ ID NO:170
HuVμ9	5′-CWGCCTGTGCTGACT CAGCCMCC-3′	SEQ ID NO:171

5

Table 12: Human kappa chain variable region primers (sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuVμ1B	5′-GACATCCAGWTGACCC AGTCTCC-3′	SEQ ID NO:172
HuVμ2	5′-GATGTTGTGATGACT CAGTCTCC-3′	SEQ ID NO:173
HuVμ3	5′-GAAATTGTGWTGACR CAGTCTCC-3′	SEQ ID NO:174
HuVμ4	5′-GATATTGTGATGACC CACACTCC-3′	SEQ ID NO:175
HuVμ5	5′-GAAACGACACTCACG CAGTCTCC-3′	SEQ ID NO:176
HuVμ6	5′-GAAATTGTGCTGACTC AGTCTCC-3′	SEQ ID NO:177

Table 13: Human lambda chain J-region primers (anti-sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuJμ1	5′-ACCTAGGACGGTGACC TTGGTCCC-3′	SEQ ID NO:178
HuJμ2/3	5′-ACCTAGGACGGTCAG CTTGGTCCC-3′	SEQ ID NO:179
HuJμ4/5	5′-ACYTAAAACGGTGAG CTGGGTCCC-3′	SEQ ID NO:180

5

Table 14: Human lambda chain J-region primers (anti-sense).

Primer name	Primer nucleotide	SEQ ID NO

	sequence	
HuJμ1	5′-ACGTTTGATTTCCAC CTTGGTCCC-3′	SEQ ID NO:181
HuJμ2	5′-ACGTTTGATCTCCAG CTTGGTCCC-3′	SEQ ID NO:182
HuJμ3	5′-ACGTTTGATATCCAC TTTGGTCCC-3′	SEQ ID NO:183
HuJμ4	5′-ACGTTTGATCTCCAC CTTGGTCCC-3′	SEQ ID NO:184
HuJμ5	5′-ACGTTTAATCTCCAG TCGTGTCCC-3′	SEQ ID NO:185

Table 15: Human kappa chain variable region primers extended with SalI restriction sites (sense), human kappa chain J-region primers extended with NotI restriction sites (anti-sense), human lambda chain variable region primers extended with SalI restriction sites (sense) and human lambda chain J-region primers extended with NotI restriction sites (anti-sense).

Primer name	Primer nucleotide sequence	SEQ ID NO
HuVμ1B-SalI	5′-TGAGCACACAGGTCG ACGGACATCCAGWTGACC CAGTCTCC-3′	SEQ ID NO:186
HuVμ2-SalI	5′-TGAGCACACAGGTCG ACGGATGTTGTGATGACT CAGTCTCC-3′	SEQ ID NO:187
HuVμ3B-SalI	5′-TGAGCACACAGGTCG ACGGAAATTGTGWTGACR CAGTCTCC-3′	SEQ ID NO:188

HuVμ4B-SalI	5′-TGAGCACACAGGTCG ACGGATATTGTGATGACC CACACTCC-3′	SEQ ID NO:189
HuVμ5-SalI	5′-TGAGCACACAGGTCGACG GAAACGACACTCACGCAGTCT CC-3′	SEQ ID NO:190
HuVμ6-SalI	5′-TGAGCACACAGGTCG ACGGAAATTGTGCTGACT CAGTCTCC-3′	SEQ ID NO:191
HuJμ1-NotI	5′-GAGTCATTCTCGACTTGC GGCCGCACGTTTGATTTCCAC CTTGGTCCC-3′	SEQ ID NO:192
HuJμ2-NotI	5′-GAGTCATTCTCGACT TGCGGCCGCACGTTTGAT CTCCAGCTTGGTCCC-3′	SEQ ID NO:193
HuJμ3-NotI	5′-GAGTCATTCTCGACTTGC GGCCGCACGTTTGATATCCAC TTTGGTCCC-3′	SEQ ID NO:194
HuJμ4-NotI	5′-GAGTCATTCTCGACT TGCGGCCGCACGTTTGAT CTCCACCTTGGTCCC-3′	SEQ ID NO:195
HuJμ5-NotI	5′-GAGTCATTCTCGACTTGC GGCCGCACGTTTAATCTCCAG TCGTGTCCC-3′	SEQ ID NO:196
HuVμ1A-SalI	5′-TGAGCACACAGGTCGACG CAGTCTGTGCTGACTCAGCCA CC-3′	SEQ ID NO:197
HuVμ1B-SalI	5′-TGAGCACACAGGTCGACG CAGTCTGTGYTGACGCAGCCG CC-3′	SEQ ID NO:198
HuVμ1C-SalI	5′-TGAGCACACAGGTCGACG	SEQ ID NO:199

	CAGTCTGTCGTGACGCAGCCG CC-3′	
HuVμ2-SalI	5′-TGAGCACACAGGTCGACG CARTCTGCCCTGACTCAGCCT-3′	SEQ ID NO:200
HuVμ3A-SalI	5′-TGAGCACACAGGTCGACG TCCTATGWGCTGACTCAGCCA CC-3′	SEQ ID NO:201
HuVμ3B-SalI	5′-TGAGCACACAGGTCGACG TCTTCTGAGCTGACTCAGGAC CC-3′	SEQ ID NO:202
HuVμ4-SalI	5′-TGAGCACACAGGTCGACG CACGTTATACTGACTCAACCG CC-3′	SEQ ID NO:203
HuVμ5-SalI	5′-TGAGCACACAGGTCGACG CAGGCTGTGCTGACTCAGCCG TC-3′	SEQ ID NO:204
HuVμ6-SalI	5′-TGAGCACACAGGTCGACG AATTTTATGCTGACTCAGCCC CA-3′	SEQ ID NO:205
HuVμ7/8-SalI	5′-TGAGCACACAGGTCGACG CAGRCTGTGGTGACYCAGGAG CC-3′	SEQ ID NO:206
HuVμ9-SalI	5′-TGAGCACACAGGTCGACG CWGCCTGTGCTGACTCAGCCM CC-3′	SEQ ID NO:207
HuJμ1-NotI	5′-GAGTCATTCTCGACTTGC GGCCGCACCTAGGACGGTGAC CTTGGTCCC-3′	SEQ ID NO:208
HuJμ2/3-NotI	5′-GAGTCATTCTCGACTTGC GGCCGCACCTAGGACGGTCAG	SEQ ID NO:209

	CTTGGTCCC-3′	
HuJμ4/5-NotI	5′-GAGTCATTCTCGACTTGC GGCCGCACYTAAAACGGTGAG CTGGGTCCC-3′	SEQ ID NO:210

Table 16: Distribution of the different light chain products over the 10 fractions.

Light chain products	Number of alleles	Fraction number	alleles/fraction
Vk1B/Jk1-5	19	1 and 2	9.5
Vk2/Jk1-5	9	3	9
Vk3B/Jk1-5	7	4	7
Vk4B/Jk1-5	1	5	5
Vk5/Jk1-5	1		
Vk6/Jk1-5	3		
Vμ1A/Jl1-3	5	6	5
Vμ1B/Jl1-3			
Vμ1C/Jl1-3			
Vμ2/Jl1-3	5	7	5
Vμ3A/Jl1-3	9	8	9
Vμ3B/Jl1-3			
Vμ4/Jl1-3	3	9	5
Vμ5/Jl1-3	1		
Vμ6/Jl1-3	1		
Vμ7/8/Jl1-3	3	10	6
Vμ9/Jl1-3	3		

Table 17: Binding of single-chain (scFv) phage antibodies selected from a naïve or an immune phage display library to a SARS-CoV preparation (Frankfurt 1 strain).

Name phage antibody	SARS-CoV preparation (OD492nm)	Number of ELISA plate
sc03-019	0.333	1
sc03-020	0.671	2
sc03-021	0.215	2
sc03-022	1.18	2
sc03-023	1.311	2
sc03-024	0.235	2
sc03-025	1.636	2
sc03-026	1.071	2
sc03-027	1.163	2
sc03-029	0.629	4
sc03-030	1.15	3
sc03-031	0.635	4
sc03-032	1.219	3
sc03-033	0.288	4
sc03-034	0.802	3
sc03-035	0.596	3
sc03-036	0.24	3
sc03-037	0.287	4
sc03-038	0.314	4
sc03-039	0.851	3
sc03-040	0.616	4
sc03-041	0.861	4
sc03-042	0.645	4
sc03-043	1.271	3
sc03-044	0.518	4
sc03-045	0.577	4
sc03-046	1.897	3
sc03-047	0.866	4
sc03-048	0.397	3
sc03-049	1.006	3
sc03-050	1.184	3
sc03-051	0.602	3
sc03-052	0.355	4
sc03-053	0.218	3
sc03-054	0.428	4
sc03-055	0.608	3
sc03-056	0.924	3
sc03-057	1.19	3

sc03-058	0.355	4
sc03-059	0.293	1

plate 1: SARS-CoV preparation (OD492nm) for no single chain phage antibody was 0.060.

plate 2: SARS-CoV preparation (OD492nm) for no single chain phage antibody was 0.211.

plate 3: SARS-CoV preparation (OD492nm) for no single chain phage antibody was 0.054.

plate 4: SARS-CoV preparation (OD492nm) for no single chain phage antibody was 0.051.

Table 18: Data of the single-chain Fv's capable of binding SARS-CoV and obtained from a naïve and an immune phage display library.

Name scFv	SEQ ID NO of nucleo-tide sequence	SEQ ID NO of amino acid sequence	HCDR3	V_H-germline	V_1-germline
sc03-019	211	212	FPGGTRSRGYMDV (SEQ ID NO:291)	V_H3-30.3 (DP-46)	V_KIII (L6)
sc03-020	213	214	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-021	215	216	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-022	217	218	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-023	219	220	RVEVVEYQLLRPRYKSWFDP (SEQ ID NO:293)	V_H4-34 (DP-63)	V_LII (2a2-V1-04)
sc03-024	221	222	KSAGSNAFDI (SEQ ID NO:294)	V_H7-04.1 (DP-21)	V_L1 (1b-V1-19)
sc03-025	223	224	TTNRAFDI (SEQ ID NO:295)	V_H3-64	VKIV (B3-DPK24)
sc03-026	225	226	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-027	227	228	TTNRAFDI	V_H3-64	V_KIV (B3-

			(SEQ ID NO:295)		DPK24)
sc03-029	229	230	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-030	231	232	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-031	233	234	ESGGGYDNHFDY (SEQ ID NO:296)	V_H1-69 (DP-10)	V_L1 (1c-V1-16)
sc03-032	235	236	DGWDLTGSFLGYGMDV (SEQ ID NO:297)	V_H1-e (DP-88)	V_L1 (1c-V1-16)
sc03-033	237	238	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-034	239	240	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-035	241	242	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-036	243	244	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-037	245	246	DAHRGFGMDV (SEQ ID NO:298)	V_H3-53 (DP-42)	V_L3 (3l-V2-13)
sc03-038	247	248	DAHRGFGMDV (SEQ ID NO:298)	V_H3-53 (DP-42)	V_L3 (3l-V2-13)
sc03-039	249	250	GSKWNDVGGGDY (SEQ ID NO:299)	V_H3-23 (DP-47)	V_L6 (6A-V1-22)
sc03-040	251	252	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-041	253	254	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-042	255	256	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-043	257	258	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-044	259	260	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-045	261	262	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-046	263	264	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)

sc03-047	265	266	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-048	267	268	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-049	269	270	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-050	271	272	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-051	273	274	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-052	275	276	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-053	277	278	GTGYLRSYHGMDV (SEQ ID NO:300)	V_H1-03 (DP-25)	V_KII (A19/A03-DPK15)
sc03-054	279	280	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KIV (B3-DPK24)
sc03-055	281	282	RVEVVEYQLLRPRYKSWFDP (SEQ ID NO:293)	V_H4-34 (DP-63)	V_L1 (1b-V1-19)
sc03-056	283	284	GSGISTPMDV (SEQ ID NO:292)	V_H5-51 (DP-73)	V_KIV (B3-DPK24)
sc03-057	285	286	PDIVVAGHSPPHYTMDV (SEQ ID NO:301)	V_H1-69 (DP-10)	V_KI L11-DPK3
sc03-058	287	288	TTNRAFDI (SEQ ID NO:295)	V_H3-64	V_KVI A14-DPK25
sc03-059	289	290	FPGGTRSRGYMDV (SEQ ID NO:291)	V_H1-46 (DP-7)	V_KIII (L6)

Table 19: Scheme of the *in vivo* ferret experiment.

					Sampling (days) [c]							
Group	Animals /group	Challenge (intratracheal) [a]		Split[b]	0	1	2	3	4	5	6	7
1	4	1,000 ($TCID_{50}$/ml)	03-014 Ab	2	S		S		S+LT			
				2	S		S		S			S+LT
2	4	10,000 ($TCID_{50}$/ml)		2	S		S		S+LT			
				2	S		S		S			S+LT
3	4	1,000 ($TCID_{50}$/ml)	Contr Ab	2	S		S		S+LT			
				2	S		S		S			S+LT
4	4	10,000 ($TCID_{50}$/ml)		2	S		S		S+LT			
				2	S		S		S			S+LT

a premix of challenge dose and optimal concentration antibody

b split based on sacrification

c S means swabs; LT means lung tissue after sacrification

Table 20: Scheme for tissue and fluid sampling

				Sampling (days)					
Group	No/Group	Challenge/ mAb		-1	0	1	2	3	4
I	4	1x10E4 $TCID_{50}$	Contr Ab	B*	B,S		S		S,LT
II	4	1x10E4 $TCID_{50}$	03-014	B	B,S		S		S,LT

*B, blood; S, pharyngeal swab, LT, lung tissue to be processed for virus titration and pathology

Table 21. List of SARS-CoV strains having a region 318-510 of the S protein not identical to the region 318-510 of the S protein of SARS-CoV Frankfurt 1 strain.

Mutation	Strain	Genbank
K344R	GZ02	AY390556
	GZ60	AY304491
	JMD	AY394988
	ZS-B	AY394996
	GZ43	AY304490
	HGZ8L1-A	AY394981
	ZS-A	AY394997
	ZS-C	AY395003
K344R F501Y	GD01	AY278489
K344R F360S L472P D480G T487S	GD03T0013	AY525636
S353F	Sin3408	AY559083
	Sin3765V	AY559084
	Sin845	AY559093
	Sin847	AY559095
	Sin849	AY559086
	Sin852	AY559082
	Sin3725V	AY559087
	Sin842	AY559081
	Sin846	AY559094
	Sin848	AY559085
	Sin850	AY559096
R426G	Shanghai LY	AY322205S3

N437D		
Y436H	GZ-C	AY394979
Y442S	Sino1-11	AY485277
N479S	BJ302 cl. 2	AY429073
	BJ302 cl. 4	AY429075
	BJ302 cl. 6	AY429077
	BJ302 cl. 3	AY429074
	BJ302 cl. 5	AY429076
	BJ302 cl. 8	AY429079

The amino acid substitutions compared to the Frankfurt 1 S protein are indicated in the left column. Strain and GenBank accession number are indicated in second and third column.

Table 22. Concentrations of the monoclonal anti-SARS-CoV antibody 03-014 giving complete protection against 100 TCID50 of the different SARS-CoV isolates indicated in an *in vitro* neutralization assay.

SARS-CoV Strain*	Concentration of 03-014 (µg/ml) resulting in 100% protection against 100 TCID50
36 (3)	12.5
39849 (3)	12.5
66 (2)	12.5
61567 (2)	12.5
61644 (1)	12.5
61644 (15)	12.5

* Between brackets the passage numbers of the respective strains is indicated

SEQUENCE LISTING

<110> Crucell Holland B.V.
Ter Meulen, Jan H.
De Kruif, Cornelis A.
Van den Brink, Edward N.
Goudsmit, Jaap

<120> Binding molecules against SARS -coronavirus and uses thereof

<130> 0091 WO 00 ORD

<160> 478

<170> PatentIn version 3.1

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<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-008

<400> 7

Arg Val Arg Pro Arg Arg Phe Asp Tyr
1 5

<210> 8

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-009

<400> 8

Gly Leu Phe Met Val Thr Thr Tyr Ala Phe Asp Tyr
1 5 10

<210> 9

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-010

<400> 9

Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr
1 5 10

<210> 10

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-012

<400> 10

Met Phe Arg Lys Ser Ser Phe Asp Ser
1 5

<210> 11

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-013

<400> 11

Gly Leu Thr Pro Leu Tyr Phe Asp Tyr
1 5

<210> 12

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03 -014

<400> 12

Gly Ile Ser Pro Phe Tyr Phe Asp Tyr
1 5

<210> 13

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03 -015

<400> 13

Gly Leu Ser Leu Arg Pro
1 5

<210> 14

<211> 354

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -001

<220>

<221> CDS

<222> (1)..(354)

<223>

<400> 14
atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aa g cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc 96
Gly Gly Ser Leu Arg L eu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

ggc tac tcg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag 144
Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly L eu Glu
35 40 45

tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc agg 192
Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
50 55 60

aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctt cag atg aac aac ctg aga gct gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aga cac cgg tt c cgg cac gtc ttc gat tac tgg ggc cag ggc acc 336
Ala Arg His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

ctg gtg acc gtg ctc gag 354
Leu Val Thr Val Leu Glu
115

<210> 15

<211> 118

<212> PRT

<213> Artificial sequence

<220>

<223> Variable h eavy chain of SC03 -001

<400> 15

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

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

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

Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
50 55 60

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

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

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

Leu Val Thr Val Leu Glu
115

<210> 16

<211> 372

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -002

<220>

<221> CDS

<222> (1)..(372)

<223>

<400> 16

atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtc aag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

ggc tac agc atg agc tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag 144
Gly Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac 192
Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
50 55 60

gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag 240

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

aac tca ctg tat ctg c aa atg aac agc ctg aaa acc gag gac acg gcc 288
Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
85 90 95

gtg tat tac tgt gct aga tac tac tcc cgc tcc ctc aag gcc t tc gat 336
Val Tyr Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp
100 105 110

tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag 372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 17

<211> 124

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -002

<400> 17

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

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

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

Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
50 55 60

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

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

Val Tyr Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp
100 105 110

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

<210> 18

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -003

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 18

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atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct       48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  Thr Phe Ser
            20                  25                  30

agc tac ccg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag      144
Ser Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac      192
Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
    50                  55                  60

tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat      288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gcc aga cgc agc tac ttc cgc cgc ttc gat  tac tgg ggc cag      336
Tyr Cys Ala Arg Arg Ser Tyr Phe Arg Arg Phe Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtg acc gtg ctc gag                                      360
Gly Thr Leu Val Thr Val Leu Glu
        115                 120
```

<210> 19

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -003

<400> 19

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

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

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

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Arg Arg Ser Tyr Phe Arg Arg Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 20

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -005

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 20

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atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg atc cag cct       48
Met Ala Glu Val Gln Leu Val Glu Ser Gl y Gly Gly Leu Ile Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

ggc tac act atg agc tgg gtc cgc cag gcg ccc ggg cag ggg ctg gag      144
Gly Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
        35                  40                  45

tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc agg      192
Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
    50                  55                  60

aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat      240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

ctt caa atg aac aac ctg aga gct gag  gac acg gcc gtg tat tac tgt      288
Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gca aaa ggc ggc ggc cgc ccg tac aac ccc ttc gat tac tgg ggc cag      33 6
Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtg acc gtg ctc gag                                     360
Gly Thr Leu Val Thr Val Leu Glu
        115                 120
```

<210> 21

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -005

<400> 21

```
Met Ala Glu Val Gl n Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro
1               5                   10                  15

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

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

Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
50 55 60

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

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

Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 22

<211> 366

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -006

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 22

atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

ggc tac cct atg cac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag 144
Gly Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtg gca gtt ata tca tat gac gga agt aat aaa tac tat gca gac 192

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
50 55 60

tcc gtg aag ggc cga tt c acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gct gt g tat 288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

tac tgt gct aaa gac ggc agc ccc cgc acc ccc agc ttc gat tac tgg 336
Tyr Cys Ala Lys Asp G ly Ser Pro Arg Thr Pro Ser Phe Asp Tyr Trp
100 105 110

ggc cag ggc acc ctg gtg acc gtg ctc gag 366
Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 23

<211> 122

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -006

<400> 23

Met Ala Glu Val Gln Leu Val Glu Ser Gly G ly Gly Leu Val Gln Pro
1 5 10 15

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

Gly Tyr Pro Met His Trp Val Arg G ln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Lys A sp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 24

<211> 366

<212> DNA

<213> Artificial sequ ence

<220>

<223> Variable heavy chain of SC03 -007

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 24

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atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct       48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

agg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc       96
Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

gac tac cgg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag      144
Asp Tyr Arg Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

agg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac      192
Arg Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
    50                  55                  60

tcc gtg aag ggc cga ttc acc a tc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg tat       288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gca aga ggc tac tgg acg tcg ctc acg ggc ttc gat tac tgg      336
Tyr Cys Ala Arg Gly Tyr Trp  Thr Ser Leu Thr Gly Phe Asp Tyr Trp
            100                 105                 110

ggc cag ggc acc ctg gtg acc gtg ctc gag                             366
Gly Gln Gly Thr Leu Val Thr Val Leu Glu
        115                 120
```

<210> 25

<211> 122

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -007

<400> 25

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

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

Asp Tyr Arg Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

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

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

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

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

Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 26

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -008

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 26

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atg gct gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct       48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
1               5                   10                  15

ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc       96
Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agc tac ccg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag      144
Ser Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac      192
Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
    50                  55                  60

tcc gtg aag ggc cgg ttc acc atc tcc  aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctg caa atg aac agc ctg aga gcc gag gac aca gcc gtg tat      288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gca aga cgc gtc cgc ccc cgc cgc ttc gat tat tgg ggc cag      336
Tyr Cys Ala Arg Arg Val Arg Pro Arg  Arg Phe Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtg acc gtg ctc gag                                     360
Gly Thr Leu Val Thr Val Leu Glu
        115                 120
```

<210> 27

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -008

<400> 27

```
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val  Gln Pro
1               5                   10                  15
```

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

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

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Arg Arg Val Arg Pro Arg Arg Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 28

<211> 369

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03-009

<220>

<221> CDS

<222> (1)..(369)

<223>

<400> 28

atg gct gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
1 5 10 15

ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc 96
Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

gac tac ccc atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag 144

Asp Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtc tca tcc att agt ggt agt ggt ggt agc aca tac tac gca gac 192
Trp Val Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctg caa atg aac agc ctg aga gcc gag gac aca gcc gtg tat 288
Leu Tyr Leu Gln Met As n Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

tac tgt gca aaa ggc ctc ttc atg gtc acc acg tac gcg ttc gat tac 336
Tyr Cys Ala Lys Gly Leu Phe Met Val Thr Thr Tyr Ala Phe As p Tyr
100 105 110

tgg ggc cag ggc acc ctg gtg acc gtg ctc gag 369
Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 29

<211> 123

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -009

<400> 29

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

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

Asp Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Trp Val Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Lys Gly Leu Phe Met Val Thr Thr Tyr Ala Ph e Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 30

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03-010

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 30

atg gct gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
1 5 10 15

ggg agg tcc ctg aga ctc tcc tgt gca acc tct gga ttc acc ttc agc 96
Gly Arg Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser
20 25 30

ggc tac acg atg cac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag 144
Gly Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc agg 192
Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
50 55 60

aag ggc aga ttc acc atc tcc aga gac aac tcc aag aac acg ct g tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctt caa atg aac aac ctg aga gct gag gac aca gct gtg tat tac tgt 288
Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aaa ggc ggc ggc ctc ccc tac ttg agc ttc gat tac tgg ggc cag 336
Ala Lys Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr Trp G ly Gln
100 105 110

ggc acc ctg gtg acc gtg ctc gag 360

Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 31

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -010

<400> 31

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

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

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

Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
50 55 60

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

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

Ala Lys Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr T rp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Leu Glu
115 120

<210> 32

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -012

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 32

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atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct       48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1               5                   10                  15

ggg gcc tca gtg aag gtc tcc tgc aag gct tct ggt tac acc ttt acc       96
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20                  25                  30

agc tat ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag      144
Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
        35                  40                  45

tgg atg gga tgg atc agc gct tac aat ggt aac a ca aac tat gca cag      192
Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln
    50                  55                  60

aag ctc cag ggc aga gtc acc atg acc aca gac aca tcc acg agc aca      240
Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr
65                  70                  75                  80

gcc tac atg gag ctg agc agc ctg aga tct gac gac acg gcc gtg tat      288
Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp  Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gca agg atg ttt agg aag agt tcc ttt gac tcc tgg ggc caa      336
Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly Gln
            100                 105                 110

ggt acc ctg gtc acc gtc tcg aga                                      360
Gly Thr Leu Val Thr Val Ser Arg
        115                 120
```

<210> 33

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -012

<400> 33

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

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

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

Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln
50 55 60

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

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

Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Arg
115 120

<210> 34

<211> 366

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -013

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 34

atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96

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

gac cac tac atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg gag      144
Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac      192
Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
    50                  55                  60

gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag      240
Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
65                  70                  75                  80

aac tca ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg gcc      288
Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
                85                  90                  95

gtg tat tac tgt gca aag ggg ttg act cct ttg tac ttt gac tac tgg      336
Val Tyr Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr Trp
            100                 105                 110

ggc caa ggt acc ctg gtc acc gtc tcg agt                             366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 35

<211> 122

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -013

<400> 35

```
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

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

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

Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
    50                  55                  60

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
65                  70                  75                  80
```

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

Val Tyr Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr Trp
100 10 5 110

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

<210> 36

<211> 366

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -014

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 36

atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

gac cac tac atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg gag 144
Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac 192
Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
50 55 60

gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag 240
Ala Ala Ser Val Lys Gly Arg Phe Thr Il e Ser Arg Asp Asp Ser Lys
65 70 75 80

aac tca ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg gcc 288
Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
85 90 95

gtg tat tac tgt gca agg ggg att tcg ccg ttt tac ttt gac tac tgg 336

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

ggc caa ggt acc ctg gtc acc gtc tcg agt 366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37

<211> 122

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -014

<400> 37

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

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

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

Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
50 55 60

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

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

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

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

<210> 38

<211> 351

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -015

<220>

<221> CDS

<222> (1)..(351)

<223>

<400> 38

```
atg gcc gag gtg cag ctg gtg gag tct ggg gga ggt gtg gta cgg cct       48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt gat       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
            20                  25                  30

gat tat ggc atg agc tgg gtc cgc caa gct cca gg g aag ggg ctg gag      144
Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtc tct ggt att aat tgg aat ggt ggt agc aca ggt tat gca gac      192
Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp
    50                  55                  60

tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tcc      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp A sn Ala Lys Asn Ser
65                  70                  75                  80

ctg tat ctg caa atg aac agt ctg aga gcc gag gac acg gcc gtg tat      288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gca aga ggt ttg tct ctt cgt cct tgg ggc caa ggt acc ctg      336
Tyr Cys Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr Leu
            100                 105                 110

gtc acc gtc tcg aga                                                 351
Val Thr Val Ser Arg
        115
```

<210> 39

<211> 117

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -015

<400> 39

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro
1 5 10 15

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

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

Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Arg
115

<210> 40

<211> 318

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -001, SC03-002, SC03-003, SC03-004, SC03-005, SC03-007, SC03-008, SC03-009, SC03-010, SC03-013, SC03-014, SC03 -016 and SC03-018

<220>

<221> CDS

<222> (1)..(318)

<223>

<400> 40
gag ctc acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

gtc acc atc act tgc cgg gca agt cag agc att agc agc tac tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
20 25 30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45

gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

tct ggg aca gat ttc act ct c acc atc agc agt ctg caa cct gaa gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt acc cct cca acg tt c 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe
85 90 95

ggc caa ggg acc aag gtg gag atc aaa cgt 318
Gly Gln Gly Thr Lys Val G lu Ile Lys Arg
100 105

<210> 41

<211> 106

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -001, SC03-002, SC03-003, SC03-004, S C03-005, SC03-007, SC03-008, SC03-009, SC03-010, SC03-013, SC03-0 14, SC03-016 and SC03-018

<400> 41

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

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

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

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50 55 60

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

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

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

<210> 42

<211> 324

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -006

<220>

<221> CDS

<222> (1)..(324)

<223>

<400> 42

gac atc cag atg act cag tct cca cac tct ctg tct gca tct gta gga 48
Asp Ile Gln Met Thr Gln Ser Pro His Ser Leu Ser Ala Ser Val Gly
1 5 10 15

gac aga gtc acc atc act tgc cgg gcg agt cag ggc att agc aat tat 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

tta gcc tgg tat cag cag aaa cca ggg aaa gtt cct aag ctc ctg atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

tat gct gca tcc act ttg caa tca ggg gtc cca tct cgg ttc agt ggc 192
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gaa gat gtt ggg gtt tat tac tgc cag cag agg ttc cgc acg ccg gtc 288
Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Arg Phe Arg Thr Pro Val
85 90 95

acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc 324
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 43

<211> 108

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-006

<400> 43

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

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

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

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

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

Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Arg Phe Arg Thr Pro Val
85 90 95

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

<210> 44

<211> 324

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC 03-012 and SC03-015

<220>

<221> CDS

<222> (1)..(324)

<223>

<400> 44

```
tct gag ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag aca        48
Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
1               5                   10                  15

gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca agc        96
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
            20                  25                  30

tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat ggt       144
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly
        35                  40                  45

aaa aac aac cgg ccc tca ggg  atc cca gac cga ttc tct ggc tcc agc      192
Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
    50                  55                  60

tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa gat       240
Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
65                  70                  75                  80

gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac cat gtg       288
Glu Ala Asp Tyr Tyr Cys Asn  Ser Arg Asp Ser Ser Gly Asn His Val
                85                  90                  95

gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt                      324
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105
```

<210> 45

<211> 108

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -012 and SC03-015

<400> 45

```
Ser Glu Leu Thr Gln Asp Pro Ala Va l Ser Val Ala Leu Gly Gln Thr
1               5                   10                  15

Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
            20                  25                  30
```

Trp Tyr Gln Gln Lys Pro Gl y Gln Ala Pro Val Leu Val Ile Tyr Gly
35 40 45

Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
50 55 60

Ser Gly Asn Thr Al a Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
65 70 75 80

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val
85 90 95

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

<210> 46

<211> 729

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-001

<220>

<221> CDS

<222> (1)..(729)

<223>

<400> 46

tcc atg gct gag gt g cag ctg gtg gag tct ggg gga ggc ttg gta aag 48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga tt c acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agc ggc tac tcg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 144
Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc 192
Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr A la Asp Ser
50 55 60

agg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 240
Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80

tat ctt cag atg aac aac ctg aga gct gag gac acg gct gtg tat tac 288
Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

tgt gca aga cac cgg ttc cgg cac gtc ttc gat tac tgg ggc cag ggc 336
Cys Ala Arg His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly
100 105 110

acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc gga acc ggg 384
Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly Thr Gly
115 120 125

tct ggg act ggt acg agc gag ctc acc cag tct cca tc c tcc ctg tct 432
Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser
130 135 140

gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt cag agc 480
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
145 150 155 160

att agc agc tac tta aat tgg tat cag cag aaa cca ggg aaa gcc cct 528
Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro G ly Lys Ala Pro
165 170 175

aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg gtc cca tca 576
Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
180 185 190

agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc atc agc 624
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
195 200 205

agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag agt tac 672
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
210 215 220

agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag atc aaa cgt 720
Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
225 230 235 240

gcg gcc gca 729
Ala Ala Ala

<210> 47

<211> 243

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-001

<400> 47

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

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

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

Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

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

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

Cys Ala Arg His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly Thr Gly
115 120 125

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

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

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

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

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

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

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

Ala Ala Ala

<210> 48

<211> 747

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-002

<220>

<221> CDS

<222> (1)..(747)

<223>

<400> 48

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tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtc aag       48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu  Val Lys
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agc ggc tac agc atg agc tgg gtc cgc cag gcg ccc ggg aag ggg ctg      144
Ser Gly Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa      192
Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
    50                  55                  60

tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca      240
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
65                  70                  75                  80

aag aac tca ctg tat ctg caa atg aac agc ctg aaa acc g ag gac acg      288
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
                85                  90                  95

gcc gtg tat tac tgt gct aga tac tac tcc cgc tcc ctc aag gcc ttc      336
Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe
            100                 105                 110

gat tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga      384
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu  Gly Thr Gly
        115                 120                 125

ggt tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc acc cag      432
Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln
    130                 135                 140
```

tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act 480
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

tgc cgg gca agt cag agc att agc agc tac tta aat tgg tat cag cag 528
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
165 170 175

aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg 576
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
180 185 190

caa agt ggg gtc cca tca agg ttc agt ggc agt gga t ct ggg aca gat 624
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

ttc act ctc acc atc agc agt ctg caa cct gaa gat ttt gca act tac 672
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
210 215 220

tac tgt caa cag agt tac agt acc cct cca acg ttc ggc caa ggg acc 720
Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
225 230 235 240

aag gtg gag atc aaa cgt gcg gcc gca 747
Lys Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 49

<211> 249

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-002

<400> 49

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

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

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

Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
50 55 60

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser

65 70 75 80

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

Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
115 120 125

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

Lys Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 50

<211> 735

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-003

<220>

<221> CDS

<222> (1)..(735)

<223>

<400> 50

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tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag       48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agc agc tac ccg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg      144
Ser Ser Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtc tca gct att agt ggt agt ggt ggt  agc aca tac tac gca      192
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac      240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg      288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  Glu Asp Thr Ala Val
                85                  90                  95

tat tac tgt gcc aga cgc agc tac ttc cgc cgc ttc gat tac tgg ggc      336
Tyr Tyr Cys Ala Arg Arg Ser Tyr Phe Arg Arg Phe Asp Tyr Trp Gly
            100                 105                 110

cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc gga      384
Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
        115                 120                 125

acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc tcc      432
Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
    130                 135                 140

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt      480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

cag agc att agc agc tac tta aat tgg tat  cag cag aaa cca ggg aaa      528
Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg gtc      576
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc      624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  Thr Asp Phe Thr Leu Thr
        195                 200                 205

atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag      672
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
```

210 215 220

agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag atc 720
Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

aaa cgt gcg gcc gca 735
Lys Arg Ala Ala Ala
245

<210> 51

<211> 245

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-003

<400> 51

Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 120 125

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

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

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

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

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

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

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

Lys Arg Ala Ala Ala
245

<210> 52

<211> 735

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-005

<220>

<221> CDS

<222> (1)..(735)

<223>

<400> 52

tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg atc cag 48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agc ggc tac act atg agc tgg gtc cgc cag gcg ccc ggg cag ggg ctg 144
Ser Gly Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

```
          35                  40                  45

gag tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc      192
Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
     50                  55                  60

agg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg      240
Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65                  70                  75                  80

tat ctt caa atg aac aac ctg aga gct gag gac acg gcc gtg tat tac      288
Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gca aaa ggc ggc ggc cgc ccg tac aac ccc ttc gat tac tgg ggc      336
Cys Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly
            100                 105                 110

cag ggc acc ctg gtg acc gtg  ctc gag ggt acc gga ggt tcc ggc gga      384
Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
        115                 120                 125

acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc tcc       432
Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
    130                 135                 140

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt      480
Leu Ser Ala Ser Val Gly As p Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg aaa      528
Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Ly s
                165                 170                 175

gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg gtc      576
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc      624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag      672
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

agt tac agt acc cct cca  acg ttc ggc caa ggg acc aag gtg gag atc      720
Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

aaa cgt gcg gcc gca                                                  735
Lys Arg Ala Ala Ala
                245
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<210> 53

<211> 245

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-005

<400> 53

Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln
1 5 10 15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 3 0

Ser Gly Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
35 40 45

Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 6 0

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

Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 9 0 95

Cys Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 1 20 125

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

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 1 50 155 160

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

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

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

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

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

Lys Arg Ala Ala Ala
245

<210> 54

<211> 753

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-006

<220>

<221> CDS

<222> (1)..(753)

<223>

<400> 54

tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag 48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly L eu Val Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agc ggc tac cct atg cac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 144
Ser Gly Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtg gca gtt ata tca tat gac gga agt aat aaa tac tat gca 192
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
50 55 60

gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac 240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75 80

acg ctg tat ctg caa atg aac agc ctg aga gct gag ga c aca gct gtg 288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
85 90 95

tat tac tgt gct aaa gac ggc agc ccc cgc acc ccc agc ttc gat tac 336
Tyr Tyr Cys Ala Lys Asp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr
100 105 110

tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc 384

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly T hr Gly Gly Ser
115 120 125

ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag atg 432
Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
130 135 140

act cag tct cca cac tct ctg tct gca tct gta gga gac aga gtc acc 480
Thr Gln Ser Pro His Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

atc act tgc cgg gcg agt cag ggc att agc aat tat tta gcc tgg tat 528
Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr
165 170 175

cag cag aaa cca ggg aaa gtt cct aag ctc ctg atc tat gct gca tcc 576
Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser
180 185 190

act ttg caa tca ggg gtc cca tct cgg ttc agt gg c agt gga tct ggg 624
Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

aca gat ttc act ctc acc atc agc agc ctg cag cct gaa gat gtt ggg 672
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Gly
210 215 220

gtt tat tac tgc cag cag agg ttc cgc acg ccg gtc acc ttc ggc cag 720
Val Tyr Tyr Cys Gln Gln Arg Phe Arg Thr Pro V al Thr Phe Gly Gln
225 230 235 240

ggc acc aaa ctg gaa atc aaa cgc gcg gcc gca 753
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala
245 250

<210> 55

<211> 251

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-006

<400> 55

Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
50 55 60

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

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

Tyr Tyr Cys Ala Lys Asp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
115 120 125

Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile G ln Met
130 135 140

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

Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr L eu Ala Trp Tyr
165 170 175

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

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

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

Val Tyr Tyr Cys Gln Gln Arg Phe A rg Thr Pro Val Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala
245 250

<210> 56

<211> 741

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-007

<220>

<221> CDS

<222> (1)..(741)

<223>

<400> 56

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tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag       48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

cct agg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agc gac tac cgg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg      144
Ser Asp Tyr Arg Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag agg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca      192
Glu Arg Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
    50                  55                  60

gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac      240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg      288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                85                  90                  95

tat tac tgt gca aga ggc tac tgg acg tcg ctc acg ggc ttc gat tac      336
Tyr Tyr Cys Ala Arg Gly Tyr Trp Thr Ser Leu Thr Gly Phe Asp Tyr
            100                 105                 110

tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc      384
Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
        115                 120                 125

ggc gga acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca      432
Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro
    130                 135                 140

tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg      480
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

gca agt cag agc att agc agc tac tta aat tgg tat cag cag aaa cca      528
Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

ggg aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt      576
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190
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ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act 624
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

ctc acc atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt 672
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

caa cag agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg 720
Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val
225 230 235 240

gag atc aaa cgt gcg gcc gca 741
Glu Ile Lys Arg Ala Ala Ala
245

<210> 57

<211> 247

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-007

<400> 57

Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

Ser Asp Tyr Arg Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

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

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

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

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

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
115 120 125

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

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

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

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

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

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

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

Glu Ile Lys Arg Ala Ala Ala
245

<210> 58

<211> 735

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-008

<220>

<221> CDS

<222> (1)..(735)

<223>

<400> 58

tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag 48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10 15

```
cct ggg agg tcc ctg aga ctc tcc  tgt gca gcc tct gga ttc acc ttc        96
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agc agc tac ccg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg       144
Ser Ser Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca       192
Glu Trp Val Ser Ala Ile Ser Gly  Ser Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac       240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac aca gcc gtg       288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                85                  90                  95

tat tac tgt gca aga cgc gtc cgc ccc cgc cgc ttc gat tat tgg ggc       336
Tyr Tyr Cys Ala Arg Arg Val Arg Pro Arg Arg Phe Asp Tyr Trp Gly
            100                 105                 110

cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc gga       384
Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
        115                 120                 125

acc ggg tct ggg act ggt acg  agc gag ctc acc cag tct cca tcc tcc       432
Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
    130                 135                 140

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt       480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg aaa       528
Gln Ser Ile Ser Ser Tyr Leu  Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg gtc       576
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc       624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag       672
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag atc       720
Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

aaa cgt gcg gcc gca                                                   735
Lys Arg Ala Ala Ala
                245
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<210> 59

<211> 245

<212> PRT

<213> Artificial sequen ce

<220>

<223> SC03-008

<400> 59

Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10 15

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

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

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 120 125

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

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

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

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

195 200 205

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

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

Lys Arg Ala Ala Ala
245

<210> 60

<211> 744

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-009

<220>

<221> CDS

<222> (1)..(744)

<223>

<400> 60

tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag 48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10 15

cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 96
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agc gac tac ccc atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 144
Ser Asp Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtc tca tcc att agt ggt agt ggt ggt agc aca tac tac gca 192
Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75 80

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac aca gcc gtg 288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
85 90 95

tat tac tgt gca aaa ggc ctc ttc atg gtc acc acg tac gcg ttc gat 336
Tyr Tyr Cys Ala Lys Gly Leu Phe Met Val Thr Thr Tyr Ala Phe Asp
100 105 110

tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt 384
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly
115 120 125

tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc acc cag tct 432
Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Le u Thr Gln Ser
130 135 140

cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc 480
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

cgg gca agt cag agc att agc agc tac tta aat tgg tat cag cag aaa 528
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

cca ggg aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa 576
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
180 185 190

agt ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc 624
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

act ctc acc atc agc agt ctg caa cct gaa gat ttt gca act tac tac 672
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

tgt caa cag agt tac agt acc cct cca acg ttc ggc caa ggg acc aag 720
Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

gtg gag atc aaa cgt gcg gcc gca 744
Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 61

<211> 248

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-009

<400> 61

Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Va l Val Gln
1 5 10 15

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

210

20 25 30

Ser Asp Tyr Pro Met Asn Trp Val Arg Gln Ala Pr o Gly Lys Gly Leu
35 40 45

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

Tyr Tyr Cys Ala Lys Gly Leu Ph e Met Val Thr Thr Tyr Ala Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly
115 120 125

Ser Gly Gly Thr Gly Se r Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser
130 135 140

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

Arg Ala Ser Gl n Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

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

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

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

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

Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 62

<211> 735

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-010

<220>

<221> CDS

<222> (1)..(735)

<223>

<400> 62

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tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag        48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1               5                   10                  15

cct ggg agg tcc ctg aga ctc tcc tgt gca acc tct gga ttc acc ttc        96
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
            20                  25                  30

agc ggc tac acg atg cac tgg gtc cgc cag gcg ccc ggg aag ggg ctg       144
Ser Gly Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc       192
Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
    50                  55                  60

agg aag ggc aga ttc acc atc tcc aga gac aac tcc aag aac acg ctg       240
Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65                  70                  75                  80

tat ctt caa atg aac aac ctg aga gct gag gac aca gct gtg tat tac       288
Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gca aaa ggc ggc ggc ctc ccc tac ttg agc ttc gat tac tgg ggc       336
Cys Ala Lys Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr Trp Gly
            100                 105                 110

cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc gga       384
Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
        115                 120                 125

acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc tcc       432
Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
    130                 135                 140

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt       480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg aaa       528
Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
```

```
                    165                 170                 175

gcc cct aag ctc ctg atc tat gct gca tcc agt tt g caa agt ggg gtc      576
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc      624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag      672
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr T yr Tyr Cys Gln Gln
    210                 215                 220

agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag atc      720
Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

aaa cgt gcg gcc gca                                                  735
Lys Arg Ala Ala Ala
                245
```

<210> 63

<211> 245

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-010

<400> 63

```
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1               5                   10                  15

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

Ser Gly Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
    50                  55                  60

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

Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
```

Cys Ala Lys Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 120 125

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

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

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

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

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

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

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

Lys Arg Ala Ala Ala
245

<210> 64

<211> 741

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-012

<220>

<221> CDS

<222> (1)..(741)

<223>

<400> 64

```
gcc atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag        48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1               5                   10                  15

cct ggg gcc tca gtg aag gtc tcc tgc a ag gct tct ggt tac acc ttt        96
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
            20                  25                  30

acc agc tat ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt       144
Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        35                  40                  45

gag tgg atg gga tgg atc agc gct tac aat ggt aac aca aac tat gca       192
Glu Trp Met Gly Trp Ile Ser Ala Tyr  Asn Gly Asn Thr Asn Tyr Ala
    50                  55                  60

cag aag ctc cag ggc aga gtc acc atg acc aca gac aca tcc acg agc       240
Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
65                  70                  75                  80

aca gcc tac atg gag ctg agc agc ctg aga tct gac gac acg gcc gtg       288
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
                85                  90                  95

tat tac tgt gca agg atg ttt agg aag agt tcc ttt gac tcc tgg ggc       336
Tyr Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly
            100                 105                 110

caa ggt acc ctg gtc acc gtc tcg aga ggt gga ggc ggt tca ggc gga       384
Gln Gly Thr Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

ggt ggc tct ggc ggt ggc gga tcg t ct gag ctg act cag gac cct gct       432
Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala
    130                 135                 140

gtg tct gtg gcc ttg gga cag aca gtc agg atc aca tgc caa gga gac       480
Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp
145                 150                 155                 160

agc ctc aga agc tat tat gca agc tgg tac cag cag aag cca gga cag       528
Ser Leu Arg Ser Tyr Tyr Ala Ser  Trp Tyr Gln Gln Lys Pro Gly Gln
                165                 170                 175

gcc cct gta ctt gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc       576
Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile
            180                 185                 190

cca gac cga ttc tct ggc tcc agc tca gga aac aca gct tcc ttg acc       624
Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr
        195                 200                 205

atc act ggg gct cag gcg gaa gat gag gct gac tat tac tgt aac tcc       672
Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser
    210                 215                 220

cgg gac agc agt ggt aac cat gtg gta ttc ggc gga ggg acc aag ctg       720
Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240
```

acc gtc cta ggt gcg gcc gca 741
Thr Val Leu Gly Ala Ala Ala
245

<210> 65

<211> 247

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-012

<400> 65

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

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

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

Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala
50 55 60

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

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

Tyr Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala
130 135 140

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

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

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

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

Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser
210 215 220

Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala
245

<210> 66

<211> 747

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-013

<220>

<221> CDS

<222> (1)..(747)

<223>

<400> 66

gcc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag 48
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agt gac cac tac atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg 144
Ser Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa 192
Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
50 55 60

```
tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca      240
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
65                  70                  75                  80

aag aac tca ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg      288
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
                85                  90                  95

gcc gtg tat tac tgt gca aag ggg ttg act  cct ttg tac ttt gac tac      336
Ala Val Tyr Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr
            100                 105                 110

tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca      384
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc acc cag      432
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  Glu Ile Glu Leu Thr Gln
    130                 135                 140

tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act      480
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

tgc cgg gca agt cag agc att agc agc tac tta aat tgg tat cag cag      528
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 17 0                175

aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg      576
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

caa agt ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat      624
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

ttc act ctc acc atc agc agt ctg caa  cct gaa gat ttt gca act tac      672
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

tac tgt caa cag agt tac agt acc cct cca acg ttc ggc caa ggg acc      720
Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
225                 230                 235                 240

aag gtg gag atc aaa cgt gcg gcc gca                                  747
Lys Val Glu Ile Lys Arg Ala Ala Ala
                245
```

<210> 67

<211> 249

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-013

<400> 67

Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

Ser Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
50 55 60

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
65 70 75 80

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

Ala Val Tyr Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr
100 105 110

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

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

Lys Val Glu Ile Lys Arg Ala Ala Ala

245

<210> 68

<211> 747

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-014

<220>

<221> CDS

<222> (1)..(747)

<223>

<400> 68

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gcc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag       48
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt gac cac tac atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg      144
Ser Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa      192
Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
    50                  55                  60

tac gcc gcg tct gtg aaa ggc aga  ttc acc atc tca aga gat gat tca      240
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
65                  70                  75                  80

aag aac tca ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg       288
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
                85                  90                  95

gcc gtg tat tac tgt gca agg ggg att tcg ccg ttt tac ttt gac tac      336
Ala Val Tyr Tyr Cys Ala Arg Gly Ile Ser Pro Phe Tyr Phe Asp Tyr
            100                 105                 110

tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca      384
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc acc cag      432
Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln
    130                 135                 140
```

```
tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act      480
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

tgc cgg gca agt cag agc att agc agc tac tta aat tgg tat cag cag      528
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

aaa cca ggg aaa gcc cct aag  ctc ctg atc tat gct gca tcc agt ttg      576
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

caa agt ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat       624
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

ttc act ctc acc atc agc agt ctg caa cct gaa gat ttt gca act tac      672
Phe Thr Leu Thr Ile Ser Se r Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

tac tgt caa cag agt tac agt acc cct cca acg ttc ggc caa ggg acc      720
Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Th r
225                 230                 235                 240

aag gtg gag atc aaa cgt gcg gcc gca                                  747
Lys Val Glu Ile Lys Arg Ala Ala Ala
                245
```

<210> 69

<211> 249

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-014

<400> 69

```
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

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

Ser Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
    50                  55                  60

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
```

65 70 75 80

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu 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 Ser Ile Ser Ser Tyr 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 Th r 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 Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gl y Gln Gly Thr
225 230 235 240

Lys Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 70

<211> 732

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-015

<220>

<221> CDS

<222> (1)..(732)

<223>

<400> 70

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gcc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggt gtg gta cgg       48
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

gat gat tat ggc atg agc tgg gtc cgc caa gct cca ggg aag ggg ctg      144
Asp Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtc tct ggt att aat tgg aat ggt ggt agc aca ggt ta t gca      192
Glu Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala
    50                  55                  60

gac tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac      240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
65                  70                  75                  80

tcc ctg tat ctg caa atg aac agt ctg aga gcc gag gac acg gcc gtg      288
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr A la Val
                85                  90                  95

tat tac tgt gca aga ggt ttg tct ctt cgt cct tgg ggc caa ggt acc      336
Tyr Tyr Cys Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtc acc gtc tcg aga ggt gga ggc ggt tca ggc gga ggt ggc tct      384
Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

ggc ggt ggc gga tcg tct gag ctg act cag gac cct gct gtg tct gtg      432
Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val
    130                 135                 140

gcc ttg gga cag ac a gtc agg atc aca tgc caa gga gac agc ctc aga      480
Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg
145                 150                 155                 160

agc tat tat gca agc tgg tac cag cag aag cca gga cag gc c cct gta      528
Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val
                165                 170                 175

ctt gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc cca gac cga      576
Leu Val Ile Tyr G ly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg
            180                 185                 190

ttc tct ggc tcc agc tca gga aac aca gct tcc ttg acc atc act ggg      624
Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr I le Thr Gly
        195                 200                 205

gct cag gcg gaa gat gag gct gac tat tac tgt aac tcc cgg gac agc      672
Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser
```

210 215 220

agt ggt aac cat gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta 720
Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
225 230 235 240

ggt gcg gcc gca 732
Gly Ala Ala Ala

<210> 71

<211> 244

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-015

<400> 71

Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg
1 5 10 15

Pro Gly Gly Ser Leu Arg Leu Ser Cys A la Ala Ser Gly Phe Thr Phe
20 25 30

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

Glu Trp Val Ser Gly Ile Asn T rp Asn Gly Gly Ser Thr Gly Tyr Ala
50 55 60

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

Ser Leu Tyr Leu Gln M et Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val
130 135 140

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

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

Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg
180 185 190

Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly
195 200 205

Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser
210 215 220

Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
225 230 235 240

Gly Ala Ala Ala

<210> 72

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZalphaB

<400> 72
tctctcgaga aaagagaggc tgaagctgca ggaattcacg tggcccagcc ggccg 55

<210> 73

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFVH

<400> 73
tctctcgaga aaagagccat ggaagctgca ggaattcacg tggcccagcc ggccg 55

<210> 74

<211> 92

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic hinge fragment

<400> 74
gcggccgcgc caaagccaag taccccacca ggttcttcat gtccaccatg tccaggctct 60

ggcggtgcgc caatcgatag cggctttcta ga 92

<210> 75

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-004

<400> 75

Asp Gly Ser Arg Phe Pro Ala Arg Phe Asp Tyr
1 5 10

<210> 76

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-016

<400> 76

Tyr Gly Ser Ala Tyr Arg Pro Pro Phe Asp Tyr
1 5 10

<210> 77

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03 -017

<400> 77

Ser Arg Ser Ala Gly Phe Phe Asp Tyr
1 5

<210> 78

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03 -018

<400> 78

Phe Asn Pro Phe Thr Ser Phe Asp Tyr
1 5

<210> 79

<211> 372

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -004

<220>

<221> CDS

<222> (1)..(372)

<223>

<400> 79

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atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct       48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

gac tac ttg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag      144
Asp Tyr Leu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtt ggc cgt att aga agc aaa gct aac agt tac gcg aca gca tat      192
Trp Val Gly Arg Ile Arg Ser Lys Ala Asn Ser Tyr Ala Thr Ala Tyr
    50                  55                  60

gct gcg tcg gtg aaa ggc agg ttc acc a tc tcc aga gat gat tca aag      240
Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
65                  70                  75                  80

aac acg gcg tat ctg caa atg aac agc ctg aaa acc gag gac acg gcc      288
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
                85                  90                  95

gtg tat tac tgt gct aaa gac ggc agc cgg ttc ccc gcc cgc ttc gat      336
Val Tyr Tyr Cys Ala Lys Asp Gly Ser  Arg Phe Pro Ala Arg Phe Asp
            100                 105                 110

tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag                     372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
        115                 120
```

<210> 80

<211> 124

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -004

<400> 80

```
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val  Gln Pro
1               5                   10                  15

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

Asp Tyr Leu Met Asn Trp Val Arg Gln Ala Pro Gly  Lys Gly Leu Glu
        35                  40                  45

Trp Val Gly Arg Ile Arg Ser Lys Ala Asn Ser Tyr Ala Thr Ala Tyr
    50                  55                  60
```

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

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

Val Tyr Tyr Cys Ala Lys Asp Gly Ser Arg Phe Pro Ala Arg Phe Asp
100 105 110

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

<210> 81

<211> 372

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -016

<400> 81
atggctgagg tgtagctggt ggagtctggg ggaggcttgg tccagcctgg agggtccctg 60

agactctccc gtgcagcctc tggattcacc tttagcaact accccatgcg ctgggtccgc 120

caggcgcccg ggaaggggct ggagtgggta ggtttcat ta gaaacaaagc taatggtggg 180

acaacagaat agaccacgtc tgtgagaggc agattcacaa tctcaagaga tgattccaaa 240

agcatcacct atctgcaaat gaacagcctg agagccgagg acacagccgt gtattactgt 300

gctaaatacg gcagcgccta ccgcccgccc ttcgattact ggggccaggg caccctggtg 360

accgtgctcg ag 372

<210> 82

<211> 125

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -016

<400> 82

Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Va l Gln
1 5 10 15

Pro Gly Gly Ser Leu Arg Leu Ser Arg Ala Ala Ser Gly Phe Thr Phe
20 25 30

Ser Asn Tyr Pro Met Arg Trp Val Arg Gln Ala Pro Gl y Lys Gly Leu
35 40 45

Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu
50 55 60

Gln Thr Thr Ser Val Arg Gly Arg Phe Thr Il e Ser Arg Asp Asp Ser
65 70 75 80

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

Ala Val Tyr Tyr Cys Ala Lys Tyr Gl y Ser Ala Tyr Arg Pro Pro Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
115 120 125

<210> 83

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -017

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 83

atg gcc cag gtg cag ctg cag gag tcg ggc gca gga ctg ttg aag cct 48
Met Ala Gln Val Gln Leu Gln Glu Ser Gly Ala Gly Leu Leu Lys P ro
1 5 10 15

tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc gtc agc 96

Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser
20 25 30

agt ggt agt tac tac tgg agc tgg atc cgg cag ccc cca ggg aag gga 144
Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
35 40 45

ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac tac aac 192
Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn
50 55 60

ccc tcc ctc aag agt cg a gtc acc ata tca gta gac acg tcc aag aac 240
Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
65 70 75 80

cag ttc tcc ctg aag ctg agc tct gtg acc gct gcg gac acg gc c gtg 288
Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
85 90 95

tat tac tgt gca aag tct cgt tct gct ggt ttc ttt gac tac tgg ggc 336
Tyr Tyr Cys Ala Lys S er Arg Ser Ala Gly Phe Phe Asp Tyr Trp Gly
100 105 110

caa ggt acc ctg gtc acc gtc tcg agt 363
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 84

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -017

<400> 84

Met Ala Gln Val Gln Leu Gln Glu Ser Gly A la Gly Leu Leu Lys Pro
1 5 10 15

Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser
20 25 30

Ser Gly Ser Tyr Tyr Trp Ser Trp I le Arg Gln Pro Pro Gly Lys Gly
35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn
50 55 60

Pro Ser Leu Lys Ser Arg V al Thr Ile Ser Val Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Lys Ser Arg Ser Ala Gly Phe Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 85

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -018

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 85

atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag 144
Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac 192
Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

tcc gtg aag ggc cgg ttc acc atc tcc a ga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat 288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

tac tgt gca aag ttt aat ccg ttt act tcc ttt gac tac tgg ggc caa 336

Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly Gln
100 105 110

ggt acc ctg gtc acc gtc tcg agt 360
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 86

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -018

<400> 86

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

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

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

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 87

<211> 324

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-017

<220>

<221> CDS

<222> (1)..(324)

<223>

<400> 87

```
gaa att gag ctc aca cag tct cca gcc acc ctg tct ttg tct cca ggg       48
Glu Ile Glu Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                  10                  15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac       96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc      144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc      192
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag  cct      240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

gaa gat ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccg      288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
                85                  90                  95

gct ttc ggc gga ggg acc aag gtg gag atc aaa cgt                      324
Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 88

<211> 108

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-017

<400> 88

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

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

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

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

<210> 89

<211> 747

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-004

<220>

<221> CDS

<222> (1)..(747)

<223>

<400> 89

tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag 48
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agc gac tac ttg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 144

```
Ser Asp Tyr Leu Met Asn Tr p Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtt ggc cgt att aga agc aaa gct aac agt tac gcg aca gca      192
Glu Trp Val Gly Arg Ile Arg Ser Lys Ala Asn Ser Tyr Ala Thr Al a
    50                  55                  60

tat gct gcg tcg gtg aaa ggc agg ttc acc atc tcc aga gat gat tca      240
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
65                  70                  75                  80

aag aac acg gcg tat ctg caa atg aac agc ctg aaa acc gag gac acg      288
Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
                85                  90                  95

gcc gtg tat tac tgt gct aaa gac ggc agc cgg ttc ccc gcc cgc ttc      336
Ala Val Tyr Tyr Cys Ala Lys Asp Gly Ser Arg Phe Pro Ala Arg Phe
            100                 105                 110

gat tac tgg ggc cag ggc  acc ctg gtg acc gtg ctc gag ggt acc gga      384
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
        115                 120                 125

ggt tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc acc  cag      432
Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln
    130                 135                 140

tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act      480
Ser Pro Ser Ser Leu Se r Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

tgc cgg gca agt cag agc att agc agc tac tta aat tgg tat cag cag      528
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gl n Gln
                165                 170                 175

aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg      576
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

caa agt ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat      624
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

ttc act ctc acc atc agc agt ctg caa cct gaa gat ttt gca act tac      672
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

tac tgt caa cag agt  tac agt acc cct cca acg ttc ggc caa ggg acc      720
Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
225                 230                 235                 240

aag gtg gag atc aaa cgt gcg gcc gca                                  747
Lys Val Glu Ile Lys Arg Ala Ala Ala
                245
```

<210> 90

<211> 249

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-004

<400> 90

```
Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

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

Ser Asp Tyr Leu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

Glu Trp Val Gly Arg Ile Arg Ser Lys Ala Asn Ser Tyr Ala Thr Ala
    50                  55                  60

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
65                  70                  75                  80

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

Ala Val Tyr Tyr Cys Ala Lys Asp Gly Ser Arg Phe Pro Ala Arg Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
        115                 120                 125

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

Lys Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 91

<211> 747

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-016

<400> 91
gccatggctg aggtgtagct ggtggagtct gggggaggct tggtccagcc tggagggtcc 60

ctgagactct cccgtgcagc ctctggattc acctttagca actaccccat gcgctgggtc 120

cgccaggcgc ccgggaaggg gctggagtgg gtaggtttca ttagaaacaa agctaatggt 180

gggacaacag aatagaccac gtctgtgaga ggcagattca caatctcaag agatgattcc 240

aaaagcatca cctatctgca aatgaacagc ctgagagccg aggacacagc cgtgtattac 300

tgtgctaaat acggcagcgc cta ccgcccg cccttcgatt actggggcca gggcaccctg 360

gtgaccgtgc tcgagggtac cggaggttcc ggcggaaccg ggtctgggac tggtacgagc 420

gagctcaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact 480

tgccgggcaa gtcagagcat tagcagctac ttaaattggt atcagcagaa acca gggaaa 540

gcccctaagc tcctgatcta tgctgcatcc agtttgcaaa gtggggtccc atcaaggttc 600

agtggcagtg gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat 660

tttgcaactt actactgtca acagagttac agtacccctc caacgttcgg ccaagggacc 720

aaggtggaga tcaaacgt gc ggccgca 747

<210> 92

<211> 249

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-016

<400> 92

```
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

Pro Gly Gly Ser Leu Arg Leu Ser Arg Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

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

Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu
    50                  55                  60

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

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

Ala Val Tyr Tyr Cys Ala Lys Tyr Gly Ser Ala Tyr Arg Pro Pro Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
        115                 120                 125

Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu 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 Ser Ile Ser Ser Tyr 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 Gln Gln Ser Tyr Ser Thr Pro Pro Thr  Phe Gly Gln Gly Thr
```

225 230 235 240

Lys Val Glu Ile Lys Arg Ala Ala Ala
245

<210> 93

<211> 744

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-017

<220>

<221> CDS

<222> (1)..(744)

<223>

<400> 93

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gcc atg gcc cag gtg cag ctg cag gag tcg ggc gca gga ctg ttg aag       48
Ala Met Ala Gln Val Gln Leu Gln Glu Ser Gly Ala Gly Leu Leu Lys
1               5                   10                  15

cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc gtc       96
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val
            20                  25                  30

agc agt ggt agt tac tac tgg agc tgg atc cgg cag ccc cca ggg aag      144
Ser Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
        35                  40                  45

gga ctg gag tgg att ggg tat atc tat tac agt ggg agc  acc aac tac      192
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
    50                  55                  60

aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag      240
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
65                  70                  75                  80

aac cag ttc tcc ctg aag ctg agc tct gtg acc gct gcg gac acg gcc      288
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  Asp Thr Ala
                85                  90                  95

gtg tat tac tgt gca aag tct cgt tct gct ggt ttc ttt gac tac tgg      336
Val Tyr Tyr Cys Ala Lys Ser Arg Ser Ala Gly Phe Phe Asp Tyr Trp
            10 0                105                 110

ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca ggc      384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 12 5
```

```
gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag tct      432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser
    130                 135                 140

cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc tgc      480
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

agg gcc agt cag agt gtt agc agc tac tta gcc tgg  tac caa cag aaa      528
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg gcc      576
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala
            180                 185                 190

act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac ttc      624
Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser  Gly Thr Asp Phe
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act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat tac      672
Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
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tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc aag      720
Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys
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Ser Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
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Gly Leu Glu Trp Ile Gly  Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
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Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
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Val Tyr Tyr Cys Ala Lys Ser Arg Ser Ala Gly Phe Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

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

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
165 170 17 5

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

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 20 5

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
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cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga  ttc acc ttt      96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
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agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg      144
Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
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gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca      192
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Th r Tyr Tyr Ala
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gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac      240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
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acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg      288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
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tat tac tgt gca aag ttt aat ccg ttt act tcc ttt gac tac tgg ggc      336
Tyr Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly
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caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca ggc gga      384
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc  acc cag tct cca      432
Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser Pro
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tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg      480
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

gca agt cag agc att agc agc tac tta aat tgg tat cag cag aaa cca      528
Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Ty r Gln Gln Lys Pro
                165                 170                 175

ggg aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt      576
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
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ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act      624
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

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

gag atc aaa cgt gcg gcc gca 741
Glu Ile Lys Arg Ala Ala Ala
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35 40 45

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

Tyr Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

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

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

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

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

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

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Ty r Tyr Cys
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tgaatactca tactcttcct ttttcaatat tattgaagca tttatcaggg ttattgtctc 6180

atgagcggat acatatttga atgtatttag aaaaataaac aaataggggt tccgcg caca 6240

tttccccgaa aagtgccacc tgacgtc 6267

<210> 112

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide 5K-I

<400> 112
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<210> 113

<211> 42

<212> DNA

<213> Artificial sequence

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<223> Oligonucleotide sy3K-C

<400> 113
gggaccaagg tggagatcaa acggaccgtg gccgccccca gc 42

<210> 114

<211> 46

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide 5H-B

<400> 114
acctgtcttg aattctccat ggccgaggtg cagctggtgg agtctg 46

<210> 115

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide sy3H -A

<400> 115
gcccttggtg ctagcgctgg agacggtcac cagggtgccc tggcccc 47

<210> 116

<211> 1338

<212> DNA

<213> Artificial sequence

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<223> IgG heavy chain sequence 03 -001

<220>

<221> CDS

<222> (1)..(1338)

<223>

<400> 116
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc a cc ttc agc ggc tac 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

tcg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag tgg gtc 144
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca tcc att agt ggt ggt agc aca tac tac gca gac tcc agg aag ggc 192
Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt cag 240
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

atg aac aac ctg aga gct gag gac acg gct gtg tat tac tgt gca aga 288
Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

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cac cgg ttc cgg cac gtc ttc gat tac tgg ggc cag ggc acc ctg gtg      336
His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

acc gtc tcc agc gct agc acc aag ggc ccc agc gtg ttc ccc ctg gcc      384
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

ccc agc agc aag agc acc agc ggc ggc aca g cc gcc ctg ggc tgc ctg      432
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc tgg aac agc ggc      480
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

gcc ttg acc agc ggc gtg cac acc ttc ccc gcc gtg ctg cag agc agc      528
Ala Leu Thr Ser Gly Val His Thr Phe Pro  Ala Val Leu Gln Ser Ser
                165                 170                 175

ggc ctg tac agc ctg agc agc gtg gtg acc gtg ccc agc agc agc ctg      576
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

ggc acc cag acc tac atc tgc aac gtg aac cac aag ccc agc aac acc      624
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

aag gtg gac aaa cgc gtg gag ccc aag agc tgc gac aag acc cac acc      672
Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

tgc ccc ccc tgc cct gcc ccc gag ctg ctg ggc gga ccc tcc gtg ttc      720
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

ctg ttc ccc ccc aag ccc aag gac acc c tc atg atc agc cgg acc ccc      768
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

gag gtg acc tgc gtg gtg gtg gac gtg agc cac gag gac ccc gag gtg      816
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cac aac gcc aag acc      864
Lys Phe Asn Trp Tyr Val Asp Gly Val  Glu Val His Asn Ala Lys Thr
        275                 280                 285

aag ccc cgg gag gag cag tac aac agc acc tac cgg gtg gtg agc gtg      912
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

ctc acc gtg ctg cac cag gac tgg ctg aac ggc aag gag tac aag tgc      960
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

aag gtg agc aac aag gcc ctg cct gcc ccc atc gag aag acc atc agc     1008
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

aag gcc aag ggc cag ccc cgg gag ccc cag gtg tac acc ctg ccc ccc     1056
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350
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agc cgg gag gag atg acc aag aac c ag gtg tcc ctc acc tgt ctg gtg 1104
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

aag ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aac ggc 1 152
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

cag ccc gag aac aac tac aag acc acc ccc cct gtg ctg gac agc gac 1200
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

ggc agc ttc ttc ctg tac agc aag ctc acc gtg gac aag agc cgg tgg 1248
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

cag cag ggc aac gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac 1296
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

aac cac tac acc cag aag agc ctg agc ctg agc ccc ggc aag 1338
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 117

<211> 446

<212> PRT

<213> Artificial sequence

<220>

<223> IgG heavy chain sequence 03 -001

<400> 117

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

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

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

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

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

Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

260

85 90 95

His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 10 5 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 13 5 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
16 5 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
19 5 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 118

<211> 1356

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain sequence of 03 -002

<220>

<221> CDS

<222> (1)..(1356)

<223>

<400> 118

gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtc aag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc ggc tac 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

agc atg agc tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag tgg gtt 144
Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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          35                  40                  45

    ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac gcc gcg      192
    Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala
 5      50                  55                  60

    tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag aac tca      240
    Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
    65                  70                  75                  80
10
    ctg tat ctg caa atg aac agc c tg aaa acc gag gac acg gcc gtg tat      288
    Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                    85                  90                  95

15  tac tgt gct aga tac tac tcc cgc tcc ctc aag gcc ttc gat tac tgg      336
    Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp Tyr Trp
                100                 105                 110

    ggc cag ggc acc ctg gtg acc gtc tcc agc gct agc acc aag ggc ccc      384
20  Gly Gln Gly Thr Leu Val Thr  Val Ser Ser Ala Ser Thr Lys Gly Pro
            115                 120                 125

    agc gtg ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca      432
    Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
25      130                 135                 140

    gcc gcc ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc      480
    Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
    145                 150                 155                 160
30
    gtg agc tgg aac agc ggc gcc ttg acc agc ggc gtg cac acc ttc ccc      528
    Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                    165                 170                 175

35  gcc gtg ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc      576
    Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                180                 185                 190

    gtg ccc agc agc agc ctg g gc acc cag acc tac atc tgc aac gtg aac      624
40  Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
            195                 200                 205

    cac aag ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag a gc      672
    His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
45      210                 215                 220

    tgc gac aag acc cac acc tgc ccc ccc tgc cct gcc ccc gag ctg ctg      720
    Cys Asp Lys Thr His Thr  Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
    225                 230                 235                 240
50
    ggc gga ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc      768
    Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  Leu
                    245                 250                 255

55  atg atc agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc      816
    Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                260                 265                 270

    cac gag gac ccc gag gtg aag ttc aac tgg tac gtg gac ggc gtg gag      864
60  His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
            275                 280                 285

    gtg cac aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc      912
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Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

tac cgg gtg gtg agc g tg ctc acc gtg ctg cac cag gac tgg ctg aac      960
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

ggc aag gag tac aag tgc aag gtg agc aac aag gcc ctg cct g cc ccc     1008
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

atc gag aag acc atc agc aag gcc aag ggc cag ccc cgg gag ccc cag     1056
Ile Glu Lys Thr Ile  Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

gtg tac acc ctg ccc ccc agc cgg gag gag atg acc aag aac cag gtg     1104
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  Gln Val
        355                 360                 365

tcc ctc acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg     1152
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

gag tgg gag agc aac ggc cag ccc gag aac aac tac aag acc acc ccc     1200
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

cct gtg ctg gac agc gac ggc agc ttc ttc ctg tac agc aag ctc acc     1248
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

gtg gac aag agc c gg tgg cag cag ggc aac gtg ttc agc tgc agc gtg     1296
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

atg cac gag gcc ctg cac aac cac tac acc cag aag agc c tg agc ctg     1344
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

agc ccc ggc aag                                                     1356
Ser Pro Gly Lys
    450
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<210> 119

<211> 452

<212> PRT

<213> Artificial sequence

<220>

<223> IgG heavy chain sequence of 03 -002

<400> 119

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30

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

Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala
    50                  55                  60

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

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

Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270
```

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 120

<211> 1353

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain sequenc e 03-009

<220>

<221> CDS

<222> (1)..(1353)

<223>

<400> 120

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gag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg       48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc gac tac       96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

ccc atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag tgg gtc      144
Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

tca tcc att agt ggt agt ggt ggt agc a ca tac tac gca gac tcc gtg      192
Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat      240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

ctg caa atg aac agc ctg aga gcc gag gac aca gcc gtg tat tac tgt      288
Leu Gln Met Asn Ser Leu Arg Ala Glu  Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gca aaa ggc ctc ttc atg gtc acc acg tac gcg ttc gat tac tgg ggc      336
Ala Lys Gly Leu Phe Met Val Thr Thr Tyr Ala Phe Asp Tyr Trp Gly
            100                 105                 110

cag ggc acc ctg gtg acc gtc tcc agc gct agc acc aag ggc ccc agc      384
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

gtg ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca gcc      432
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

gcc ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg      480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

agc tgg aac agc ggc gcc ttg acc a gc ggc gtg cac acc ttc ccc gcc      528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

gtg ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc gtg       576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

ccc agc agc agc ctg ggc acc cag acc tac atc tgc aac gtg aac cac      624
Pro Ser Ser Ser Leu Gly Thr Gln  Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
```

```
aag ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag agc tgc      672
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
    210                 215                 220

gac aag acc cac acc tgc ccc ccc tgc cct gcc ccc gag ctg ctg ggc      720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

gga ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc atg      768
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

atc agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc cac      816
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

gag gac ccc gag gtg aag ttc a ac tgg tac gtg gac ggc gtg gag gtg      864
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

cac aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc tac      912
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

cgg gtg gtg agc gtg ctc acc gtg ctg cac cag gac tgg ctg aac ggc      960
Arg Val Val Ser Val Leu Thr  Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

aag gag tac aag tgc aag gtg agc aac aag gcc ctg cct gcc ccc atc     1008
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

gag aag acc atc agc aag gcc aag ggc cag ccc cgg gag ccc cag gtg     1056
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

tac acc ctg ccc ccc agc cgg gag gag atg acc aag aac cag gtg tcc     1104
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

ctc acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag     1152
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

tgg gag agc aac ggc cag c cc gag aac aac tac aag acc acc ccc cct     1200
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

gtg ctg gac agc gac ggc agc ttc ttc ctg tac agc aag ctc acc g tg     1248
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

gac aag agc cgg tgg cag cag ggc aac gtg ttc agc tgc agc gtg atg     1296
Asp Lys Ser Arg Trp Gln  Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

cac gag gcc ctg cac aac cac tac acc cag aag agc ctg agc ctg agc     1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  Ser
        435                 440                 445

ccc ggc aag                                                        1353
Pro Gly Lys
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450

<210> 121

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> IgG heavy chain sequence 03 -009

<400> 121

Glu 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 Asp Tyr
20 25 30

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

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Leu Phe Met Val Thr Thr Tyr Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 122

<211> 1350

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03 -013

<220>

<221> CDS

<222> (1)..(1350)

<223>

<400> 122

gag gtg cag ctg gtg gag tc t ggg gga ggc ttg gtc cag cct gga ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt gac ca c 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
20 25 30

tac atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt 144
Tyr Met Asp Trp Val Arg G ln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac gcc gcg 192
Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala A la
50 55 60

tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag aac tca 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat 288
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

tac tgt gca aag ggg ttg act cct ttg tac ttt gac tac tgg ggc cag 336
Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

ggc acc ctg gtg acc gt c tcc agc gct agc acc aag ggc ccc agc gtg 384

```
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca gc c gcc      432
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc      480
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

tgg aac agc ggc gcc ttg acc agc ggc gtg cac acc ttc ccc gcc gtg      528
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro A la Val
                165                 170                 175

ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc gtg ccc      576
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

agc agc agc ctg ggc acc cag acc tac atc tgc aac gtg aac cac aag      624
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag agc tgc gac      672
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

aag acc cac acc tg c ccc ccc tgc cct gcc ccc gag ctg ctg ggc gga      720
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ct c atg atc      768
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc cac gag      816
Ser Arg Thr Pro G lu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

gac ccc gag gtg aag ttc aac tgg tac gtg gac ggc gtg gag gtg cac      864
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val G lu Val His
        275                 280                 285

aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc tac cgg      912
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

gtg gtg agc gtg ctc acc gtg ctg cac cag gac tgg ctg aac ggc aag      960
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

gag tac aag tgc aag gtg agc aac aag gcc ctg cct gcc ccc atc gag     1008
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

aag acc atc ag c aag gcc aag ggc cag ccc cgg gag ccc cag gtg tac     1056
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

acc ctg ccc ccc agc cgg gag gag atg acc aag aac ca g gtg tcc ctc     1104
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
```

```
acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag tgg      1152
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

gag agc aac ggc cag ccc gag aac aac tac aag acc acc ccc cct gtg      1200
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr T hr Pro Pro Val
385                 390                 395                 400

ctg gac agc gac ggc agc ttc ttc ctg tac agc aag ctc acc gtg gac      1248
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

aag agc cgg tgg cag cag ggc aac gtg ttc agc tgc agc gtg atg cac      1296
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

gag gcc ctg cac aac cac tac acc cag aag agc ctg agc ctg agc ccc      1344
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

ggc aag                                                             1350
Gly Lys
    450
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<210> 123

<211> 450

<212> PRT

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03 -013

<400> 123

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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 Ph e Ser Asp His
            20                  25                  30

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

Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Th r Thr Glu Tyr Ala Ala
    50                  55                  60

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

Leu Tyr Leu Gln Met Asn Ser Leu Ly s Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95
```

Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Se r Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 2 40

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 2 70

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 3 00

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 3 30 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 3 60 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 3 90 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 124

<211> 1350

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03 -014

<220>

<221> CDS

<222> (1)..(1350)

<223>

<400> 124

gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct gga ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt gac cac 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
20 25 30

```
tac atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt      144
Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35                  40                  45

ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac gcc gcg      192
Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala
      50                  55                  60

tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag aac tca      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg gcc gtg t at      288
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gca agg ggg att tcg ccg ttt tac ttt gac tac tgg ggc cag      336
Tyr Cys Ala Arg Gly Ile  Ser Pro Phe Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtg acc gtc tcc agc gct agc acc aag ggc ccc agc gtg      384
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  Val
          115                 120                 125

ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca gcc gcc      432
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
      130                 135                 140

ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc      480
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

tgg aac agc ggc gcc ttg acc agc ggc gtg cac acc ttc ccc gcc gtg      528
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc gtg ccc      576
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

agc agc agc ctg ggc acc cag acc tac atc tgc aac gtg aac c ac aag      624
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
          195                 200                 205

ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag agc tgc gac      672
Pro Ser Asn Thr Lys  Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
      210                 215                 220

aag acc cac acc tgc ccc ccc tgc cct gcc ccc gag ctg ctg ggc gga      720
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu   Gly Gly
225                 230                 235                 240

ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc atg atc      768
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc cac gag      816
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

gac ccc gag gtg aag ttc aac tgg tac gtg gac ggc gtg gag gtg cac      864
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
```

```
          275                 280                 285

     aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc tac cgg      912
     Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 5       290                 295                 300

     gtg gtg agc gtg ctc acc gtg ctg cac cag gac tgg ctg a ac ggc aag      960
     Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
     305                 310                 315                 320
10
     gag tac aag tgc aag gtg agc aac aag gcc ctg cct gcc ccc atc gag      1008
     Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                     325                 330                 335

15   aag acc atc agc aag gcc aag ggc cag ccc cgg gag ccc cag gtg tac      1056
     Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  Gln Val Tyr
                 340                 345                 350

     acc ctg ccc ccc agc cgg gag gag atg acc aag aac cag gtg tcc ctc      1104
20   Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
             355                 360                 365

     acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag tgg      1152
     Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
25       370                 375                 380

     gag agc aac ggc cag ccc gag aac aac tac aag acc acc ccc cct gtg      1200
     Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
     385                 390                 395                 400
30
     ctg gac agc gac ggc agc ttc ttc ctg tac agc aag ctc acc gtg gac      1248
     Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                     405                 410                 415

35   aag agc cgg tgg cag cag ggc aac gtg ttc agc tgc a gc gtg atg cac      1296
     Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                 420                 425                 430

     gag gcc ctg cac aac cac tac acc cag aag agc ctg agc ctg agc ccc      1344
40   Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
             435                 440                 445

     ggc aag                                                             1350
     Gly Lys
45       450


     <210>  125

50   <211>  450

     <212>  PRT

     <213>  Artificial sequence
55


     <220>

60   <223>  IgG heavy chain of 03 -014

     <400>  125
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```
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 Ser Asp His
            20                  25                  30

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

Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala
    50                  55                  60

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

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

Tyr Cys Ala Arg Gly Ile Ser Pro Phe Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
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Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu S er Pro
435 440 445

Gly Lys
450

<210> 126

<211> 1344

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03 -018

<220>

<221> CDS

<222> (1)..(1344)

<223>

<400> 126

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

tcc ctg aga ctc tcc tgt gca  gcc tct gga ttc acc ttt agc agc tat       96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc       144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac tcc gtg       192
Ser Ala Ile Ser Gly Ser Gly  Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat       240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt       288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gca aag ttt aat ccg ttt act tcc ttt gac tac tgg ggc cag ggc acc       336
Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtg acc gtc tcc agc gct agc acc aag ggc ccc agc gtg ttc ccc       384
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

ctg gcc ccc agc agc aag  agc acc agc ggc ggc aca gcc gcc ctg ggc       432
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc tgg  aac       480
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

agc ggc gcc ttg acc agc ggc gtg cac acc ttc ccc gcc gtg ctg cag       528
Ser Gly Ala Leu Thr Ser  Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

agc agc ggc ctg tac agc ctg agc agc gtg gtg acc gtg ccc agc agc       576
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  Ser
            180                 185                 190
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agc ctg ggc acc cag acc tac atc tgc aac gtg aac cac aag ccc agc      624
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

aac acc aag gtg gac aaa cgc gtg gag ccc aag agc tgc gac aag acc      672
Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

cac acc tgc ccc ccc tgc cct gcc ccc gag ctg ctg ggc gga ccc tcc      720
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc atg atc agc cgg      768
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc cac gag  gac ccc      816
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

gag gtg aag ttc aac tgg tac gtg gac ggc gtg gag gtg cac aac gcc      864
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

aag acc aag ccc cgg gag gag cag tac aac agc acc tac cgg gtg gtg      912
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg  Val Val
    290                 295                 300

agc gtg ctc acc gtg ctg cac cag gac tgg ctg aac ggc aag gag tac      960
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

aag tgc aag gtg agc aac aag gcc ctg cct gcc ccc atc gag aag acc     1008
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

atc agc aag gcc aag ggc cag ccc cgg gag ccc cag gtg tac acc ctg     1056
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

ccc ccc agc cgg gag gag atg acc aag aac cag gtg tcc ctc acc tgt     1104
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag  tgg gag agc     1152
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

aac ggc cag ccc gag aac aac tac aag acc acc ccc cct gtg ctg gac     1200
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

agc gac ggc agc ttc ttc ctg tac agc aag ctc acc gtg gac aag agc     1248
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  Asp Lys Ser
                405                 410                 415

cgg tgg cag cag ggc aac gtg ttc agc tgc agc gtg atg cac gag gcc     1296
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            42 0                425                 430

ctg cac aac cac tac acc cag aag agc ctg agc ctg agc ccc ggc aag     1344
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 44 5
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<210> 127

<211> 448

<212> PRT

<213> Artificial sequence

<220>

<223> TgG heavy chain of 03 -018

<400> 127

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 Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

```
                180                 185                 190

    Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
5           195                 200                 205

    Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
        210                 215                 220
10
    His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  Pro Ser
    225                 230                 235                 240

15
    Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                    245                 250                 255

20  Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  His Glu Asp Pro
                260                 265                 270

    Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
25          275                 280                 285

    Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  Ser Thr Tyr Arg Val Val
        290                 295                 300
30
    Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
    305                 310                 315                 320

35
    Lys Cys Lys Val Ser Asn Lys Ala  Leu Pro Ala Pro Ile Glu Lys Thr
                    325                 330                 335

40  Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
                340                 345                 350

    Pro Pro Ser Arg Glu Glu  Met Thr Lys Asn Gln Val Ser Leu Thr Cys
45          355                 360                 365

    Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
        370                 375                 380
50
    Asn Gly Gln Pro  Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
    385                 390                 395                 400

55
    Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                    405                 410                 415

60  Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                420                 425                 430
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 128

<211> 642

<212> DNA

<213> Artificial sequence

<220>

<223> IgG light chain of 03-001, 03-002, 03-009, 03-013, 03-014 and 03-018

<220>

<221> CDS

<222> (1)..(642)

<223>

<400> 128

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

gac aga gtc acc atc act tgc cgg gca agt cag agc att agc agc tac 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc 144
Leu Asn Trp Tyr Gln Gln Lys Pro Gly L ys Ala Pro Lys Leu Leu Ile
35 40 45

tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc 192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gaa gat ttt gca act tac tac tgt caa cag agt tac agt acc cct cca 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

acg ttc ggc caa ggg acc aag gtg gag atc aaa cgg acc gtg gcc gct 336
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

ccc agc gtg ttc atc ttc ccc ccc tc c gac gag cag ctg aag agc ggc 384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

acc gcc agc gtg gtg tgc ctg ctg aac aac ttc tac ccc cgg gag gcc 4 32

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

aag gtg cag tgg aag gtg gac aac gcc ctg cag agc ggc aac agc cag 480
Lys Val Gln Trp Lys Val Asp Asn A la Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

gag agc gtg acc gag cag gac agc aag gac tcc acc tac agc ctg agc 528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

agc acc ctc acc ctg agc aag gcc gac tac gag aag cac aag gtg tac 576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

gcc tgc gag gtg acc cac cag ggc ctg agc agc ccc gtg acc aag agc 624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

ttc aac cgg ggc gag tgt 642
Phe Asn Arg Gly Glu Cys
210

<210> 129

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> IgG light chain of 03 -001, 03-002, 03-009, 03-013, 03-014 and 03-018

<400> 129

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 130

<211> 4914

<212> DNA

<213> Artificial sequence

<220>

<223> Vector pDV-C05

<400> 130

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tggggcgcgc ctcagggaac cctggtcacc gtctcgagcg gtacgggcgg ttcaggcgga 180

accggcagcg gcactggcgg gtcgacggaa attgtgctca cacagtctcc agccaccctg 240

tctttgtctc caggggaaag agccaccctc tcctgcaggg ccagtcagag tgttagcagc 300

tacttagcct ggtaccaaca gaaacctggc caggctccca ggctcctcat ctatgatgca 360

tccaacaggg ccactggcat cccagccagg ttcagtggca gtgggtctgg gacagacttc 420

actctcacca tcagcagcct aga gcctgaa gattttgcag tttattactg tcagcagcgt 480

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<210> 131

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuCIgG

<400> 131
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<210> 132

<211> 23

<212> DNA

<213> Artificial sequence

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<223> primer HuVH1B/7A

<400> 132
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<210> 133

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuVH1C

<400> 133
saggtccagc tggtrcagtc tgg 23

<210> 134

<211> 23

<212> DNA

<213> Artificial sequence

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<223> primer HuVH2B

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<223> primer HuVH4B

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caggtgcagc tacagcagtg ggg 23

<210> 138

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<223> primer HuVH4C

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<210> 139

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<223> primer HuVH6A

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<223> primer HuJH1/2

<400> 141
tgaggagacg gtgaccaggg tgcc 24

<210> 142

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<220>

<223> primer HuJH3

<400> 142
tgaagagacg gtgaccattg tccc 24

<210> 143

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<220>

<223> primer HuJH4/5

<400> 143
tgaggagacg gtgaccaggg ttcc 24

<210> 144

<211> 24

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<220>

<223> primer HuJH6

<400> 144
tgaggagacg gtgaccgtgg tccc 24

<210> 145

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<223> primer HuVH1B/7A -NcoI

<400> 145
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<210> 146

<211> 56

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<223> primer HuVH1C -NcoI

<400> 146
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<210> 147

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<223> primer HuVH2B -NcoI

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<210> 148

<211> 56

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<223> primer HuVH3B -NcoI

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<210> 149

<211> 56

<212> DNA

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<223> primer HuVH3C -NcoI

<400> 149
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<210> 150

<211> 56

<212> DNA

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<223> primer HuVH4B -NcoI

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<223> primer HuVH5B -NcoI

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<210> 153

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<223> primer HuVH6A -NcoI

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<210> 154

<211> 36

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<220>

<223> primer HuJH1/2-XhoI

<400> 154
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<210> 155

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuJH3-XhoI

<400> 155
gagtcattct cgactcgaga cggtgaccat tgtccc 36

<210> 156

<211> 36

<212> DNA

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<223> primer HuJH4/5-XhoI

<400> 156
gagtcattct cgactcgaga cggtgaccag ggttcc 36

<210> 157

<211> 36

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<220>

<223> primer HuJH6 - XhoI

<400> 157
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<210> 158

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acactctccc ctgttgaagc tctt 24

<210> 159

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<220>

<223> primer HuClambda2

<400> 159
tgaacattct gtaggggcca ctg 23

<210> 160

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<220>

<223> primer HuClambda7

<400> 160
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<210> 161

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<220>

<223> primer HuVlambda1A

<400> 161
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<210> 162

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<223> primer HuVlambda1B

<400> 162
cagtctgtgy tgacgcagcc gcc 23

<210> 163

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<223> primer HuVlambda1C

<400> 163
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<210> 164

<211> 21

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<213> Artificial sequence

<220>

<223> primer HuVlambda2

<400> 164
cartctgccc tgactcagcc t 21

<210> 165

<211> 23

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<220>

<223> primer HuVlambda3A

<400> 165
tcctatgwgc tgactcagcc acc 23

<210> 166

<211> 23

<212> DNA

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<220>

<223> primer HuVlambda3B

<400> 166
tcttctgagc tgactcagga ccc 23

<210> 167

<211> 23

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<223> primer HuVlambda4

<400> 167
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<210> 168

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<220>

<223> primer HuVlambda5

<400> 168
caggctgtgc tgactcagcc gtc 23

<210> 169

<211> 23

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<223> primer HuVlambda6

<400> 169
aattttatgc tgactcagcc cca 23

<210> 170

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<223> primer HuVlambda7/8

<400> 170
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<210> 171

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<223> primer HuVlambda9

<400> 171
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<210> 172

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<223> primer HuVkappa1B

<400> 172
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<210> 173

<211> 23

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<223> primer HuVkappa2

<400> 173
gatgttgtga tgactcagtc tcc 23

<210> 174

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<223> primer HuVkappa3

<400> 174
gaaattgtgw tgacrcagtc tcc 23

<210> 175

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<223> primer HuVkappa4

<400> 175
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<210> 176

<211> 23

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<223> primer HuVkappa5

<400> 176
gaaacgacac tcacgcagtc tcc 23

<210> 177

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuVkappa6

<400> 177
gaaattgtgc tgactcagt c tcc 23

<210> 178

<211> 24

<212> DNA

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<220>

<223> primer HuJlambda1

<400> 178
acctaggacg gtgaccttgg tccc 24

<210> 179

<211> 24

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<223> primer HuJlambda2/3

<400> 179
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<210> 180

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<223> primer HuJlambda4/5

<400> 180
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<210> 181

<211> 24

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<223> primer HuJkappa1

<400> 181
acgtttgatt tccaccttgg tccc 24

<210> 182

<211> 24

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<223> primer HuJkappa2

<400> 182
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<210> 183

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<223> primer HuJkappa3

<400> 183
acgtttgata tccactttgg tccc 24

<210> 184

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<223> primer HuJkappa4

<400> 184
acgtttgatc tccaccttgg tccc 24

<210> 185

<211> 24

<212> DNA

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<223> primer HuJkappa5

<400> 185
acgtttaatc tccagtcgtg tccc 24

<210> 186

<211> 41

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<223> primer HuVkappa1B -SalI

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<210> 187

<211> 41

<212> DNA

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<223> primer HuVkappa2 -SalI

<400> 187
tgagcacaca ggtcgacgga tgttgtgatg actcagtctc c 41

<210> 188

<211> 41

<212> DNA

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<220>

<223> primer HuVkappa3B -SalI

<400> 188
tgagcacaca ggtcgacgga aattgtgwt g acrcagtctc c 41

<210> 189

<211> 41

<212> DNA

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<223> primer HuVkappa4B -SalI

<400> 189
tgagcacaca ggtcgacgga tattgtgatg acccacactc c 41

<210> 190

<211> 41

<212> DNA

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<223> primer HuVkappa5 -SalI

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tgagcacaca ggtcgacgga aacgacactc acgcagtctc c 41

<210> 191

<211> 41

<212> DNA

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<220>

<223> primer HuVka ppa6-SalI

<400> 191
tgagcacaca ggtcgacgga aattgtgctg actcagtctc c 41

<210> 192

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuJkappa1 -NotI

<400> 192
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<210> 193

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuJkappa2 -NotI

<400> 193
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<210> 194

<211> 48

<212> DNA

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<223> primer HuJkappa3 -NotI

<400> 194
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<210> 195

<211> 48

<212> DNA

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<223> primer HuJkappa4 -NotI

<400> 195
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<210> 196

<211> 48

<212> DNA

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<223> primer HuJkappa5 -NotI

<400> 196
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<210> 197

<211> 41

<212> DNA

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<223> primer HuVlambda1A -SalI

<400> 197
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<210> 198

<211> 41

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<223> primer HuVlambda1B -SalI

<400> 198
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<210> 199

<211> 41

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<223> primer HuVlambda1C -SalI

<400> 199
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<210> 200

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<212> DNA

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<223> primer HuVlambda2 -SalI

<400> 200
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<210> 201

<211> 41

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<223> primer HuVlambda3A -SalI

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<210> 202

<211> 41

<212> DNA

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<223> primer HuVlambda3B -SalI

<400> 202
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<210> 203

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<212> DNA

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<223> primer HuVlambda4 -SalI

<400> 203
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<210> 204

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<212> DNA

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<223> primer HuVlambda5 -SalI

<400> 204
tgagcacaca ggtcgacgca ggctgtgctg actcagccgt c 41

<210> 205

<211> 41

<212> DNA

<213> Artificial sequence

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<223> primer HuVlambda6 -SalI

<400> 205
tgagcacaca ggtcgacgaa ttttatgctg actcagcccc a 41

<210> 206

<211> 41

<212> DNA

<213> Artificial sequence

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<223> primer HuVlambda7/8 -SalI

<400> 206
tgagcacaca ggtcgacgca grctgtggtg acycaggagc c 41

<210> 207

<211> 41

<212> DNA

<213> Artificial sequence

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<223> primer HuVlambda9 -SalI

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<210> 208

<211> 48

<212> DNA

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<220>

<223> primer HuJlambda1 -NotI

<400> 208
gagtcattct cgacttgcgg ccgcacctag gacggtgacc ttggtccc 48

<210> 209

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuJlambda2/3 -NotI

<400> 209
gagtcattct cgacttgcgg ccgcacctag gacggtcagc ttggtccc 48

<210> 210

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> primer HuJlambda4/5-NotI

<400> 210
gagtcattct cgacttgcgg ccgcacytaa aacggtgagc tgggtccc 48

<210> 211

<211> 753

<212> DNA

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<223> SC03-019

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<222> (1)..(753)

<223>

<400> 211

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Ala Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
1               5                   10                  15

cct ggg agg tcc ctg aga ctc tcc  tgt gca gcc tct gga ttc acc ttc      96
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt ggc tat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg       144
Ser Gly Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca       192
Glu Trp Val Ala Val Ile Ser Tyr  Asp Gly Ser Asn Lys Tyr Tyr Ala
    50                  55                  60

gac tcc gtg aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac       240
Asp Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80
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acg ctg tat ctg caa atg aac agc ctg aga gct gag gac acg gct gtg      288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                85                  90                  95

tat tac tgt gcg aga ttc cct ggt ggt acc aga agc cgc ggc tac atg      336
Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met
            100                 105                 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcg agc ggt acg ggc      384
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly
        115                 120                 125

ggt tca ggc gga acc ggc agc  ggc act ggc ggg tcg acg gaa att gtg      432
Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Glu Ile Val
    130                 135                 140

ctc aca cag tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc      480
Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160

acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg      528
Thr Leu Ser Cys Arg Ala Ser  Gln Ser Val Ser Ser Tyr Leu Ala Trp
                165                 170                 175

tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca      576
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
            180                 185                 190

tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct      624
Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

ggg aca gac ttc act ctc acc atc agc agc cta gag cct gaa gat ttt      672
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc      720
Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly
225                 230                 235                 240

gga ggg acc aag gtg gag  atc aaa cgt gcg gcc                        753
Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
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<211> 251

<212> PRT

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<223> SC03-019

<400> 212

Ala Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln

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Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30
Ser Gly Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
    50                  55                  60
Asp Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                85                  90                  95
Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met
            100                 105                 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly T hr Gly
        115                 120                 125
Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Glu Ile Val
    130                 135                 140
Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro G ly Glu Arg Ala
145                 150                 155                 160
Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp
                165                 170                 175
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg L eu Leu Ile Tyr Asp Ala
            180                 185                 190
Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205
Gly Thr Asp Phe Thr Leu Thr Ile S er Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220
Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly
225                 230                 235                 240
Gly Gly Thr Lys Val Glu I le Lys Arg Ala Ala
                245                 250
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<212> DNA

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<223> SC03-020

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<221> CDS

<222> (1)..(762)

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1               5                   10                  15

ccg ggg gag tct ctg aag atc tct tgt aag ggt tct gga tac ggc ttt       96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gl n Met Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg      336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg  agc ggt acg ggc ggt tca ggc      384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag      43 2
Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac      480
Ser Pro Asp Ser Leu Ala Val Ser Le u Gly Glu Arg Ala Thr Ile Asn
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145 150 155 160

tgc aag tcc agc cag aaa att tta cac agc tcc aac aat aag aac tac 528
Cys Lys Ser Ser Gln Lys Ile Leu His Ser Ser Asn Asn Lys Asn Tyr
165 170 175

tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att 576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
180 185 190

tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc 624
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

agc ggg tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct 672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
210 215 220

gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act cct ccg 720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro
225 230 235 240

gtt ttc ggc gga ggg acc aag gtg gaa atc aaa cgt gcg gcc 762
Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 214

<211> 254

<212> PRT

<213> Artificial sequence

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<223> SC03-020

<400> 214

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

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

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

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser Gln Lys Ile Leu His Ser Ser Asn Asn Lys Asn Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro
225 230 235 240

Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 215

<211> 762

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-021

<220>

<221> CDS

<222> (1)..(762)

<223>

<400> 215

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gcc atg gcc cag gtc cag ctg gta cag tct gga aca gag gtg aa a aag       48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys
1               5                   10                  15

ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt       96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys G ly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg gg g ggt tcg ggg att tct acc cct atg gac gtc tgg      336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc gg t tca ggc      384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag      432
Gly Thr Gly Ser G ly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac      480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala T hr Ile Asn
145                 150                 155                 160

tgc aag tcc agc cag agt gtt tta cac agc tcc aac aat aag aac tac      528
Cys Lys Ser Ser Gln Ser Val Leu His Ser Ser Asn Asn Lys Asn Tyr
                165                 170                 175

cta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att      576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

tac tgg gca tct acc cgg caa tcc ggg gtc cct gac cga ttc agt ggc      624
Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

agc ggg tct gg g aca gat ttc act ctc acc atc agc agc ctg cag gct      672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
    210                 215                 220
```

gaa gat gtg gca gtt tat tac tgt cag caa tat tat ag t act cct ccg 720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro
225 230 235 240

acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt gcg gcc 762
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 216

<211> 254

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-021

<400> 216

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

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

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

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser Gln Ser Val Leu His Ser Ser Asn Asn Lys Asn Tyr
165 170 175

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

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro
225 230 235 240

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 217

<211> 762

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-022

<220>

<221> CDS

<222> (1)..(762)

<223>

<400> 217

gcc atg gcc cag atg cag ctg gtg caa tct gga aca gag gtg aaa aag 48
Ala Met Ala Gln Met Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys
1 5 10 15

ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt 96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg 144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

```
gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att t ct acc cct atg gac gtc tgg      336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc      384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag      432
Gly Thr Gly Ser Gly Thr Gly Gly Ser  Thr Asp Ile Gln Leu Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac      480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145                 150                 155                 160

tgc aag tcc agc cag agt gtt tta tac agc tcc atc aat aag aac tac      528
Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Ile Asn Lys Asn Tyr
                165                 170                 175

tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att      576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc      624
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

agc ggg tct ggg aca gat ttc act c tc acc atc agc agc ctg cag gct      672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
    210                 215                 220

gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac       720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
225                 230                 235                 240

act ttt ggc cag ggg acc aag gtg gaa atc aaa cgt gcg gcc               762
Thr Phe Gly Gln Gly Thr Lys Val  Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 218

<211> 254

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-022

<400> 218

Ala Met Ala Gln Met Gln Leu Val Gln Se r Gly Thr Glu Val Lys Lys
1 5 10 15

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Tle Thr Tyr Trp Tle Gly Trp Va l Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

Pro Ser Phe Gln Gly Gl n Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65 70 75 80

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Al a Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Ile Asn Lys Asn Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr

225 230 235 240

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 219

<211> 780

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-023

<220>

<221> CDS

<222> (1)..(780)

<223>

<400> 219

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gcc atg gcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag       48
Ala Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
1               5                   10                  15

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tct ttc       96
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser  Phe
            20                  25                  30

agt ggt ttc tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg      144
Ser Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg      192
Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
    50                  55                  60

tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag      240
Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
65                  70                  75                  80

ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat      288
Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gcg aga agg gtg gag gta gta gag tac cag ctg ctc  cgt ccc      336
Tyr Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro
            100                 105                 110

cga tat aaa agt tgg ttc gac ccc tgg ggc cag ggc acc ctg gtc acc      384
Arg Tyr Lys Ser Trp  Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
        115                 120                 125
```

gtc tcg agc ggt acg ggc ggt tca ggc gga acc ggc agc ggc act ggc 432
Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly
130 135 140

ggg tcg acg cag tct gcc ctg act cag cct cgc tca gtg tcc ggg tct 480
Gly Ser Thr Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser
145 150 155 160

cct gga cag tca gtc acc atc tcc tgc act gga tcc agc agt act gtt 528
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Thr Val
165 170 175

ggt ggt tat aac tat gtc tcc tgg tac caa cag cac cca ggc aaa gcc 576
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
180 185 190

ccc aaa ctc atg att tat gat gtc agt aag cgg ccc tca ggg gtt tct 624
Pro Lys Leu Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser
195 200 205

aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc 672
Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
210 215 220

tct ggg ctc cag gct gag gac gag gct gat tat tac tgc agc tca tat 720
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr
225 230 235 240

aca agc agc agc act tat gtc ttc gga act ggg acc aag gtc acc gtc 768
Thr Ser Ser Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val
245 250 255

cta ggt gcg gcc 780
Leu Gly Ala Ala
260

<210> 220

<211> 260

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-023

<400> 220

Ala Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
1 5 10 15

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

Ser Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu

35 40 45

Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
50 55 60

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

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro
100 105 110

Arg Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
115 120 125

Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr G ly
130 135 140

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

Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Ser Ser S er Thr Val
165 170 175

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
180 185 190

Pro Lys Leu Met Ile Tyr Asp Val Ser Lys Arg P ro Ser Gly Val Ser
195 200 205

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
210 215 220

Ser Gly Leu Gln Ala Glu Asp Glu Ala A sp Tyr Tyr Cys Ser Ser Tyr
225 230 235 240

Thr Ser Ser Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val
245 250 255

Leu Gly Ala Ala
260

<210> 221

<211> 753

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-024

<220>

<221> CDS

<222> (1)..(753)

<223>

<400> 221

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gcc atg gcc cag gtg cag ctg gtg gag tct ggg tct gag ttg aag atc       48
Ala Met Ala Gln Val Gln Le u Val Glu Ser Gly Ser Glu Leu Lys Ile
1               5                   10                  15

cct ggg gcc tca gtg aag gtt tcc tgc aag gct act gga tac acc ttc       96
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Thr Gly Tyr Thr Ph e
            20                  25                  30

act cgt tat tct ctg aat tgg gtg cgg cag gcc cct gga caa ggg ctt      144
Thr Arg Tyr Ser Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        35                  40                  45

gag tgg gtg ggg tgg att aac acc cag act gga aac tca aac tat ggc      192
Glu Trp Val Gly Trp Ile Asn Thr Gln Thr Gly Asn Ser Asn Tyr Gly
    50                  55                  60

cag gcc ttc tca gga cgg ttt gtc ttc tcc ttg gac acc tca gtc agc      240
Gln Ala Phe Ser Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
65                  70                  75                  80

acg gca tat ttg caa atc  agc agc cta cag gcc gag gac act gcc aca      288
Thr Ala Tyr Leu Gln Ile Ser Ser Leu Gln Ala Glu Asp Thr Ala Thr
                85                  90                  95

tac tac tgt gcg agg aag agt gcg ggt tcg aat gct ttc gac att  tgg      336
Tyr Tyr Cys Ala Arg Lys Ser Ala Gly Ser Asn Ala Phe Asp Ile Trp
            100                 105                 110

ggc caa ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc      384
Gly Gln Gly Thr Met Va l Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg cag tct gtc gtg acg cag      432
Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Gln Ser Val Val Th r Gln
    130                 135                 140

ccg ccc tca gtg tct gcg gcc cca gga cag aag gcc acc atc tcc tgc      480
Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Ala Thr Ile Ser Cys
145                 1 50                155                 160

tct gga agc agc tcc aac att ggg aat aat tat gta tcc tgg tac cag      528
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln
```

165 170 1 75

cag ctc cca gga aca gcc ccc aaa ctc ctc att tat gac aat aat aag 576
Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn Lys
180 185 190

cga ccc tca ggg att cct aac cga ttc tct ggc tcc aag tct ggc acg 624
Arg Pro Ser Gly Ile Pro Asn Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

tca gcc acc ctg ggc atc acc gga ctc cag act ggg gac gag gcc gat 672
Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp
210 215 220

tat tac tgc gga aca tgg gat agc agc ctg agt gct tat gtc ttc gga 720
Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu Ser Ala Tyr Val Phe Gly
225 230 235 240

act ggg acc aag gtc acc gtc cta ggt gcg gcc 753
Thr Gly Thr Lys Val Thr Val Leu Gly Ala Ala
245 250

<210> 222

<211> 251

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-024

<400> 222

Ala Met Ala Gln Val Gln Leu Val Glu Ser Gly Ser Glu Leu Lys Ile
1 5 10 15

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

Thr Arg Tyr Ser Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
35 40 45

Glu Trp Val Gly Trp Ile Asn Thr Gln Thr Gly Asn Ser Asn Tyr Gly
50 55 60

Gln Ala Phe Ser Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
65 70 75 80

Thr Ala Tyr Leu Gln Ile Ser Ser Leu Gln Ala Glu Asp Thr Ala Thr
85 90 95

Tyr Tyr Cys Ala Arg Lys Ser Ala Gly Ser Asn Ala Phe Asp Ile Trp
100 105 110

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

Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Gln Ser Val Val Thr Gln
130 135 140

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

Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln
165 170 175

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

Arg Pro Ser Gly Ile Pro Asn Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu Ser Ala Tyr Val Phe Gly
225 230 235 240

Thr Gly Thr Lys Val Thr Val Leu Gly Ala Ala
245 250

<210> 223

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-025

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 223

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gcc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag        48
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc        96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg       144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca       192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc ac c atc tcc aga gac aat tcc aag aac       240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg        288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa       336
Tyr Tyr Cys Ala Arg Thr Thr A sn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc       384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca       432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag       480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct       528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gg a cag cct cct aag ctg ctc att tac tgg       576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct atc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc gg g       624
Ala Ser Ile Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat       672
Ser Gly Thr Asp Phe Thr L eu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat aat att ccg tat gct ttc       720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Ile Pro Tyr Ala P he
225                 230                 235                 240
```

ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc 756
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 224

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-025

<400> 224

Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

Ala Ser Ile Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

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

Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Ile Pro Tyr Ala Phe
225 230 235 240

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 225

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-026

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 225

gcc atg gcc cag gtc cag ctg gta cag tct ggg gga ggc ttg gtc cag 48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agt agt tat gcc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gaa tat gtt tca ggt att agt a gt aat ggg ggt agc aca tat tat gca 192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac 240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75 80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg 288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
85 90 95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa 336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
100 105 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc 384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
115 120 125

ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tct cca 432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag 480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

tcc agc cag agt att tta tac agc tcc aac agt aag aac tac tta ggt 528
Ser Ser Gln Ser Ile Leu Tyr Ser Ser Asn Ser Lys Asn Tyr Leu Gly
165 170 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg 576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
180 185 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg 624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat 672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
210 215 220

gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac agt ttt 720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
225 230 235 240

ggc cag ggg acc aag gtg gag atc aaa cgt gcg gcc 756
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 226

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-026

<400> 226

```
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Ile Leu Tyr Ser Ser Asn Ser Lys Asn Tyr Leu Gly
                165                 170                 175

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

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

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

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

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
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245 250

<210> 227

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-027

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 227

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gcc atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag        48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc        96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg  gtc cgc cag gct cca ggg aag gga ctg       144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca       192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac       240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg       288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa       336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc       384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tct cca       432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140
```

```
gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac agt ttt      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
225                 230                 235                 240

ggc cag ggg acc aaa gtg gat atc aaa cgt gcg gcc                      756
Gly Gln Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
                245                 250
```

<210> 228

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-027

<400> 228

```
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala A la Ser Gly Phe Thr Phe
            20                  25                  30

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

Glu Tyr Val Ser Gly Ile Ser Ser A sn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
```

65 70 75 80

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
245 250

<210> 229

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-029

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 229

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gcc atg gcc gaa gtg cag ctg gtg cag tct ggg gga ggc ttg gtt cag       48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

ccg ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Se r Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys As n
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc  aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Le u Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ty r Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
```

210 215 220

gtg gca gtt tat tac tgt cag caa tat tat agt act cct ctc act ttc 720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
225 230 235 240

ggc gca ggg acc aag ctg gag atc aaa cgt gcg gcc 756
Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 230

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-029

<400> 230

Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 231

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-030

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 231
gcc atg gcg gag gtc cag gt g gta cag tct gga gga ggc ttg gtc cag 48
Ala Met Ala Glu Val Gln Val Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggg ggg tcc ctc aaa ctc tcc tgt gca gcc tct gga ttc acc tt c 96
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 144
Ser Ser Tyr Ala Met His T rp Val Arg Gln Ala Pro Gly Lys Gly Leu

```
          35                  40                  45

    gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
    Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr A la
5       50                  55                  60

    aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
    Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    65                  70                  75                  80
10
    acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
    Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

15  tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
    Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

    ggg aca atg gtc acc gt c tcg agc ggt acg ggc ggt tca ggc gga acc      384
20  Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

    ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tc t cca      432
    Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
25      130                 135                 140

    gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
    Asp Ser Leu Ala Val S er Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
    145                 150                 155                 160
30
    tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
    Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr L eu Ala
                165                 170                 175

35  tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
    Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

    gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
40  Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

    tct ggg aca gat ttt act ctc acc atc agc agt ctg cag gct gaa gat      672
    Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
45      210                 215                 220

    gtg gca gtt tat ta c tgt cag caa tat tat agt act cct ctg acg ttc      720
    Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
    225                 230                 235                 240
50
    ggc caa ggg acc aag gtg gaa atc aaa cgt gcg gcc                       756
    Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
                245                 250

55
    <210>  232

    <211>  252

60  <212>  PRT

    <213>  Artificial sequence
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<220>

<223> SC03-030

<400> 232

```
Ala Met Ala Glu Val Gln Val Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

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

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

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

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

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 233

<211> 759

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-031

<220>

<221> CDS

<222> (1)..(759)

<223>

<400> 233

gcc atg gcc cag gtg cag ctg gtg caa tct ggg gct gac gtg aag a ag 48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Asp Val Lys Lys
1 5 10 15

cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga ggc acg ttc 96
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Gly Thr Phe
20 25 30

agc agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt 144
Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
35 40 45

gag tgg atg gga agg atc atc cct atc ctt ggt ata aca aac tac gca 192
Glu Trp Met Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
50 55 60

cag aag ttc cag ggc aga gtc aca att acc gcg gac aaa tcc acg ggc 240
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Gly
65 70 75 80

aca ggc aac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 288
Thr Gly Asn Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
85 90 95

tat tac tgt gcg aga g aa tcg ggt ggt ggc tac gat aac cac ttt gac 336
Tyr Tyr Cys Ala Arg Glu Ser Gly Gly Gly Tyr Asp Asn His Phe Asp
100 105 110

tac tgg ggc cag gga acc ctg gtc acc gtc tcg agc ggt acg g gc ggt 384

```
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Thr Gly Gly
        115                 120                 125

tca ggc gga acc ggc agc ggc act ggc ggg tcg acg cag tct gtg ctg      432
Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Gln Ser Val Leu
    130                 135                 140

acg cag ccg ccc tca gcg tct ggg acc ccc gga cag agg gtc acc atc      480
Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile
145                 150                 155                 160

tct tgt tct gga ggc agc tcc aac atc gga agt aat act gta aac tgg      528
Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ser Asn Thr Val Asn Trp
                165                 170                 175

tac cag caa ctc cca gga acg gcc ccc aaa ctc gtc atc tat gct aat      576
Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val Ile Tyr Ala Asn
            180                 185                 190

aat cag cgg ccc tca ggg gtc cct gac cga ttc tct gcc tcc aag tct      624
Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Ala Ser Lys Ser
        195                 200                 205

ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag gat gag      672
Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu
    210                 215                 220

gct gat tat tac tgt gca gct tgg gat gac agc ctg act g gt gga gtg      720
Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Thr Gly Gly Val
225                 230                 235                 240

ttc ggc gga ggg acc cag ctc acc gtt tta agt gcg gcc                  759
Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Ser Ala Ala
                245                 250
```

<210> 234

<211> 253

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-031

<400> 234

```
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Asp Val Lys Lys
1               5                   10                  15

Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Gly Thr Phe
            20                  25                  30

Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        35                  40                  45
```

Glu Trp Met Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
50 55 60

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

Thr Gly Asn Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Thr Gly Gly
115 120 125

Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Gln Ser Val Leu
130 135 140

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

Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ser Asn Thr Val Asn Trp
165 170 175

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

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

Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu
210 215 220

Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Thr Gly Gly Val
225 230 235 240

Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Ser Ala Ala
245 2 50

<210> 235

<211> 771

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-032

<220>

<221> CDS

<222> (1)..(771)

<223>

<400> 235

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gcc atg gcc gag gtg cag ctg gtg gag tct ggg gct gag gtg aag aag       48
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys
1               5                  10                  15

cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc       96
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  Gly Thr Phe
            20                  25                  30

agc agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt      144
Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        35                  40                  45

gag tgg atg gga aag atc atc cct att ctt ggt aaa gtc act tac gca      192
Glu Trp Met Gly Lys Ile Ile Pro Ile Leu Gly Lys Val Thr Tyr Ala
    50                  55                  60

cag aag ttc cag gcc aga gtc acg att acc gcg gac gaa tcc acg agc      240
Gln Lys Phe Gln Ala Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
65                  70                  75                  80

aca gcc tac ctg gag ctg agc agc ctg aga tct gag gac acg gcc gtt      288
Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
                85                  90                  95

ttt tac tgt gcg aga gac ggc tgg gat ttg act ggt  tct ttt tta ggc      336
Phe Tyr Cys Ala Arg Asp Gly Trp Asp Leu Thr Gly Ser Phe Leu Gly
            100                 105                 110

tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcg agc      384
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

ggt acg ggc ggt tca ggc gga acc ggc agc ggc act ggc ggg tcg acg      432
Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr  Gly Gly Ser Thr
    130                 135                 140

cag tct gtc gtg acg cag ccg ccc tca gcg tct ggg acc ccc ggg cag      480
Gln Ser Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
145                 150                 155                 160

agg gtc acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat      528
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
                165                 170                 175

act gta agc tgg tac cag cag gtt cca ggg acg gcc ccc aag ctc ctc      576
Thr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
            180                 185                 190
```

atc tat agg aat aat cag cgg ccc cca ggg gtc cyt gac cga ttc tct 624
Ile Tyr Arg Asn Asn Gln Arg Pro Pro Gly Val Xaa Asp Arg Phe Ser
195 200 205

ggc tcc aag tct ggc acc tca gcc tcc ytg gcc atc agt ggg ctc cag 672
Gly Ser Lys Ser Gly Thr Ser Ala Ser Xaa Ala Ile Ser Gly Leu Gln
210 215 220

tct gac gat gag gcc ttt tat tac tgt gca gca tgg gat ggc agc mtg 720
Ser Asp Asp Glu Ala Phe Tyr Tyr Cys Ala Ala Trp Asp Gly Ser Xaa
225 230 235 240

aat ggt ctg gcc ttc ggc gga ggg acc aag ctg acc gtc cta ggt gcg 768
Asn Gly Leu Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
245 250 255

gcc 771
Ala

<210> 236

<211> 257

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> (204)..(204)

<223> The 'Xaa' at location 204 stands for Pro, or Leu.

<220>

<221> misc_feature

<222> (218)..(218)

<223> The 'Xaa' at location 218 stands for Leu.

<220>

<221> misc_feature

<222> (240)..(240)

<223> The 'Xaa' at location 240 stands for Met, or Leu.

<220>

<223> SC03-032

<400> 236

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

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

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

Glu Trp Met Gly Lys Ile Ile Pro Ile Leu Gly Lys Val Thr Tyr Ala
50 55 60

Gln Lys Phe Gln Ala Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
65 70 75 80

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

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

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

Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr
130 135 140

Gln Ser Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
145 150 155 160

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
165 170 175

Thr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
180 185 190

Ile Tyr Arg Asn Asn Gln Arg Pro Pro Gly Val Xaa Asp Arg Phe Ser
195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Xaa Ala Ile Ser Gly Leu Gln
210 215 220

Ser Asp Asp Glu Ala Phe Tyr Tyr Cys Ala Ala Trp Asp Gly Ser Xaa
225 230 235 240

Asn Gly Leu Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
245 250 255

Ala

<210> 237

<211> 765

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-033

<220>

<221> CDS

<222> (1)..(765)

<223>

<400> 237

```
gcc atg gcc cag gtc cag ctg gta cag tct gga aca gag gtg  aaa aag       48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys
1               5                   10                  15

ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt       96
Pro Gly Glu Ser Le u Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Ly s Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg      336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc  ggt tca ggc      384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag      432
Gly Thr Gly Se r Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln
    130                 135                 140
```

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac 480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Al a Thr Ile Asn
145 150 155 160

tgc aag acc agc cac aat att ttc tcc aga tcc aac aat aag gac tac 528
Cys Lys Thr Ser His Asn Ile Phe Ser Arg Ser Asn Asn Lys Asp Tyr
165 170 175

tta gct tgg tac cag cag aaa cca ggc cag cct ccc aga tta ctc att 576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile
180 185 190

tac tgg gcg tct acc cgg gca tcc ggg gtc cct gaa cga ttc agt ggc 624
Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val Pro Glu Arg Phe Ser Gly
195 200 205

agc ggc tct ggg aca gac ttc agt ctc acc atc agc agc ctg cag gct 672
Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Ala
210 215 220

gaa gat gtg gcg gtt tat tac tgt cag caa tat tat agt tcc cct atg 720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Ser Pro Met
225 230 235 240

tac agt ttt ggc cag ggg acc aag gtg gag atc aaa cgt gcg gcc 765
Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250 255

<210> 238

<211> 255

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-033

<400> 238

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

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn

65 70 75 80

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Thr Ser His Asn Ile Phe Ser Arg Ser Asn Asn Lys Asp Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val Pro Glu Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Ser Pro Met
225 230 235 240

Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250 255

<210> 239

<211> 762

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-034

<220>

<221> CDS

<222> (1)..(762)

<223>

<400> 239

```
gcc atg gcc gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag        48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1               5                  10                  15

ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt        96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg       144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc       192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac       240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata       288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tc g ggg att tct acc cct atg gac gtc tgg       336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca gg c       384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag       432
Gly Thr Gly Ser Gly Thr G ly Gly Ser Thr Asp Val Val Met Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac       480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile A sn
145                 150                 155                 160

tgc aag tcc agc cag agt att tta aac aga tcc aac aat aag aac tac       528
Cys Lys Ser Ser Gln Ser Ile Leu Asn Arg Ser Asn Asn Lys Asn Tyr
                165                 170                 175

tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att       576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc       624
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

agc ggg tct ggg aca ga t ttc aat ctc acc atc agc agc ctg cag gct       672
Ser Gly Ser Gly Thr Asp Phe Asn Leu Thr Ile Ser Ser Leu Gln Ala
```

210 215 220

gag gat gtg gca gtt tat tac tgt cag cag tat aat aac tgg cc t ctc 720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
225 230 235 240

act ttc ggc gga ggg acc aaa gtg gat atc aaa cgt gcg gcc 762
Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
245 250

<210> 240

<211> 254

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-034

<400> 240

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

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

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

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser Gln Ser Ile Leu Asn Arg Ser Asn Asn Lys Asn Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
245 25 0

<210> 241

<211> 765

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-035

<220>

<221> CDS

<222> (1)..(765)

<223>

<400> 241

gcc atg gcc gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag 48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10 15

ccc ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt 96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg 144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu

```
          35                  40                  45

    gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
    Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
 5      50                  55                  60

    ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
    Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
    65                  70                  75                  80
10
    acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
    Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

15  tat tac tgt gcg ggg ggt tcg ggg att tct acc c ct atg gac gtc tgg      336
    Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

    ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc      384
20  Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

    gga acc ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag      432
    Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp  Ile Gln Met Thr Gln
25      130                 135                 140

    tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac      480
    Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
    145                 150                 155                 160
30
    tgc aag tcc agt cag agt gtt tta tac agc tcc aac aat aag aac tac      528
    Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
                165                 170                 175

35  tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att      576
    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

    tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc      624
40  Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

    agc ggg tct ggg aca gat ttc act ctc acc a tc agc agc ctg cag gct      672
    Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
45      210                 215                 220

    gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccc ctg      720
    Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu
    225                 230                 235                 240
50
    tac agt ttt ggc cag ggg acc aag gtg gag atc aaa cct gcg gcc          765
    Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu  Ile Lys Pro Ala Ala
                245                 250                 255

55
    <210>  242

    <211>  255

60  <212>  PRT

    <213>  Artificial sequence
```

<220>

<223> SC03-035

<400> 242

Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Al a Glu Val Lys Lys
1 5 10 15

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gl n Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

Pro Ser Phe Gln Gly Gln Val Th r Ile Ser Ala Asp Lys Ser Ile Asn
65 70 75 80

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gl y Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu
225 230 235 240

Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Pro Ala Ala
245 250 255

<210> 243

<211> 759

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-036

<220>

<221> CDS

<222> (1)..(759)

<223>

<400> 243

```
gcc atg gcc gag gtg cag ctg gtg cag tct gga aca gag gtg aaa aag       48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys
1               5                   10                  15

ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt       96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac  gtc tgg      336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc      384
```

```
Gly Gln Gly Thr Thr  Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag      432
Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met  Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac      480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145                 150                 155                 160

tgc aag tcc agc cag agt gtt tta cac agc ccc aac aat aag aac tac      528
Cys Lys Ser Ser Gln Ser Val Leu His Ser Pro Asn Asn Lys Asn Tyr
                165                 170                 175

ttg gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att      576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc      624
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

agc ggg tct ggg aca gat ttc act ctc acc atc agc agc  ctg cag gct      672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
    210                 215                 220

gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act aac agt      720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Asn Ser
225                 230                 235                 240

ttt ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc                  759
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 244

<211> 253

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-036

<400> 244

```
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val L ys Lys
1               5                   10                  15

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro G ly Lys Gly Leu
        35                  40                  45
```

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser A la Asp Lys Ser Ile Asn
65 70 75 80

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gly Ser Gly I le Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser G ln Ser Val Leu His Ser Pro Asn Asn Lys Asn Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Asn Ser
225 230 235 240

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 245

<211> 744

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-037

<220>

<221> CDS

<222> (1)..(744)

<223>

<400> 245

```
gcc atg gcc aaa gtg cag ctg gtg cag tct gga gga ggc ttg atc cag       48
Ala Met Ala Lys Val Gln Leu Val Gln Ser Gly Gly Gl y Leu Ile Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc gtc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val
            20                  25                  30

agt agc aac tac atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg      144
Ser Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  4 5

gag tgg gtc tca att gtt ttt agc ggt ggt agc aca tac tac gca gac      192
Glu Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
    50                  55                  60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg aac agc ctg aga gcc gag gac  acg gcc gta tat      288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

tat tgt gcg aga gat gcc cac cgg ggg ttc ggt atg gac gtc tgg ggc      336
Tyr Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga      384
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gl y Gly Ser Gly Gly
        115                 120                 125

acc ggc agc ggc act ggc ggg tcg acg tct tct gag ctg act cag gac      432
Thr Gly Ser Gly Thr Gly Gly Ser Thr Ser Ser Glu Leu Thr Gln Asp
    130                 135                 140

cct gct gtg tct gtg gcc ttg gga cag aca gtc agg atc aca tgc caa      480
Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln
145                 150                 155                 160

gga gac agc ctc aga agc tat tat gca agc tgg tac cag cag aag cca      528
Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro
                165                 170                 175

gga cag gcc cct gta ctt gtc atc tat ggc aaa aac aac cgg ccc tca      576
Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
            180                 185                 190
```

ggg atc cca gac cgg ttc tct ggc tcc agc tca gga aac aca gct tcc 624
Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser
195 200 205

ttg acc atc act ggg gct cag gcg gaa gat gag gcc gac tat tat tgt 672
Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

aac ggc cgg gac agc agt ggt aac cat tgg gtg ttc ggc gga ggg acc 720
Asn Gly Arg Asp Ser Ser Gly Asn His Trp Va l Phe Gly Gly Gly Thr
225 230 235 240

aag ctg acc gtc cta ggt gcg gcc 744
Lys Leu Thr Val Leu Gly Ala Ala
245

<210> 246

<211> 248

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-037

<400> 246

Ala Met Ala Lys Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln
1 5 10 15

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

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

Glu Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly
100 105 110

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

Thr Gly Ser Gly Thr Gly Gly Ser Thr Ser Ser Glu Leu Thr Gln Asp
130 135 140

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

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

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser
195 200 205

Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

Asn Gly Arg Asp Ser Ser Gly Asn His Trp Val Phe Gly Gly Gly Thr
225 230 235 240

Lys Leu Thr Val Leu Gly Ala Ala
245

<210> 247

<211> 744

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-038

<220>

<221> CDS

<222> (1)..(744)

<223>

<400> 247
gcc atg gcc gag gtg cag ctg gtg cag tct gga gga ggc ttg atc cag 48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln
1 5 10 15

```
cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct ggg ttc acc gtc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val
            20                  25                  30

agt agc aac tac atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg      144
Ser Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtc tca att gtt ttt agc ggt ggt ag c aca tac tac gca gac      192
Glu Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
    50                  55                  60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg aac agc ctg aga gcc gag gac acg gcc gta tat      288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala G lu Asp Thr Ala Val Tyr
                85                  90                  95

tat tgt gcg aga gat gcc cat cgg ggg ttc ggt atg gac gtc tgg ggc      336
Tyr Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly
            100                 105                 110

cag ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga      384
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly
        115                 120                 125

acc ggc agc ggc act ggc ggg tcg acg tct tct gag ctg act cag gac      432
Thr Gly Ser Gly Thr Gly Gly Ser Thr Ser Ser Glu Leu Thr Gln Asp
    130                 135                 140

cct gct gtg tct gtg gcc ttg gga cag aca gtc agg atc aca tgc caa      480
Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln
145                 150                 155                 160

gga gac agc ctc aga agc tat tat gca ag c tgg tac cag cag aag cca      528
Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro
                165                 170                 175

gga cag gcc cct gta ctt gtc atc tat ggt aaa aac aac cgg ccc tca      576
Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
            180                 185                 190

ggg atc cca gac cga ttc tct ggc tcc agc tca gga gac aca gct tcc      624
Gly Ile Pro Asp Arg Phe Ser Gly Ser S er Ser Gly Asp Thr Ala Ser
        195                 200                 205

ttg acc atc act ggg gct cag gcg gaa gat gag gct gac tat tac tgt      672
Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
    210                 215                 220

aac tcc cgg gac agc agt ggt aac cat tgg gtg ttc ggc gga ggg acc      720
Asn Ser Arg Asp Ser Ser Gly Asn His Trp Val Phe Gly Gly Gly Thr
225                 230                 235                 240

aag ctg acc gtc cta ggt gcg gcc                                      744
Lys Leu Thr Val Leu Gly Ala Ala
                245

<210>  248
```

<211> 248

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-038

<400> 248

Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln
1 5 10 15

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

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

Glu Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly
100 105 110

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

Thr Gly Ser Gly Thr Gly Gly Ser Thr Ser Ser Glu Leu Thr Gln Asp
130 135 140

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

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

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asp Thr Ala Ser

195 200 205

Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

Asn Ser Arg Asp Ser Ser Gly Asn His Trp Val Phe Gly Gly Gly Thr
225 230 235 240

Lys Leu Thr Val Leu Gly Ala Ala
245

<210> 249

<211> 759

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-039

<220>

<221> CDS

<222> (1)..(759)

<223>

<400> 249

```
gcc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag        48
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt g ca gcc tct gga ttc acc ttt        96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg       144
Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg gtc tca gtt att tat agc ggt ggt act agt aca tac tat gca       192
Glu Trp Val Ser Val Ile Tyr Ser Gly  Gly Thr Ser Thr Tyr Tyr Ala
    50                  55                  60

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gat aat tcc aag aac       240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

aca ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta       288
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                85                  90                  95
```

```
tat ttc tgt gcg aaa gga tct aaa tgg aac gac gtg ggg ggg ggt gac      336
Tyr Phe Cys Ala Lys Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp
            100                 105                 110

tac tgg ggc cag gga acc ctg gtc acc gtc tcg agc ggt acg ggc ggt      384
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Thr Gly Gly
        115                 120                 125

tca ggc gga acc ggc agc ggc act g gc ggg tcg acg aat ttt atg ctg      432
Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asn Phe Met Leu
    130                 135                 140

act cag ccc cac tct gtg tcg gag tct ccg ggg aag acg gta acc atc       480
Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys Thr Val Thr Ile
145                 150                 155                 160

tcc tgc gcc ggc agc agt ggc agc att gcc agc aac tat gtg cag tgg      528
Ser Cys Ala Gly Ser Ser Gly Ser  Ile Ala Ser Asn Tyr Val Gln Trp
                165                 170                 175

tac cag caa cgc ccg ggc agt gcc ccc act act gtg atc tat gag gat      576
Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val Ile Tyr Glu Asp
            180                 185                 190

aac caa aga ccc tct ggg gtc cct gat cgg ttc tct ggc tcc atc gac      624
Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Asp
        195                 200                 205

agc tcc tcc aac tct gcc tcc ctc acc atc tct gga ctg aag act gag      672
Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly Leu Lys Thr Glu
    210                 215                 220

gac gag gct gac tac tac tgt cag tct tat gat ggt tat ctt tgg att      720
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly Tyr Leu Trp Ile
225                 230                 235                 240

ttc ggc gga ggg acc aag ctg a cc gtc cta ggt gcg gcc                 759
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
                245                 250
```

<210> 250

<211> 253

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-039

<400> 250

```
Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
```

20 25 30

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

Glu Trp Val Ser Val Ile Tyr Ser Gly Gly Thr Ser Thr Tyr Tyr Ala
50 55 60

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

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

Tyr Phe Cys Ala Lys Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Thr Gly Gl y
115 120 125

Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asn Phe Met Leu
130 135 140

Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys Thr Va l Thr Ile
145 150 155 160

Ser Cys Ala Gly Ser Ser Gly Ser Ile Ala Ser Asn Tyr Val Gln Trp
165 170 175

Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Va l Ile Tyr Glu Asp
180 185 190

Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Asp
195 200 205

Ser Ser Ser Asn Ser Ala Ser Leu Thr Il e Ser Gly Leu Lys Thr Glu
210 215 220

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly Tyr Leu Trp Ile
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Th r Val Leu Gly Ala Ala
245 250

<210> 251

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-040

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 251

```
gcc atg gcc cag gtc cag ctg gta cag tct ggg gga ggc ttg gtc cag       48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tct  cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc agg      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Arg
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu  Ala
```

```
                    165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat agt agt ccg tac agt ttt      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Ser Pro Tyr Ser Phe
225                 230                 235                 240

ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc                      756
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 252

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-040

<400> 252

```
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

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

Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95
```

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

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

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

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

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Ser Pro Tyr Ser Phe
225 230 235 240

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 253

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-041

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 253

```
gcc atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag        48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc        96
Pro Gly Gly Ser Leu Arg Le u Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg       144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Le u
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca       192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  5 5                 60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac       240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  8 0

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg       288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa       336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga  acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gat atc cag atg acc cag tct cca       432
Gly Ser Gly Thr Gly Gl y Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag cgg acc acc atc aac tgc aag       480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Thr Thr Ile Asn Cy s Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct       528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg       576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg       624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat       672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac  agt ttt      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
225                 230                 235                 240
```

ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc 756
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 254

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-041

<400> 254

Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Thr Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 255

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-042

<220>

<221> misc_feature

<222> (153)..(154)

<223> n can be a, g, c or t

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 255

gcc atg gcc cag atg cag ctg gtg caa tct ggg gga ggc tta gtt cag 48
Ala Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctt tcc tgt gca gcc tct gga t tc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

```
                20                  25                  30

    agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
    Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 5          35                  40                  45

    gaa tat gtn tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
    Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr  Tyr Tyr Ala
        50                  55                  60
10
    aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
    Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    65                  70                  75                  80

15  acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
    Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                    85                  90                  95

    tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
20  Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
                100                 105                 110

    ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
    Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
25          115                 120                 125

    ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg a ct cag tct cca      432
    Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln Ser Pro
        130                 135                 140
30
    gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
    Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
    145                 150                 155                 160

35  tcc agc cag agt gtt tta tac agc tcc aac gat aag aac tac tta gct      528
    Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asp Lys  Asn Tyr Leu Ala
                    165                 170                 175

    tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
40  Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
                180                 185                 190

    gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agc ggc agc ggg      624
    Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
45          195                 200                 205

    tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
    Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
        210                 215                 220
50
    gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac agt ttt      720
    Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
    225                 230                 235                 240

55  ggc cag ggg acc aag ctg gag atc aaa cgt gcg g cc                     756
    Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
                    245                 250


60  <210>  256

    <211>  252
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<212> PRT

<213> Artificial sequence

<220>

<223> SC03-042

<220>

<221> misc_feature

<222> (153)..(154)

<223> n can be a, g, c or t

<400> 256

```
Ala Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asp Lys Asn Tyr Leu Ala
                165                 170                 175
```

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

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

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

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

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 257

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-043

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 257

```
gcc atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag        48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc        96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct c ca ggg aag gga ctg       144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca       192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac       240
```

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

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg g cc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agg tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Arg Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aag cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgt gaa tcc ggg gtc tct gag cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Ser Glu Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat agt acc ccg tac agt ttt      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
225                 230                 235                 240

ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc                      756
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 258

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-043

<400> 258

```
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Th r Phe
            20                  25                  30

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Th r Tyr Tyr Ala
    50                  55                  60

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

Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Al a Glu Asp Met Ala Val
                85                  90                  95

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

Gly Thr Met Val Thr Val Ser Ser Gl y Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

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

Asp Ser Leu Ala Val Ser Le u Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Val Leu Tyr Arg Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

Trp Tyr Gln Gln Ly s Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

Ala Ser Thr Arg Glu Ser Gly Val Ser Glu Arg Phe Ser Gly Ser Gly
        195                 200                 205

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

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

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 259

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-044

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 259

```
gcc atg gcc gag gtg cag ctg gtg gag act ggg gga ggc ttg gtc cag       48
Ala Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc  tct gga ttc acc ttc      96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly  Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc  cag atg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140
```

```
gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn  Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agg ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Arg Gly Ser Gly
        195                 200                 205

tcc ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

ctg gca gtt tat tac tgt cag caa tat tat agt act ccg tac agt ttt      720
Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
225                 230                 235                 240

ggc cag ggg acc aag ctg gag atc aaa  cgt gcg gcc                     756
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 260

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-044

<400> 260

```
Ala Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln
1               5                   10                  15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 261

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-045

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 261

```
gcc atg gcc cag ctg cag ctg cag gag tcg ggg  gga ggc ttg gtc cag       48
Ala Met Ala Gln Leu Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Al a Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agt aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  7 5                 80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc cag      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg  ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ctg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Ar g Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
```

210 215 220

gtg gca gtt tat tac tgt cag caa tat tat agt act cca ttc act ttc 720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr Phe
225 230 235 240

ggc cct ggg acc aaa gtg gat atc aaa cgt gcg gcc 75 6
Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
245 250

<210> 262

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-045

<400> 262

Ala Met Ala Gln Leu Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
245 250

<210> 263

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-046

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 263
gcc atg gcc gag gtc cag ctg gta cag tct ggg gga ggc ttg gtc cag 48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala A la Ser Gly Phe Thr Phe
20 25 30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

```
          35                  40                  45

     gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
     Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 5       50                  55                  60

     aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
     Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
     65                  70                  75                  80
10
     acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
     Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                 85                  90                  95

15   tat tac tgt gcg aga act act aat cgg gc t ttt gat atc tgg ggc caa      336
     Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
             100                 105                 110

     ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
20   Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
         115                 120                 125

     ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag tct cca      432
     Gly Ser Gly Thr Gly Gly Ser Thr Asp V al Val Met Thr Gln Ser Pro
25       130                 135                 140

     gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
     Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
     145                 150                 155                 160
30
     tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
     Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                 165                 170                 175

35   tgg tac cag cag aaa cca ggg cag cct cct aag ctg ctc att tac tgg      576
     Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
             180                 185                 190

     gca tct acc cgg gaa tcc ggg gtc cct gac agg ttc agt ggc agc ggg      624
40   Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
         195                 200                 205

     tct ggg aca gac ttc agt ctc acc at c agc agc ctg cag gct gaa gat      672
     Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
45       210                 215                 220

     gtg gcg gtt tat tac tgt cag caa tat tac agt cct ccg tac act ttt      7 20
     Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Pro Pro Tyr Thr Phe
     225                 230                 235                 240
50
     ggc ccg ggg acc aag gtg gaa atc aaa cgt gcg gcc                      756
     Gly Pro Gly Thr Lys Val Glu Ile L ys Arg Ala Ala
                 245                 250

55
     <210>  264

     <211>  252

60   <212>  PRT

     <213>  Artificial sequence
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<220>

<223> SC03-046

<400> 264

```
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                  10                  15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

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

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

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

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

Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 265

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-047

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 265

gcc atg gcc gag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cag 48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca 192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac 240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75 80

acg ctg tat ctt caa atg ggc agc ctg a ga gct gag gac atg gct gtg 288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
85 90 95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc cag 336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
100 105 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc 384

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

ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag tct cca 432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln Ser Pro
130 135 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag 480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

tcc agc cag agt gtt tta tat agc tcc aac aat aag aac tac tta gct 528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg 576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
180 185 190

gca tct acc cgg gaa tcc ggg gtc c ct gac cga ttc agt ggc agc ggg 624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat 672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
210 215 220

gtg gca gtt tat tac tgt cag caa tat tat agt act cct ctc act ttc 720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
225 230 235 240

ggc gga ggg acc aag gtg gaa atc aaa cgt gcg gcc 756
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 266

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-047

<400> 266

Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Il e Trp Gly Gln
100 105 110

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

Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Va l Met Thr Gln Ser Pro
130 135 140

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Se r Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

Ala Ser Thr Arg Glu Ser Gl y Val Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

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

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

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 267

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-048

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 267

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gcc atg gcc gag gtg cag ctg gtg gag act ggg gga ggc ttg gtc cag       48
Ala Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc  tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg  Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag  cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190
```

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg 624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat 672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
210 215 220

gtg gca gtt tat tac tgt cag caa tat tac agt act ccg ctc act ttc 720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
225 230 235 240

ggc gga ggg acc aag gtg gaa atc aaa cgt gcg gcc 756
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 268

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-048

<400> 268

Ala Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser G ly
195 200 205

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

Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro L eu Thr Phe
225 230 235 240

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 269

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-049

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 269
gcc atg gcc cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cag 48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 1 0 15

```
cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat  ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      24 0
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Le u Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gac atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140

tcc tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Ser Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc  tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tat cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg       576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Va l Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat agt act ccg ctc act ttc      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc                      756
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 270

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-049

<400> 270

Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

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

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

195 200 205

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

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

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 271

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-050

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 271

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gcc atg gcc cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cag       48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cg c cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      1 92
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr I le Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95
```

```
tat tac tgt gcg aga act act aat cgg gct ttt gac atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140

tcc tcc ctg gct gtg tct ctg gg c gag agg gcc acc atc aac tgc aag      480
Ser Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct       528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tat cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly G ln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag caa tat tat agt act ccg ctc act ttc      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc                      756
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
                245                 250
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<210> 272

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-050

<400> 272

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Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser  Gly Phe Thr Phe
```

20 25 30

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

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

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 273

<211> 762

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-051

<220>

<221> CDS

<222> (1)..(762)

<223>

<400> 273

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gcc atg gcc cag gtg cag ctg gtg cag tct gga aca gag gtg aaa aag       48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys
1               5                   10                  15

ccg ggg gag tct ctg aag atc tcc t gt aag ggt tct gga tac ggc ttt       96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg       144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc       192
Glu Trp Met Gly Ile Ile Tyr Pro  Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac       240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata       288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg       336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc       384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc g gg tcg acg gac atc cag atg acc cag       432
Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac       480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145                 150                 155                 160

tgc aag tcc ggc cag agt att tta tac agc tcc aac gat aag aac tac       528
Cys Lys Ser Gly Gln Ser Ile  Leu Tyr Ser Ser Asn Asp Lys Asn Tyr
```

```
                    165                 170                 175

    tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctt ctc att      576
    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
5               180                 185                 190

    tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc      624
    Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
            195                 200                 205
10
    agc ggg tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct      672
    Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
        210                 215                 220

15  gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac      720
    Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
    225                 230                 235                 240

    act ttt ggc cag ggg acc a ag gtg gaa atc aaa cgt gcg gcc              762
20  Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
                    245                 250


    <210>  274
25
    <211>  254

    <212>  PRT

30  <213>  Artificial sequen ce


    <220>
35
    <223>  SC03-051

    <400>  274

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


    Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
45              20                  25                  30


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

55
    Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
    65                  70                  75                  80


60  Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                    85                  90                  95
```

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Se r Gly
115 120 125

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

Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Al a Thr Ile Asn
145 150 155 160

Cys Lys Ser Gly Gln Ser Ile Leu Tyr Ser Ser Asn Asp Lys Asn Tyr
165 170 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Le u Thr Ile Ser Ser Leu Gln Ala
210 215 220

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
225 230 235 240

Thr Phe Gly Gln Gly Thr Ly s Val Glu Ile Lys Arg Ala Ala
245 250

<210> 275

<211> 762

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-052

<220>

<221> CDS

<222> (1)..(762)

<223>

<400> 275

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gcc atg gcc gaa gtg cag ctg gtg cag tct gga aca gag gtg aaa aag       48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys
1               5                   10                  15

ccg ggg gag tct ctg aag gtc tcc tgt aag ggt tct gga  tac ggc ttt      96
Pro Gly Glu Ser Leu Lys Val Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc      192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr  Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac      240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc acc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata      288
Thr Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg      336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc      384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gac atc  cag atg acc cag      432
Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac      480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145                 150                 155                 160

tgc aag tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac      528
Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn  Asn Lys Asn Tyr
                165                 170                 175

tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att      576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc      624
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

agc ggg tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct      672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
    210                 215                 220

gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac      720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
225                 230                 235                 240
```

act ttt ggc cag ggg acc aag gtg gaa atc aaa cgt gcg gcc 762
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 276

<211> 254

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-052

<400> 276

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

Pro Gly Glu Ser Leu Lys Val Ser Cys Lys Gly Ser Gly Tyr Gly Phe
20 25 30

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
35 40 45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
50 55 60

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

Thr Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
85 90 95

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
100 105 110

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

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

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

Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
165 170 175

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu I le
180 185 190

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser L eu Gln Ala
210 215 220

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
225 230 235 240

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys A rg Ala Ala
245 250

<210> 277

<211> 768

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-053

<220>

<221> CDS

<222> (1)..(768)

<223>

<400> 277

gcc atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10 15

cct ggg gcc tca gtg atg gtt tcc tgc aag gcc tct gga tac acc ttc 96
Pro Gly Ala Ser Val Met Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
20 25 30

agt aac tat gct atg cat tgg gtg cgc cag ggc ccc gga caa agg ctt 144
Ser Asn Tyr Ala Met His Trp Val Ar g Gln Gly Pro Gly Gln Arg Leu
35 40 45

gag tgg atg gga tgg atc aac gct gac aaa ggt cag aca aaa tat tca 192
Glu Trp Met Gly Trp Ile Asn Ala Asp Lys Gly Gln Thr Lys Tyr Ser
50 55 60

```
cag aag ttc cag ggc aga gtc acc att acc ggg gac aca tcc gcc agc      240
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Gly Asp Thr Ser Ala Ser
65                  70                  75                  80

aca gcc tac atg gac ctg agc agc ctg aga tct gaa gac acg gct gtg      288
Thr Ala Tyr Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
                85                  90                  95

tat tac tgt gcg aga ggg acc gga tat ttg cgg agc tac cac ggc atg      336
Tyr Tyr Cys Ala Arg Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met
            100                 105                 110

gac gtc tgg ggc cag ggg acc acg  gtc acc gtc tcg agc ggt acg ggc      384
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly
        115                 120                 125

ggt tca ggc gga acc ggc agc ggc act ggc ggg tcg acg gat gtt gtg       432
Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val
    130                 135                 140

atg act cag tct cca ccc tcc ctg ccc gtc acc cct ggg gag ccg gcc      480
Met Thr Gln Ser Pro Pro Ser Le u Pro Val Thr Pro Gly Glu Pro Ala
145                 150                 155                 160

tcc atc tcc tgc agg tct agt cag agc ctc ctc cat agt aat gga tac      528
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
                165                 170                 175

aac tat ttg gat tgg tac ctg cag aag cca ggt cag tct cca cag ctc      576
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
            180                 185                 190

ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc      624
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
        195                 200                 205

agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg      672
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
    210                 215                 220

gag gct gag gat gtt ggg gtt  tat tac tgc atg caa gct cta caa act      720
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
225                 230                 235                 240

cct ctc acc ttc ggc caa ggg aca cga ctg gag att aaa cgt gcg gcc       768
Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
                245                 250                 255
```

<210> 278

<211> 256

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-053

<400> 278

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

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

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

Glu Trp Met Gly Trp Ile Asn Ala Asp Lys Gly Gln Thr Lys Tyr Ser
50 55 60

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

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

Tyr Tyr Cys Ala Arg Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met
100 105 110

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

Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val
130 135 140

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

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
165 170 175

Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
180 185 190

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

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

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
225 230 235 240

Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala

245 250 255

<210> 279

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-054

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 279

```
gcc atg gcc gaa gtg cag ctg gtg cag tc t ggg gga ggc gtg gtc cag       48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
1               5                   10                  15

cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg G ln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc gg t acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca      4 32
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140
```

```
gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly G lu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct      528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
                165                 170                 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg      576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc ggc ggg      624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Gly Gly
        195                 200                 205

tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat      672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
    210                 215                 220

gtg gca gtt tat tac tgt cag ca a tat tat agt act ccg tac agt ttt      720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
225                 230                 235                 240

ggc cag ggg acc aag gtg gag atc aaa cgt gcg gcc                      756
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 280

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-054

<400> 280

```
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
1               5                   10                  15

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

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
```

65 70 75 80

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
24 5 250

<210> 281

<211> 780

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-055

<220>

<221> CDS

<222> (1)..(780)

<223>

<400> 281

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gcc atg gcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag       48
Ala Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
1               5                  10                  15

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc       96
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
            20                  25                  30

agt ggt ttc tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg      144
Ser Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg      192
Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
    50                  55                  60

tcc ctc aag agt cga gtc acc ata tca gca gac acg tcc aag aac cag      240
Ser Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln
65                  70                  75                  80

ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat      288
Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gcg aga agg gtg gag gta g ta gag tac cag ctg ctc cgt ccc      336
Tyr Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro
            100                 105                 110

cga tat aaa agt tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc       384
Arg Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
        115                 120                 125

gtc tcg agc ggt acg ggc ggt tca ggc gga acc ggc agc ggc act ggc      432
Val Ser Ser Gly Thr Gly Gly Ser  Gly Gly Thr Gly Ser Gly Thr Gly
    130                 135                 140

ggg tcg acg cag tct gtg ttg acg cag ccg ccc tca gtg tct ggg gcc      480
Gly Ser Thr Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala
145                 150                 155                 160

cca ggg cag agg gtc tcc atc tcc tgc tct gga agc ggc gcc aat ggt      528
Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Gly Ala Asn Gly
                165                 170                 175

ggg act gat cct gtt tct tgg tac cag aaa ttc cca gga aca gcc ccc      576
Gly Thr Asp Pro Val Ser Trp Tyr Gln Lys Phe Pro Gly Thr Ala Pro
            180                 185                 190

cac ctc ctc att tat gac aat aat aag cga ccc tca ggg att cct gac      624
His Leu Leu Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp
        195                 200                 205

cga ttc tct ggc tcc aag tct g gc gcg tca gcc acc ctg gac atc acc      672
Arg Phe Ser Gly Ser Lys Ser Gly Ala Ser Ala Thr Leu Asp Ile Thr
```

```
        210                 215                 220

    gga ctc cag act ggg gac gag gcc gac tat tac tgc gga gca tgg gat        720
    Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp
5   225                 230                 235                 240

    ccc agt ctg agc ggt tat gtc ttc ggg act ggg acc cag ctc acc gtt        768
    Pro Ser Leu Ser Gly Tyr Val  Phe Gly Thr Gly Thr Gln Leu Thr Val
                    245                 250                 255
10
    tta agt gcg gcc                                                      780
    Leu Ser Ala Ala
                260

15
    <210>  282

    <211>  260

20  <212>  PRT

    <213>  Artificial sequence


25
    <220>

    <223>  SC03-055

30  <400>  282

    Ala Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
    1               5                   10                  15

35
    Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
                20                  25                  30


40  Ser Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Le u
            35                  40                  45


    Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
45      50                  55                  60


    Ser Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Ly s Asn Gln
    65                  70                  75                  80
50
    Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                    85                  90                  95

55
    Tyr Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gl n Leu Leu Arg Pro
                100                 105                 110


60  Arg Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
            115                 120                 125
```

Val Ser Ser Gly Thr Gly Gly Ser Gly Gl y Thr Gly Ser Gly Thr Gly
130 135 140

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

Pro Gly Gln Arg Val Ser Ile Se r Cys Ser Gly Ser Gly Ala Asn Gly
165 170 175

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

His Leu Leu Ile Tyr As p Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp
195 200 205

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

Gly Leu Gln Th r Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp
225 230 235 240

Pro Ser Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val
245 250 255

Leu Ser Ala Ala
260

<210> 283

<211> 762

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-056

<220>

<221> CDS

<222> (1)..(762)

<223>

<400> 283
gcc atg gcc gaa gtg cag ctg gtg cag tct gga aca gag gtg aaa aag 48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys

```
1               5                  10                  15

ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt      96
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys  Gly Ser Gly Tyr Gly Phe
            20                  25                  30

atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg     144
Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
        35                  40                  45

gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc     192
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac     240
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata     288
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg ggg ggt tcg ggg att  tct acc cct atg gac gtc tgg     336
Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc     384
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
        115                 120                 125

gga acc ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag     432
Gly Thr Gly Ser Gly Thr Gly Gly Ser  Thr Asp Val Val Met Thr Gln
    130                 135                 140

tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac     480
Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145                 150                 155                 160

tgc aag tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac     528
Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
                165                 170                 175

tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att     576
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            180                 185                 190

tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc     624
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

agc ggg tct ggg aca gat ttc act  ctc acc atc agc agc ctg cag gct     672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
    210                 215                 220

gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac     720
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
225                 230                 235                 240

agt ttt ggc cag ggg acc aag gtg gag atc aaa cgt gcg gcc             762
Ser Phe Gly Gln Gly Thr Lys Val  Glu Ile Lys Arg Ala Ala
                245                 250
```

<210> 284

<211> 254

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-056

<400> 284

```
Ala Met Ala Glu Val Gln Leu Val Gln S er Gly Thr Glu Val Lys Lys
1               5                   10                  15

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
            20                  25                  30

Ile Thr Tyr Trp Ile Gly Trp V al Arg Gln Met Pro Gly Lys Gly Leu
        35                  40                  45

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
    50                  55                  60

Pro Ser Phe Gln Gly G ln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
65                  70                  75                  80

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
                85                  90                  95

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
            100                 105                 110

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

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

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

Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
                165                 170                 175

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

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
225 230 235 240

Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 285

<211> 768

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-057

<220>

<221> CDS

<222> (1)..(768)

<223>

<400> 285

gcc atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 48
Ala Met Ala Gln Val Gl n Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10 15

cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc 96
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Th r Phe
20 25 30

agc aga tat gct atc agt tgg gtg cga cag gcc cct gga caa ggc ctt 144
Ser Arg Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
35 40 45

gag tgg atg gga agg atc aac cct atc ctt aat tta aca aac tac gca 192
Glu Trp Met Gly Arg Ile Asn Pro Ile Leu Asn Leu Thr Asn Tyr Ala
50 55 60

cag aag ttc cag ggc aga gtc acg att acc gcg gac aaa tcc acg agt 240
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
65 70 75 80

aca gcc tac atg gag atg agt agc ctg aga tct gag gac acg gcc att 288

```
Thr Ala Tyr Met Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
                85                  90                  95

tat tac tgt gcg agc ccg gat ata gta gta gcc ggt cac gct  tcc ccc      336
Tyr Tyr Cys Ala Ser Pro Asp Ile Val Val Ala Gly His Ala Ser Pro
            100                 105                 110

cca cac tac act atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc      384
Pro His Tyr Thr Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
        115                 120                 125

tcg agc ggt acg ggc ggt tca ggc gga acc ggc agc ggc act ggc ggg      432
Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Th r Gly Gly
    130                 135                 140

tcg acg gac atc cag atg acc cag tct cca tcc tca ctg tct gca tct      480
Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145                 150                 155                 160

gta gga gac aga gtc acc atc act tgc cgg gca agt cag ggc att aga      528
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg
                165                 170                 175

aat gat tta ggc tgg tat cag cag aaa cca ggg aaa gcc cct aac ctc      576
Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu
            180                 185                 190

ctg atc tat cag gca tct gct tta cag agt ggg gtc cca tca agg ttc      624
Leu Ile Tyr Gln Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe
        195                 200                 205

agc ggc agt gaa tct ggg gca gaa ttc act ctc acc atc  agc agc ctg      672
Ser Gly Ser Glu Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu
    210                 215                 220

cac cct gat gat ttt gca act tat tac tgc caa cag tat cat gat ttt      720
His Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asp Phe
225                 230                 235                 240

ccg atc acc ttc ggc caa ggg aca cga ctg gag att aaa cgt gcg gcc      768
Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Ly s Arg Ala Ala
                245                 250                 255
```

<210> 286

<211> 256

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-057

<400> 286

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Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val  Lys Lys
1               5                   10                  15
```

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

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

Glu Trp Met Gly Arg Ile Asn Pro Ile Leu Asn Leu Thr Asn Tyr Ala
50 55 60

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

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

Tyr Tyr Cys Ala Ser Pro Asp Ile Val Val Ala Gly His Ala Ser Pro
100 105 110

Pro His Tyr Thr Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120 125

Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly
130 135 140

Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145 150 155 160

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

Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu
180 185 190

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

Ser Gly Ser Glu Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu
210 215 220

His Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asp Phe
225 230 235 240

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
245 250 255

<210> 287

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-058

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 287

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gcc atg gcc gag gtc cag ctg gta cag tct gga gga ggc ttg gtc cag       48
Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1               5                   10                  15

cct ggg ggg tcc ctc aaa ctc tcc tgt gca gcc tct gga ttc acc ttc       96
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            20                  25                  30

agt agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      144
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        35                  40                  45

gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca      192
Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
    50                  55                  60

aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac      240
Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65                  70                  75                  80

acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg      288
Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
                85                  90                  95

tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa      336
Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc      384
Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
        115                 120                 125

ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tct cca      432
Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag      480
Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145                 150                 155                 160
```

tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct 528
Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg 576
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
180 185 190

gca tct acc cgg ga a tcc ggg gtc cct gac cga ttc agt ggc agc ggg 624
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

tct ggg aca gat ttt act ctc acc atc agc agt ctg cag gc t gaa gat 672
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
210 215 220

gtg gca gtt tat tac tgt cag caa tat tat agt act cct ctg acg ttc 720
Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
225 230 235 240

ggc caa ggg acc aag gtg gaa atc aaa cgt gcg gcc 756
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 288

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-058

<400> 288

Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

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

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
50 55 60

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

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

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

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

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

Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 289

<211> 756

<212> DNA

<213> Artificial sequence

<220>

<223> SC03-059

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 289

```
gcc atg gcc cag gtg cag ctg gtg caa tct ggg gct gag gtg aag aag       48
Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys  Lys
1               5                   10                  15

cct ggg tcc tcg gtg aag gtc tcc tgc agg gct tct ggt gga ggc gtc       96
Pro Gly Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Gly Val
            20                  25                  30

ttc cgc aat tat gct atc aac tgg gtg cga cag gcc cct gga caa ggg      144
Phe Arg Asn Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
        35                  40                  45

ctt gag tgg atg gga atg atc aac cct agt ggt ggt agc aca agc tac      192
Leu Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr
    50                  55                  60

gca cag aag ttc cag g gc aga gtc acc ctg acc agg gac acg tcc acg      240
Ala Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Thr
65                  70                  75                  80

agc aca gtc tac atg gag ctg agc agc ctg aga tct gag gac a cg gcc      288
Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
                85                  90                  95

gtg tat tac tgt gcg aga ttc cct ggt ggt acc aga agc cgc ggc tac      336
Val Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr
            100                 105                 110

atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcg agc ggt acg      384
Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  Gly Thr
        115                 120                 125

ggc ggt tca ggc gga acc ggc agc ggc act ggc ggg tcg acg gaa att      432
Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Glu Ile
    130                 135                 140

gtg ctc aca cag tct cca gcc acc ctg tct ttg tct cca ggg gaa aga      480
Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
145                 150                 155                 160

gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac tta gcc      528
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
                165                 170                 175

tgg tac caa cag a aa cct ggc cag gct ccc agg ctc ctc atc tat gat      576
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
            180                 185                 190

gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt g gc agt ggg      624
Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
        195                 200                 205

tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct gaa gat      672
Ser Gly Thr Asp  Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
    210                 215                 220

ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccg gct ttc      720
Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro  Pro Ala Phe
225                 230                 235                 240
```

ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc 756
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 290

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> SC03-059

<400> 290

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

Pro Gly Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Gly Val
20 25 30

Phe Arg Asn Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
35 40 45

Leu Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr
50 55 60

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

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

Val Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr
100 105 110

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

Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Glu Il e
130 135 140

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

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ty r Leu Ala

165 170 175

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

Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Ph e Ser Gly Ser Gly
195 200 205

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

Phe Ala Val Tyr Tyr Cys Gln Gln Arg Se r Asn Trp Pro Pro Ala Phe
225 230 235 240

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

<210> 291

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-019 and SC03-059

<400> 291

Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met Asp Val
1 5 10

<210> 292

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-020, SC03-021, SC03-022, SC03-033, SC03-034, SC03-035, SC03-036, SC03-051. SC03-052 and SC03-056

<400> 292

Gly Ser Gly Ile Ser Thr Pro Met Asp Val
1 5 10

<210> 293

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-023 and SC03-055

<400> 293

Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg Tyr Lys Ser
1 5 10 15

Trp Phe Asp Pro
20

<210> 294

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-024

<400> 294

Lys Ser Ala Gly Ser Asn Ala Phe Asp Ile
1 5 10

<210> 295

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-025, SC03-026, SC03-027, SC03-029, SC03-030, SC03-040, SC03-050, SC03-054 and SC03-058

<400> 295

Thr Thr Asn Arg Ala Phe Asp Ile

1 5

<210> 296

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-031

<400> 296

Glu Ser Gly Gly Gly Tyr Asp Asn His Phe Asp Tyr
1 5 10

<210> 297

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-032

<400> 297

Asp Gly Trp Asp Leu Thr Gly Ser Phe Leu Gly Tyr Gly Met Asp Val
1 5 10 15

<210> 298

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-037 and SC03-038

<400> 298

Asp Ala His Arg Gly Phe Gly Met Asp Val
1 5 10

<210> 299

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-039

<400> 299

Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp Tyr
1 5 10

<210> 300

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-053

<400> 300

Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met Asp Val
1 5 10

<210> 301

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> HCDR3 of SC03-057

<400> 301

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

Val

<210> 302

<211> 372

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -019

<220>

<221> CDS

<222> (1)..(372)

<223>

<400> 302

```
atg gcc cag atg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct       48
Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro
1               5                   10                  15

ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  Phe Thr Phe Ser
            20                  25                  30

ggc tat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag      144
Gly Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac      192
Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
    50                  55                  60

tcc gtg aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat      288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gcg aga ttc cct ggt ggt acc aga agc  cgc ggc tac atg gac      336
Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met Asp
            100                 105                 110

gtc tgg ggc aaa ggg acc acg gtc acc gtc tcg agc                      372
Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 303

<211> 124

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -019

<400> 303

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

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

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

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met Asp
100 105 110

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

<210> 304

<211> 330

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -019

<220>

<221> CDS

<222> (1)..(330)

<223>

<400> 304

gaa att gtg ctc aca cag tct cca gcc acc ctg tct ttg tct cca ggg 48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96
Glu Arg Ala Thr Leu Ser Cys Arg Al a Ser Gln Ser Val Ser Ser Tyr
20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccg 288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

gct ttc ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc 330
Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
100 105 110

<210> 305

<211> 110

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -019

<400> 305

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

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

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
100 105 110

<210> 306

<211> 363

<212> DNA

<213> Artificial se quence

<220>

<223> Variable heavy chain of SC03 -020

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 306

atg gcc gaa gtg cag ctg gtg cag tct ggg tca gag gtg aaa aag ccg 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Ser Glu Val Lys Lys Pro
1 5 10 15

ggg gag tct ctg aag atc tct tgt aag ggt tct gga tac ggc ttt atc 96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag 144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg 192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

tcc ttc caa ggc cag gtc ac c atc tca gcc gac aag tcc atc aac acc 240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata ta t 288

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc 336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

caa ggg acc acg gtc acc gtc tcg agc 363
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 307

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -020

<400> 307

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 308

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -020

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 308

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gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag aaa att tta cac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Lys Ile Leu His Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct g gg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act cct ccg gtt ttc ggc gga ggg acc aag gtg gaa atc      336
Tyr Tyr Ser Thr Pro Pro Val Phe Gly  Gly Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 309

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -020

<400> 309

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Lys Ile Leu His Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gl n Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gl y Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Val Ph e Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Ala Ala
115

<210> 310

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -021

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 310
atg gcc cag gtc cag ctg gta cag tct gga aca gag gtg aaa aag ccg 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1 5 10 15

ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt atc 96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag 144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg 192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc 240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat 288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc 336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

caa ggg acc acg gtc acc gtc tcg agc 363
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 311

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -021

<400> 311

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 312

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -021

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 312

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Ser
20 25 30

tcc aac aat aag aac tac cta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg caa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Se r Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gl n
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 313

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -021

<400> 313

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 314

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -022

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 314

```
atg gcc cag atg cag ctg gtg caa tct gga aca gag gtg aaa aag ccg       48
Met Ala Gln Met Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1               5                   10                  15

ggg gag tct ctg aag atc tcc tgt aag ggt tc t gga tac ggc ttt atc       96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag      144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg      192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser G lu Thr Arg Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc      240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat      288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc      336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                 363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 315

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -022

<400> 315

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 316

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -022

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 316

```
gac atc cag ttg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt t ta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc atc aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Ile Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu  Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac act ttt ggc cag ggg acc aag gtg gaa atc      336
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 317

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -022

<400> 317

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Se r Val Leu Tyr Ser
```

20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Se r Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu As p Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 318

<211> 390

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -023

<220>

<221> CDS

<222> (1)..(390)

<223>

<400> 318

atg gcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct 48
Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro
1 5 10 15

tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tct ttc agt 96
Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser
20 25 30

ggt ttc tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg gag 144
Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

```
tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg tcc      192
Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50                  55                  60

ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc      240
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat tac      288
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga agg gtg gag gta  gta gag tac cag ctg ctc cgt ccc cga      336
Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg
            100                 105                 110

tat aaa agt tgg ttc gac ccc tgg ggc cag ggc acc ctg gtc acc gtc      384
Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
        115                 120                 125

tcg agc                                                             390
Ser Ser
    130
```

<210> 319

<211> 130

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -023

<400> 319

```
Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro
1               5                   10                  15

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

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

Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50                  55                  60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
```

85 90 95

Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg
100 105 110

Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
115 120 125

Ser Ser
130

<210> 320

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -023

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 320

```
cag tct gcc ctg act cag cct cgc tca gtg  tcc ggg tct cct gga cag       48
Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15

tca gtc acc atc tcc tgc act gga tcc agc agt act gtt ggt ggt tat       96
Ser Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Thr Val Gly Gly Tyr
            20                  25                  30

aac tat gtc tcc tgg tac caa cag cac cca ggc aaa gcc ccc aaa ctc      144
Asn Tyr Val Ser Trp Tyr Gln Gln His Pr o Gly Lys Ala Pro Lys Leu
        35                  40                  45

atg att tat gat gtc agt aag cgg ccc tca ggg gtt tct aat cgc ttc      192
Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc tct ggg ctc      240
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

cag gct gag gac gag gct gat tat tac tgc agc tca tat aca agc agc      288
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95
```

agc act tat gtc ttc gga act ggg acc aag gtc acc gtc cta ggt gcg 336
Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
100 105 110

gcc 339
Ala

<210> 321

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -023

<400> 321

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

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

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
85 90 95

Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
100 105 110

Ala

<210> 322

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -024

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 322

```
atg gcc cag gtg cag ctg gtg gag tct ggg tct gag ttg aag atc cct       48
Met Ala Gln Val Gln Leu Val Glu Ser Gly S er Glu Leu Lys Ile Pro
1               5                   10                  15

ggg gcc tca gtg aag gtt tcc tgc aag gct act gga tac acc ttc act       96
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Thr Gly Tyr Thr Phe Thr
            20                  25                  30

cgt tat tct ctg aat tgg gtg cgg cag gcc cct gga caa ggg ctt gag      144
Arg Tyr Ser Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
        35                  40                  45

tgg gtg ggg tgg att aac acc cag act gga aac tca aac tat ggc cag      192
Trp Val Gly Trp Ile Asn Thr Gln Thr Gly Asn Ser Asn Tyr Gly Gln
    50                  55                  60

gcc ttc tca gga cgg ttt gtc ttc tcc ttg gac acc tca gtc agc acg      240
Ala Phe Ser Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr
65                  70                  75                  80

gca tat ttg caa atc agc agc cta cag gc c gag gac act gcc aca tac      288
Ala Tyr Leu Gln Ile Ser Ser Leu Gln Ala Glu Asp Thr Ala Thr Tyr
                85                  90                  95

tac tgt gcg agg aag agt gcg ggt tcg aat gct ttc gac att tgg ggc      336
Tyr Cys Ala Arg Lys Ser Ala Gly Ser Asn Ala Phe Asp Ile Trp Gly
            100                 105                 110

caa ggg aca atg gtc acc gtc tcg agc                                  363
Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 323

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -024

<400> 323

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

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

Arg Tyr Ser Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
35 40 45

Trp Val Gly Trp Ile Asn Thr Gln Thr Gly Asn Ser Asn Tyr Gly Gln
50 55 60

Ala Phe Ser Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr
65 70 75 80

Ala Tyr Leu Gln Ile Ser Ser Leu Gln Ala Glu Asp Thr Ala Thr Tyr
85 90 95

Tyr Cys Ala Arg Lys Ser Ala Gly Ser Asn Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 324

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -024

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 324
cag tct gtc gtg acg cag ccg ccc tca gtg tct gcg gcc cca gga cag 48
Gln Ser Val Val Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

aag gcc acc atc tcc tgc tct gga agc agc tcc aac att ggg aat aat 96
Lys Ala Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

tat gta tcc tgg tac cag cag ctc cca gga aca gcc ccc aaa ctc ctc 144
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

att tat gac aat aat aag cga ccc tca ggg att cct aac cga ttc tct 192
Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asn Arg Phe Ser
50 55 60

ggc tcc aag tct ggc acg tca gcc acc ctg ggc atc acc gga ctc cag 240
Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

act ggg gac gag gcc gat tat tac tgc gga aca tgg g at agc agc ctg 288
Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

agt gct tat gtc ttc gga act ggg acc aag gtc acc gtc cta ggt gcg 336
Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
100 105 110

gcc 339
Ala

<210> 325

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -024

<400> 325

Gln Ser Val Val Thr Gln Pro Pr o Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Ala Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Tyr Val Ser Trp Tyr Gl n Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asn Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
100 105 110

Ala

<210> 326

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -025

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 326

atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240

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

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
10 0 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 327

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -025

<400> 327

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 328

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -025

<220>

<221> CDS

<222> (1).. (348)

<223>

<400> 328

```
gac atc cag ttg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag  cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct atc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Th r Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat aat att ccg tat gct ttc ggc cag ggg acc aag ctg gag atc      336
Tyr Tyr Asn Ile Pro Tyr Ala Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 329

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -025

<400> 329

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Asn Ile Pro Tyr Ala Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg Ala Ala
115

<210> 330

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -026

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 330
atg gcc cag gtc cag ctg gta cag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc tt c agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gcc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His T rp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr A la Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

aca atg gtc acc gt c tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 331

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -026

<400> 331

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 332

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -026

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 332

gac atc cag atg acc cag tct cca gac tcc ctg gct g tg tct ctg ggc 48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt att tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Ser
20 25 30

tcc aac agt aag aac tac tta ggt tgg tac cag cag aaa cca gga cag 144
Ser Asn Ser Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aag gtg gag atc 336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 333

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -026

<400> 333

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Ser
20 25 30

Ser Asn Ser Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gl n
85 90 95

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

Lys Arg Ala Ala
115

<210> 334

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -027

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 334

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atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct       48
Met Ala Gln Val Gln Leu Val  Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa  ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                          357
Thr Met Val Thr Val Ser  Ser
        115
```

<210> 335

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -027

<400> 335

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 336

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -027

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 336

```
gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Se r Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac  tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aaa gtg gat atc      336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Asp Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 337

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -027

<400> 337

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 338

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03-029

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 338

atg gcc gaa gtg cag ctg gtg cag tct ggg gga ggc ttg gtt cag ccg 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144

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

tat gtt tca ggt att agt agt aa t ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser L eu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 339

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -029

<400> 339

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 340

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -029

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 340

gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac t ac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc g gg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ctc act ttc ggc gca ggg acc aag ctg gag atc 336
Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

aaa cgt gcg gcc 348

Lys Arg Ala Ala
115

<210> 341

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -029

<400> 341

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg Ala Ala
115

<210> 342

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -030

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 342

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atg gcg gag gtc cag gtg gta cag tct gga gga ggc ttg gtc cag cct       48
Met Ala Glu Val Gln Val Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                  10                  15

ggg ggg tcc ctc aaa ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                         357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 343

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -030

<400> 343

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

Gly Gly Ser Leu Lys Leu Ser C ys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

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

Tyr Val Ser Gly Ile S er Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 344

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -030

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 344

gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96

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

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Le u Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Va l
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttt act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agt ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ctg acg ttc ggc caa ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 345

<211> 116

<212> PRT

<213> Artificial sequ ence

<220>

<223> Variable light chain of SC03 -030

<400> 345

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 346

<211> 369

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -031

<220>

<221> CDS

<222> (1)..(369)

<223>

<400> 346

atg gcc cag gtg cag ctg gtg caa tct ggg gct gac gtg aag aag cct 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Asp Val Lys Lys Pro
1 5 10 15

ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga ggc acg ttc agc 96
Gly Ser Ser Val Lys Val Ser Cys Glu Ala S er Gly Gly Thr Phe Ser
20 25 30

agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag 144
Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
35 40 45

tgg atg gga agg atc atc cct atc ctt ggt ata aca aac tac gca cag 192
Trp Met Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala Gln
50 55 60

aag ttc cag ggc aga gtc aca att acc gcg gac aaa tcc acg ggc aca 240
Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Gly Thr
65 70 75 80

ggc aac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat 288
Gly Asn Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
85 90 95

tac tgt gcg aga gaa tcg ggt ggt ggc ta c gat aac cac ttt gac tac 336

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

tgg ggc cag gga acc ctg gtc acc gtc tcg agc 369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 347

<211> 123

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -031

<400> 347

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

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

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

Trp Met Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala Gln
50 55 60

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

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

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

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

<210> 348

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -031

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 348

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cag tct gtg ctg acg cag ccg ccc tca gcg tct ggg acc ccc gga cag       48
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15

agg gtc acc atc tct tgt tct gga ggc agc tcc aac atc gga agt aat       96
Arg Val Thr Ile Ser Cys Ser Gly Gly  Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

act gta aac tgg tac cag caa ctc cca gga acg gcc ccc aaa ctc gtc      144
Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val
        35                  40                  45

atc tat gct aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct      192
Ile Tyr Ala Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

gcc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag      240
Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80

tct gag gat gag gct gat tat tac tgt gca gct tgg gat gac agc ctg      288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

act ggt gga gtg ttc ggc gga ggg a cc cag ctc acc gtt tta agt gcg      336
Thr Gly Gly Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Ser Ala
            100                 105                 110

gcc                                                                  339
Ala
```

<210> 349

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-031

<400> 349

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

Arg Val Thr Ile Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val
35 40 45

Ile Tyr Ala Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Thr Gly Gly Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Ser Ala
100 105 110

Ala

<210> 350

<211> 381

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -032

<220>

<221> CDS

<222> (1)..(381)

<223>

<400> 350

atg gcc gag gtg cag ctg gtg gag tct ggg gct gag gtg aag aag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc 96
Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
20 25 30

agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag 144
Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
35 40 45

tgg atg gga aag atc atc cct att ctt ggt aaa gtc act tac gca cag 192
Trp Met Gly Lys Ile Ile Pro Ile Leu Gly Lys Val Thr Tyr Ala Gln
50 55 60

aag ttc cag gcc aga gtc acg att acc gcg gac gaa tcc acg agc aca 240
Lys Phe Gln Ala Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr
65 70 75 80

gcc tac ctg gag ctg agc agc ctg aga tct gag gac acg gcc gtt ttt 288
Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Phe
85 90 95

tac tgt gcg aga gac ggc tgg gat ttg act ggt tct ttt tta ggc tac 336
Tyr Cys Ala Arg Asp Gly Trp Asp Leu Thr Gly Ser Phe Leu Gly Tyr
100 105 110

ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcg agc 381
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 351

<211> 127

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -032

<400> 351

Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val L ys Lys Pro
1 5 10 15

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

Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro G ly Gln Gly Leu Glu
35 40 45

Trp Met Gly Lys Ile Ile Pro Ile Leu Gly Lys Val Thr Tyr Ala Gln
50 55 60

Lys Phe Gln Ala Arg Val Thr Ile Thr A la Asp Glu Ser Thr Ser Thr
65 70 75 80

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

Tyr Cys Ala Arg Asp Gly Trp A sp Leu Thr Gly Ser Phe Leu Gly Tyr
100 105 110

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

<210> 352

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -032

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 352

cag tct gtc gtg acg cag ccg ccc tca gcg tct ggg acc ccc ggg cag 48
Gln Ser Val Val Thr Gln Pro Pro Ser Al a Ser Gly Thr Pro Gly Gln
1 5 10 15

agg gtc acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat 96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

act gta agc tgg tac cag cag gtt cca ggg acg gcc ccc aag ctc ctc 144
Thr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

atc tat agg aat aat cag cgg ccc cca ggg gtc cyt gac cga ttc tct 192
Ile Tyr Arg Asn Asn Gln Arg Pro Pro Gly Val Xaa Asp Arg Phe Ser
50 55 60

ggc tcc aag tct ggc acc tca gcc tcc ytg gcc atc agt ggg ctc cag 240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Xaa Ala Ile Ser Gly Leu Gln
65 70 75 80

tct gac gat gag gcc ttt tat tac tgt gca gca tgg gat ggc agc mtg 288
Ser Asp Asp Glu Ala Phe Tyr Tyr Cys Ala Ala Trp Asp Gly Ser Xaa
85 90 95

aat ggt ctg gcc ttc ggc gga ggg acc aag ctg acc gtc cta ggt gcg 33 6
Asn Gly Leu Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
100 105 110

gcc 339
Ala

<210> 353

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> (60)..(60)

<223> The 'Xaa' at location 60 stands for Pro, or Leu.

<220>

<221> misc_feature

<222> (74)..(74)

<223> The 'Xaa' at location 74 stands for Leu.

<220>

<221> misc_feature

<222> (96)..(96)

<223> The 'Xaa' at location 96 stands for Met, or Leu.

<220>

<223> Variable light chain of SC03-032

<400> 353

Gln Ser Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Arg Asn Asn Gln Arg Pro Pro Gly Val Xaa Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Xaa Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Asp Asp Glu Ala Phe Tyr Tyr Cys Ala Ala Trp Asp Gly Ser Xaa
85 90 95

Asn Gly Leu Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
100 105 110

Ala

<210> 354

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -033

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 354

atg gcc cag gtc cag ctg gta cag tct gga aca gag gtg aaa aag ccg 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pr o
1 5 10 15

ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt atc 96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag 144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg 192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc 240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat 288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc 336
Tyr Cys Ala Gly Gly Se r Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

caa ggg acc acg gtc acc gtc tcg agc 363
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 355

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -033

<400> 355

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 356

<211> 351

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -033

<220>

<221> CDS

<222> (1)..(351)

<223>

<400> 356

```
gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag acc agc cac aat att ttc tcc aga       96
Glu Arg Ala Thr Ile Asn Cys Lys Thr Ser His Asn Ile Phe Ser Arg
            20                  25                  30

tcc aac aat aag gac tac tta gct tgg tac cag cag aaa cca ggc cag      144
Ser Asn Asn Lys Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct ccc aga tta ctc att tac tgg gcg tct acc cgg gca tcc ggg gtc      192
Pro Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val
    50                  55                  60

cct gaa cga ttc agt ggc agc ggc tc t ggg aca gac ttc agt ctc acc      240
Pro Glu Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gcg gtt tat tac tgt cag caa      2 88
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt tcc cct atg tac agt ttt ggc cag ggg acc aag gtg gag      336
Tyr Tyr Ser Ser Pro Met Tyr Ser P he Gly Gln Gly Thr Lys Val Glu
            100                 105                 110

atc aaa cgt gcg gcc                                                  351
Ile Lys Arg Ala Ala
        115
```

<210> 357

<211> 117

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -033

<400> 357

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

Glu Arg Ala Thr Ile Asn Cys Lys Thr Ser His Asn Ile Phe Ser Arg
20 25 30

Ser Asn Asn Lys Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Ser Pro Met Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys Arg Ala Ala
115

<210> 358

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC0 3-034

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 358

```
atg gcc gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccg       48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1               5                  10                  15

ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt atc       96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag      144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct g aa acc aga tac agc ccg      192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc      240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat      288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc      336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                 363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 359

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -034

<400> 359

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
```

20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 360

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -034

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 360

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt att tta aac aga 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Asn Arg
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc aat ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Asn Leu Thr
65 70 75 80

atc agc agc ctg cag gct gag gat gtg gca gtt tat tac tgt cag cag 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat aat aac tgg cct ctc act ttc ggc gga ggg acc aaa gtg gat atc 336
Tyr Asn Asn Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 361

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -034

<400> 361

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Asn Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Asn Asn Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile

100 105 110

Lys Arg Ala Ala
115

<210> 362

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -035

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 362

```
atg gcc gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc       48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1               5                   10                  15

ggg gag tct ctg aag atc tcc tgt  aag ggt tct gga tac ggc ttt atc       96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag       144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg       192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc       240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat       288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc       336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                  363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 363

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -035

<400> 363

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 364

<211> 351

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -035

<220>

<221> CDS

<222> (1)..(351)

<223>

<400> 364

```
gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc agt ca g agt gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser T hr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccc ctg tac agt ttt ggc cag ggg acc aag gtg gag      336
Tyr Tyr Ser Thr Pro Leu Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu
            100                 105                 110

atc aaa cct gcg gcc                                                  351
Ile Lys Pro Ala Ala
        115
```

<210> 365

<211> 117

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -035

<400> 365

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Ile Lys Pro Ala Ala
115

<210> 366

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -036

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 366
atg gcc gag gtg cag ctg gtg cag tct gga aca gag g tg aaa aag ccg 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1 5 10 15

ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt atc 96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

```
acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag      144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly  Lys Gly Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg      192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc      240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat      288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc      336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                 363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 367

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -036

<400> 367

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Ty r
                85                  90                  95
```

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 368

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -036

<220>

<221> CDS

<222> (1)..(345)

<223>

<400> 368

```
gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg  ggc       48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac agc       96
Glu Arg Ala Thr Ile Asn  Cys Lys Ser Ser Gln Ser Val Leu His Ser
            20                  25                  30

ccc aac aat aag aac tac ttg gct tgg tac cag cag aaa cca gga cag      144
Pro Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act aac  agt ttt ggc cag ggg acc aag ctg gag atc aaa      336
Tyr Tyr Ser Thr Asn Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

cgt gcg gcc 345
Arg Ala Ala
115

<210> 369

<211> 115

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-036

<400> 369

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Asn Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Ala Ala
115

<210> 370

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -037

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 370

```
atg gcc aaa gtg cag ctg gtg cag tct gga gga ggc ttg atc cag cct       48
Met Ala Lys Val Gln Leu Val Gln Ser Gly Gly Gl y Leu Ile Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc gtc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser
            20                  25                  30

agc aac tac atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag      144
Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg gtc tca att gtt ttt agc ggt ggt agc aca tac tac gca gac tcc      192
Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
    50                  55                  60

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg      240
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65                  70                  75                  80

tat ctt caa atg aac agc ctg aga gcc gag gac  acg gcc gta tat tat      288
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga gat gcc cac cgg ggg ttc ggt atg gac gtc tgg ggc caa      336
Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly Gln
            100                 105                 110

ggg acc acg gtc acc gtc tcg agc                                     360
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 371

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -037

<400> 371

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

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

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

Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

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

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

Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 372

<211> 333

<212> DNA

<213> Artificial se quence

<220>

<223> Variable light chain of SC03 -037

<220>

<221> CDS

<222> (1)..(333)

<223>

<400> 372

tct tct gag ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag 48
Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96

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

agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

ggc aaa aac aac cgg ccc tca ggg atc cca gac cgg ttc tct ggc tcc 192
Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

agc tca gga aac aca gct tc c ttg acc atc act ggg gct cag gcg gaa 240
Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

gat gag gcc gac tat tat tgt aac ggc cgg gac agc agt ggt aac ca t 288
Asp Glu Ala Asp Tyr Tyr Cys Asn Gly Arg Asp Ser Ser Gly Asn His
85 90 95

tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt gcg gcc 333
Trp Val Phe Gly Gly Gly T hr Lys Leu Thr Val Leu Gly Ala Ala
100 105 110

<210> 373

<211> 111

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -037

<400> 373

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Gly Arg Asp Ser Ser Gly Asn His
85 90 95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
100 105 110

<210> 374

<211> 360

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -038

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 374

atg gcc gag gtg cag ctg gtg cag tct gga gga ggc ttg atc cag cct 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct ggg ttc acc gtc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser
20 25 30

agc aac tac atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag 144
Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtc tca att gtt ttt agc ggt ggt agc aca tac t ac gca gac tcc 192
Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 240
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80

tat ctt caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tat 288
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

tgt gcg aga gat gcc cat cgg ggg ttc ggt atg gac gtc tgg ggc cag 336
Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly Gln
100 105 110

ggg acc acg gtc acc gtc tcg agc 360
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 375

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -038

<400> 375

Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro
1 5 1 0 15

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

Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 4 0 45

Trp Val Ser Ile Val Phe Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 7 0 75 80

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

Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly Gln
1 00 105 1.1.0

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 376

<211> 333

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -038

<220>

<221> CDS

<222> (1)..(333)

<223>

<400> 376

```
tct tct gag ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag       48
Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1               5                   10                  15

aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca       96
Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
            20                  25                  30

agc tgg tac cag cag aag cca gga  cag gcc cct gta ctt gtc atc tat      144
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45

ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc       192
Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

agc tca gga gac aca gct tcc ttg acc atc act ggg gct cag gcg gaa       240
Ser Ser Gly Asp Thr Ala Ser Leu  Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80

gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac cat       288
Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
                85                  90                  95

tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt gcg gcc           333
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
            100                 105                 110
```

<210> 377

<211> 111

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -038

<400> 377

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

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
            20                  25                  30
```

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
85 90 95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
100 105 110

<210> 378

<211> 369

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -039

<220>

<221> CDS

<222> (1)..(369)

<223>

<400> 378

atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag 144
Ser Tyr Ala Met Se r Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tgg gtc tca gtt att tat agc ggt ggt act agt aca tac tat gca gac 192
Trp Val Ser Val Ile Tyr Ser Gly Gly Thr Ser Thr Tyr Ty r Ala Asp
50 55 60

tcc gtg aag ggc cgg ttc acc atc tcc aga gat aat tcc aag aac aca 240

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

ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat 288
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

ttc tgt gcg aaa gga tct aaa tgg aac gac gtg ggg ggg ggt gac tac 336
Phe Cys Ala Lys Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp Tyr
100 105 110

tgg ggc cag gga acc ctg gtc acc gtc tcg agc 369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 379

<211> 123

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -039

<400> 379

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

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

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

Trp Val Ser Val Ile Tyr Ser Gly Gly Thr Ser Thr Tyr Tyr Ala Asp
50 55 60

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

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

Phe Cys Ala Lys Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp Tyr
100 105 110

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

<210> 380

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -039

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 380

```
aat ttt atg ctg act cag ccc cac tct gtg tcg gag tct ccg ggg aag       48
Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1               5                   10                  15

acg gta acc atc tcc tgc gcc ggc agc agt ggc agc at t gcc agc aac       96
Thr Val Thr Ile Ser Cys Ala Gly Ser Ser Gly Ser Ile Ala Ser Asn
            20                  25                  30

tat gtg cag tgg tac cag caa cgc ccg ggc agt gcc ccc act act gtg      144
Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35                  40                  45

atc tat gag gat aac caa aga ccc tct ggg gtc cct gat cgg ttc tct      192
Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro A sp Arg Phe Ser
    50                  55                  60

ggc tcc atc gac agc tcc tcc aac tct gcc tcc ctc acc atc tct gga      240
Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80

ctg aag act gag gac gag gct gac tac tac tgt cag tct tat gat ggt      288
Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly
                85                  90                  95

tat ctt tgg att ttc ggc gga ggg acc aag ctg acc gtc cta ggt gcg      336
Tyr Leu Trp Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
            100                 105                 110

gcc                                                                 339
Ala
```

<210> 381

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -039

<400> 381

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys Ala Gly Ser Ser Gly Ser Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

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

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly
85 90 95

Tyr Leu Trp Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
100 105 110

Ala

<210> 382

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -040

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 382

```
atg gcc cag gtc cag ctg gta cag tct ggg gga ggc ttg gtc cag cct       48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc t gg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                          357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 383

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -040

<400> 383

```
Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  3 0
```

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 6 0

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

Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 9 0 95

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

Thr Met Val Thr Val Ser Ser
115

<210> 384

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -040

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 384

gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc agg tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt agt ccg tac agt ttt ggc cag ggg acc aag ctg gag atc 336
Tyr Tyr Ser Ser Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 385

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -040

<400> 385

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 386

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03-041

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 386

```
atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct       48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag  aac acg     240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                         357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 387

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -041

<400> 387

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 388

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -041

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 388

```
gat atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc        48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag cgg acc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc        96
Glu Arg Thr Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag       144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cg g gaa tcc ggg gtc       192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc       240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa       288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val T yr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aag ctg gag atc       336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                       348
Lys Arg Ala Ala
        115
```

<210> 389

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -041

<400> 389

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

Glu Arg Thr Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 390

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -042

<220>

<221> misc_feature

<222> (150)..(151)

<223> n can be a, t, c, or g

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 390
atg gcc cag atg cag ctg gtg caa tct ggg gga ggc tta gtt cag cct 48
Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctt tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 3 0

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtn tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Tr p Gly Gln Gly
100 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 391

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -042

<220>

<221> misc_feature

<222> (150)..(151)

<223> n can be a, t, c, or g

<400> 391

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

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

20 25 30

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 392

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -042

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 392

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp S er Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac gat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asp Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agc ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gt g gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aag ctg gag atc 3 36
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 393

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -042

<400> 393

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

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

Ser Asn Asp Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile

100 105 110

Lys Arg Ala Ala
115

<210> 394

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -043

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 394

```
atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct       48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat t cc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                         357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 395

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -043

<400> 395

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

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

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Le u Glu
35 40 45

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe As p Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 396

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC 03-043

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 396

```
gac atc cag ttg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc        48
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agg        96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Arg
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aag cca gga cag       144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct  acc cgt gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

tct gag cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Ser Glu Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala  Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt acc ccg tac agt ttt ggc cag ggg acc aag ctg gag atc      336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 397

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -043

<400> 397

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Ser Glu Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 398

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -044

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 398
atg gcc gag gtg cag ctg gtg gag act ggg gga ggc ttg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 399

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -044

<400> 399

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 400

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -044

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 400

```
gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag ag t gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr A rg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agg ggc agc ggg tcc ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Arg Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat ctg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aag ctg gag atc      336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110
```

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 401

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -044

<400> 401

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Arg Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 402

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -045

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 402

```
atg gcc cag ctg cag ctg cag gag tcg ggg gga ggc ttg gtc cag c ct       48
Met Ala Gln Leu Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agt aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act a ct aat cgg gct ttt gat atc tgg ggc cag ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                          357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 403

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable hea vy chain of SC03 -045

<400> 403

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 404

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -045

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 404

gac atc cag ctg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96

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

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cca ttc act ttc ggc cct ggg acc aaa gtg gat atc 336
Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 405

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -045

<400> 405

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
100 105 110

Lys Arg Ala Ala
115

<210> 406

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -046

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 406

atg gcc gag gtc cag ctg gta cag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336

Tyr Cys Ala Arg Thr Thr As n Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 407

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -046

<400> 407

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 408

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-046

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 408

```
gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca ggg cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac agg ttc agt ggc agc ggg tct ggg aca gac ttc ag t ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gcg gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tac agt cct ccg tac act ttt ggc ccg ggg acc aag gtg gaa atc      336
Tyr Tyr Ser Pro Pro Tyr Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 409

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -046

<400> 409

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Pro Pro Tyr Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Ala Ala
115

<210> 410

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -047

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 410

atg gcc gag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc c ag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc cag ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 411

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -047

<400> 411

Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 1 5

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

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 4 5

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 7 5 80

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

Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 1 05 110

Thr Met Val Thr Val Ser Ser
115

<210> 412

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -047

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 412

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tat agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act cct ctc act ttc ggc gga ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 413

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -047

<400> 413

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 414

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -048

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 414

```
atg gcc gag gtg cag ctg gtg gag act ggg  gga ggc ttg gtc cag cct       48
Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro
1               5                  10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Al a Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                         357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 415

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -048

<400> 415

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 416

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -048

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 416
gac atc cag ttg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tac agt act ccg ctc ac t ttc ggc gga ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 417

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light ch ain of SC03-048

<400> 417

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 418

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -049

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 418

atg gcc cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct g ag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gac atc tgg ggc caa ggg 336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 419

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -049

<400> 419

Met Ala Gln Val Gln Le u Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 420

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -049

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 420

```
gac atc cag ttg acc cag tct cca tcc tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tat cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg  tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa       288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg ctc act ttc ggc gga ggg acc aag gtg gag atc      336
Tyr Tyr Ser Thr Pro Leu Thr Phe  Gly Gly Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 421

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -049

<400> 421

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 422

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -050

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 422

```
atg gcc gaa gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct       48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca  tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu As p Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                         357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 423

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -050

<400> 423

```
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

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

20 25 30

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 424

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -050

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 424

gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tcc aac aat aag aac tac tta gct tgg ta c cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser G ly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

tat tat agt act ccg ctc act ttc ggc gga ggg acc aag gtg gaa atc 336
Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 425

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -050

<400> 425

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

100 105 110

Lys Arg Ala Ala
115

<210> 426

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -051

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 426

```
atg gcc cag gtg cag ctg gtg cag tct gga aca gag gtg aaa aag ccg       48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1               5                   10                  15

ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac g gc ttt atc       96
Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag      144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg      192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg  Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc      240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat      288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc      336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                 363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 427

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -051

<400> 427

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

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gl y Tyr Gly Phe Ile
20 25 30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Se r Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Le u Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Th r Val Ser Ser
115 120

<210> 428

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -051

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 428

```
gac atc cag atg acc cag tct  cca gac tcc ctg gct gtg tct ctg ggc        48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc ggc cag agt att tta tac agc        96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Gly Gln Ser Ile Leu Tyr Ser
            20                  25                  30

tcc aac gat aag aac tac tta gct tgg tac cag cag aaa cca gga cag       144
Ser Asn Asp Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctt ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc       192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc       240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa       288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac act ttt ggc cag ggg acc aag gtg gaa atc       336
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                      348
Lys Arg Ala Ala
        115
```

<210> 429

<211> 116

<212> PRT

<213> Artificial seque nce

<220>

<223> Variable light chain of SC03 -051

<400> 429

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Gly Gln Ser Ile Leu T yr Ser
20 25 30

Ser Asn Asp Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg G lu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala V al Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 430

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -052

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 430

atg gcc gaa gtg cag ctg gtg cag tct gga aca gag gtg aaa aag ccg 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1 5 10 15

ggg gag tct ctg aag gtc tcc tgt aag ggt tct gga tac ggc ttt atc 96
Gly Glu Ser Leu Lys Val Ser Cys Lys Gly Se r Gly Tyr Gly Phe Ile
20 25 30

```
acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag      144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg      192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc      240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

acc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat      288
Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc  cct atg gac gtc tgg ggc      336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                  363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 431

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -052

<400> 431

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

Gly Glu Ser Leu Lys Val Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

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

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95
```

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 432

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -052

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 432

```
gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc       48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc       96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val L eu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac act ttt ggc cag ggg acc aa g gtg gaa atc      336
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110
```

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

<210> 433

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -052

<400> 433

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 434

<211> 372

<212> DNA

<213> Artificial seque nce

<220>

<223> Variable heavy chain of SC03 -053

<220>

<221> CDS

<222> (1)..(372)

<223>

<400> 434

```
atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct       48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1               5                   10                  15

ggg gcc tca gtg atg gtt tcc tgc aag gcc tct gga tac acc ttc agt       96
Gly Ala Ser Val Met Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser
            20                  25                  30

aac tat gct atg cat tgg gtg cgc cag ggc ccc gga caa agg ctt gag      144
Asn Tyr Ala Met His Trp Val Arg Gln Gly Pro Gly Gln Arg Leu Glu
        35                  40                  45

tgg atg gga tgg atc aac gct gac aaa ggt cag aca aaa tat tca cag      192
Trp Met Gly Trp Ile Asn Ala Asp Lys Gly Gln Thr Lys Tyr Ser Gln
    50                  55                  60

aag ttc cag ggc aga gtc acc a tt acc ggg gac aca tcc gcc agc aca      240
Lys Phe Gln Gly Arg Val Thr Ile Thr Gly Asp Thr Ser Ala Ser Thr
65                  70                  75                  80

gcc tac atg gac ctg agc agc ctg aga tct gaa gac acg gct gtg tat       288
Ala Tyr Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
                85                  90                  95

tac tgt gcg aga ggg acc gga tat ttg cgg agc tac cac ggc atg gac      336
Tyr Cys Ala Arg Gly Thr Gly  Tyr Leu Arg Ser Tyr His Gly Met Asp
            100                 105                 110

gtc tgg ggc cag ggg acc acg gtc acc gtc tcg agc                      372
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 435

<211> 124

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -053

<400> 435

Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Gl u Val Lys Lys Pro
1 5 10 15

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

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

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

Lys Phe Gln Gly Arg Val Thr Il e Thr Gly Asp Thr Ser Ala Ser Thr
65 70 75 80

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

Tyr Cys Ala Arg Gly Th r Gly Tyr Leu Arg Ser Tyr His Gly Met Asp
100 105 110

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

<210> 436

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -053

<220>

<221> CDS

<222> (1)..(345)

<223>

<400> 436

gat gtt gtg atg act cag tct cca ccc tcc ctg ccc gtc acc cct ggg 48
Asp Val Val Met Thr Gln Ser Pro Pro Ser Leu Pro Val Thr Pro Gly
1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ctc cat agt 96

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

aat gga tac aac tat ttg gat tgg tac ctg cag aag cca ggt cag tct 144
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

cca cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct 192
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct 288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

cta caa act cct ctc acc ttc ggc caa ggg aca cga ctg gag att aaa 336
Leu Gln Thr Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

cgt gcg gcc 345
Arg Ala Ala
115

<210> 437

<211> 115

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -053

<400> 437

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

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

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

Arg Ala Ala
115

<210> 438

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of S C03-054

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 438

atg gcc gaa gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct 48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro
1 5 10 15

ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 96
Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa 144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac 192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg 240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat 288
Leu Tyr Leu Gln Met Gly Ser Leu Arg Al a Glu Asp Met Ala Val Tyr
85 90 95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg 336

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

aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

<210> 439

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -054

<400> 439

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

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

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

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> 440

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -054

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 440

```
gac atc cag ttg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc        48
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc        96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gc t tgg tac cag cag aaa cca gga cag       144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc       192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc ggc ggg tct ggg aca gat ttc act ctc acc       240
Pro Asp Arg Phe Ser Gly Gly G ly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa       288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aag gtg gag atc       336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                      348
Lys Arg Ala Ala
        115
```

<210> 441

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -054

<400> 441

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg Ala Ala
115

<210> 442

<211> 390

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -055

<220>

<221> CDS

<222> (1)..(390)

<223>

<400> 442

```
atg gcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct       48
Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro
1               5                   10                  15

tcg gag acc ctg tcc ctc acc tgc gct gtc tat g gt ggg tcc ttc agt       96
Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser
            20                  25                  30

ggt ttc tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg gag      144
Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg tcc      192
Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr  Asn Tyr Asn Pro Ser
    50                  55                  60

ctc aag agt cga gtc acc ata tca gca gac acg tcc aag aac cag ttc      240
Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat tac      288
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga agg gtg gag gta gta gag tac cag ctg ctc cgt ccc cga      336
Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg
            100                 105                 110

tat aaa agt tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc      384
Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
        115                 120                 125

tcg agc                                                             390
Ser Ser
    130
```

<210> 443

<211> 130

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -055

<400> 443

```
Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro
1               5                   10                  15

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

Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45
```

Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Ty r Tyr
85 90 95

Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg
100 105 110

Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Le u Val Thr Val
115 120 125

Ser Ser
130

<210> 444

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -055

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 444

cag tct gtg ttg acg cag ccg ccc tca gtg tct ggg gcc cca ggg cag 48
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

agg gtc tcc atc tcc tgc tct gga agc ggc gcc aat ggt ggg act gat 96
Arg Val Ser Ile Ser Cys Ser Gly Ser Gly Ala Asn Gly Gly Thr Asp
20 25 30

cct gtt tct tgg tac cag aaa ttc cca gga aca gcc ccc cac ctc ctc 144
Pro Val Ser Trp Tyr Gln Lys Phe Pro Gly Thr Ala Pro His Leu Leu
35 40 45

att tat gac aat aat aag cga ccc tca ggg att cct gac cga ttc tct 192
Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

ggc tcc aag tct ggc gcg tca gcc acc ctg gac atc acc gga ctc cag 240
Gly Ser Lys Ser Gly Ala Ser Ala Thr Leu Asp Ile Thr Gly Leu Gln
65 70 75 80

act ggg gac gag gcc gac tat tac tgc gga gca tgg gat ccc agt ctg 288
Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Pro Ser Leu
85 90 95

agc ggt tat gtc ttc ggg act ggg acc cag ctc acc gtt tta agt gcg 336
Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser Ala
100 105 110

gcc 339
Ala

<210> 445

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -055

<400> 445

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Ser Ile Ser Cys Ser Gly Ser Gly Ala Asn Gly Gly Thr Asp
20 25 30

Pro Val Ser Trp Tyr Gln Lys Phe Pro Gly Thr Ala Pro His Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Ala Ser Ala Thr Leu Asp Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Pro Ser Leu
85 90 95

Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser Ala
100 105 110

Ala

<210> 446

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -056

<220>

<221> CDS

<222> (1)..(363)

<223>

<400> 446

```
atg gcc gaa gtg cag ctg gtg cag tct gga aca gag gtg aaa  aag ccg       48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1               5                   10                  15

ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt atc       96
Gly Glu Ser Leu Ly s Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
            20                  25                  30

acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag      144
Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gl y Leu Glu
        35                  40                  45

tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc ccg      192
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
    50                  55                  60

tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac acc      240
Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65                  70                  75                  80

gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata tat      288
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc      336
Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcg agc                                 363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 447

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03-056

<400> 447

Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
1 5 10 15

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
50 55 60

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 448

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-056

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 448

```
gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc        48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc        96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag       144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc       192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc       240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa       288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act ccg tac agt ttt ggc cag ggg acc aag gtg gag atc       336
Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                      348
Lys Arg Ala Ala
        115
```

<210> 449

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-056

<400> 449

```
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15
```

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Ala Ala
115

<210> 450

<211> 387

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -057

<220>

<221> CDS

<222> (1)..(387)

<223>

<400> 450

atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc 96
Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
20 25 30

aga tat gct atc agt tgg gtg cga cag gcc cct gga caa ggc ctt gag 144

```
Arg Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
        35                  40                  45

tgg atg gga agg atc aac cct atc ctt aat tta aca aac tac gca cag      192
Trp Met Gly Arg Ile Asn Pro Ile Leu Asn Leu Thr Asn Tyr Ala Gln
    50                  55                  60

aag ttc cag ggc aga gtc acg att acc gcg gac aaa tcc acg agt aca      240
Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr
65                  70                  75                  80

gcc tac atg gag atg agt agc ctg aga tct g ag gac acg gcc att tat      288
Ala Tyr Met Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr
                85                  90                  95

tac tgt gcg agc ccg gat ata gta gta gcc ggt cac gct tcc ccc cca      336
Tyr Cys Ala Ser Pro Asp Ile Val Val Ala Gly His Ala Ser Pro Pro
            100                 105                 110

cac tac act atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcg      384
His Tyr Thr Met Asp Val Trp Gly Gln Gly  Thr Thr Val Thr Val Ser
        115                 120                 125

agc                                                                  387
Ser
```

<210> 451

<211> 129

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -057

<400> 451

```
Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ly s Pro
1               5                   10                  15

Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
            20                  25                  30

Arg Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gl n Gly Leu Glu
        35                  40                  45

Trp Met Gly Arg Ile Asn Pro Ile Leu Asn Leu Thr Asn Tyr Ala Gln
    50                  55                  60

Lys Phe Gln Gly Arg Val Thr Ile Thr Ala As p Lys Ser Thr Ser Thr
65                  70                  75                  80
```

Ala Tyr Met Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Ser Pro Asp Ile Val Va l Ala Gly His Ala Ser Pro Pro
100 105 110

His Tyr Thr Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 452

<211> 330

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -057

<220>

<221> CDS

<222> (1)..(330)

<223>

<400> 452

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gac atc cag atg acc cag tct cca tcc tca ctg tct gca tct gta gga       48
Asp Ile Gln Met Thr Gln  Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

gac aga gtc acc atc act tgc cgg gca agt cag ggc att aga aat gat       96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn  Asp
            20                  25                  30

tta ggc tgg tat cag cag aaa cca ggg aaa gcc cct aac ctc ctg atc      144
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45

tat cag gca tct gct tta cag agt ggg gtc cca tca agg ttc agc ggc      192
Tyr Gln Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt gaa tct ggg gca gaa ttc act ctc acc atc agc agc ctg cac cct      240
Ser Glu Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu His Pro
65                  70                  75                  80

gat gat ttt gca act  tat tac tgc caa cag tat cat gat ttt ccg atc      288
```

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asp Phe Pro Ile
85 90 95

acc ttc ggc caa ggg aca cga ctg gag att aaa cgt gcg gcc 330
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
100 105 110

<210> 453

<211> 110

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03-057

<400> 453

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 Asn Leu Leu Ile
35 40 45

Tyr Gln Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu His Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asp Phe Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
100 105 110

<210> 454

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -058

<220>

<221> CDS

<222> (1)..(357)

<223>

<400> 454

```
atg gcc gag gtc cag ctg gta cag tct gga gga ggc ttg gtc cag cct       48
Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1               5                   10                  15

ggg ggg tcc ctc aaa ctc tcc tgt gca gcc tct gga ttc acc ttc agt       96
Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  3 0

agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg gaa      144
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca aac      192
Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
    50                  55                  60

tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc  aag aac acg      240
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80

ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg tat      288
Leu Tyr Leu Gl n Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
                85                  90                  95

tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa ggg      336
Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Tr p Gly Gln Gly
            100                 105                 110

aca atg gtc acc gtc tcg agc                                         357
Thr Met Val Thr Val Ser Ser
        115
```

<210> 455

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -058

<400> 455

Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 456

<211> 348

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -058

<220>

<221> CDS

<222> (1)..(348)

<223>

<400> 456

gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96

```
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag      144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

cct cct aag ctg ctc att tac tgg gca tct ac c cgg gaa tcc ggg gtc      192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttt act ctc acc      240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

atc agc agt ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa      288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala V al Tyr Tyr Cys Gln Gln
                85                  90                  95

tat tat agt act cct ctg acg ttc ggc caa ggg acc aag gtg gaa atc      336
Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

aaa cgt gcg gcc                                                     348
Lys Arg Ala Ala
        115
```

<210> 457

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -058

<400> 457

```
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
```

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Ala Ala
115

<210> 458

<211> 375

<212> DNA

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -059

<220>

<221> CDS

<222> (1)..(375)

<223>

<400> 458

atg gcc cag gtg cag ctg gtg caa tct ggg gct gag gtg aag aag cct 48
Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

ggg tcc tcg gtg aag gtc tcc tgc agg gct tct ggt gga ggc gtc ttc 96
Gly Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Gly Val Phe
20 25 30

cgc aat tat gct atc aac tgg gtg cga cag gcc cct gga caa g gg ctt 144
Arg Asn Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
35 40 45

gag tgg atg gga atg atc aac cct agt ggt ggt agc aca agc tac gca 192
Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
50 55 60

cag aag ttc cag ggc aga gtc acc ctg acc agg gac acg tcc acg agc 240
Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Thr Ser
65 70 75 80

aca gtc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 288
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
85 90 95

tat tac tgt gcg aga ttc cct ggt ggt acc aga agc cgc ggc tac atg 336

Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met
100 105 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcg agc 375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 459

<211> 125

<212> PRT

<213> Artificial sequence

<220>

<223> Variable heavy chain of SC03 -059

<400> 459

Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

Gly Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Gly Val Phe
20 25 30

Arg Asn Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
35 40 45

Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
50 55 60

Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Thr Ser
65 70 75 80

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 460

<211> 330

<212> DNA

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -059

<220>

<221> CDS

<222> (1)..(330)

<223>

<400> 460

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gaa att gtg ctc aca cag tct cca gcc acc ctg tct ttg tct cca ggg       48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                  10                  15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac       96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30

tta gcc tgg tac caa cag aaa cct ggc  cag gct ccc agg ctc ctc atc      144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc      192
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct      240
Ser Gly Ser Gly Thr Asp Phe Thr Leu  Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

gaa gat ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccg      288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
                85                  90                  95

gct ttc ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc              330
Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
            100                 10 5                110
```

<210> 461

<211> 110

<212> PRT

<213> Artificial sequence

<220>

<223> Variable light chain of SC03 -059

<400> 461

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
100 105 110

<210> 462

<211> 3789

<212> DNA

<213> Artificial sequence

<220>

<223> Codon-optimized sequence of S protein of SARS -CoV stra
in Frankfurt 1

<220>

<221> CDS

<222> (10)..(3777)

<223>

<400> 462
ggtaccgcc atg ttc atc ttc ctg ctg ttc ctg acc ctg acc agc ggc agc 51
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser
1 5 10

gat ctg gat agg tgc acc acc ttc gac gac gtg cag gcc cct aat tac 99
Asp Leu Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr
15 20 25 30

```
acc cag cac acc agc tct atg cgg ggc gtg tac tac ccc gac  gag atc      147
Thr Gln His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile
                35                  40                  45

ttc aga agc gac acc ctg tac ctg aca cag gac ctg ttc ctg ccc ttc      195
Phe Arg Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe
            50                  55                  60

tac agc aac gtg acc ggc ttc cac acc atc aac cac acc ttc ggc aac      243
Tyr Ser Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn
        65                  70                  75

ccc gtg atc cct ttc aag gac ggc atc tac ttc gcc gcc acc gag aag      291
Pro Val Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys
    80                  85                  90

agc aat gtg gtg cgg ggc tgg gtg ttc ggc agc acc atg aac aac aag      339
Ser Asn Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys
95                  100                 105                 110

agc cag agc gtg atc atc atc aac aat agc acc aac gtg gtg atc agg      387
Ser Gln Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg
                115                 120                 125

gcc tgc aac ttc gag ctg tgc gac aac cct ttc ttc gcc gtg tcc aaa      435
Ala Cys Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys
            130                 135                 140

cct atg ggc acc cag acc cac acc atg atc ttc gac aac  gcc ttc aac      483
Pro Met Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn
        145                 150                 155

tgc acc ttc gag tac atc agc gac gcc ttc agc ctg gat gtg agc gag      531
Cys Thr Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu
    160                 165                 170

aag agc ggg aac ttc aag cac ctg cgg gag ttc gtg ttc aag aac aag      579
Lys Ser Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys
175                 180                 185                 190

gac ggc ttc ctg tac gtg tac aag ggc tac cag ccc atc gac gtg gtg      627
Asp Gly Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val
                195                 200                 205

aga gat ctg ccc agc ggc ttc aac acc ctg aag ccc atc ttc aag ctg      675
Arg Asp Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu
            210                 215                 220

ccc ctg ggc atc aac atc acc aac ttc cgg gcc atc ctg acc gcc ttc      723
Pro Leu Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe
        225                 230                 235

agc cct gcc cag gac atc tgg ggc acc agc gcc gct gcc tac ttc gtg      771
Ser Pro Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val
    240                 245                 250

ggc tac ctg aag ccc acc acc ttc atg ctg aag tac  gac gag aac ggc      819
Gly Tyr Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly
255                 260                 265                 270

acc atc acc gat gcc gtg gac tgc agc cag aac ccc ctg gcc gag ctg      867
Thr Ile Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu
```

```
                    275                 280                 285

     aag tgc agc gtg aag agc ttc gag atc gac aag ggc atc tac cag acc      915
     Lys Cys Ser Val Lys Ser Phe Glu Ile Asp Lys Gl y Ile Tyr Gln Thr
 5               290                 295                 300

     agc aac ttc aga gtg gtg ccc agc ggc gat gtg gtg agg ttc ccc aac      963
     Ser Asn Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn
             305                 310                 315
10
     atc acc aac ctg tgc cct ttc ggc gag gtg ttc aac gcc acc aag ttc     1011
     Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe
         320                 325                 3 30

15   cct agc gtg tac gcc tgg gag cgg aag aag atc agc aac tgc gtg gcc     1059
     Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala
     335                 340                 345                 350

     gat tac agc gtg ctg tac aac agc acc ttc ttc agc acc ttc aag tgc     1107
20   Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys
                     355                 360                 365

     tac ggc gtg agc gcc acc aag ctg aac gac ctg  tgc ttc agc aac gtg     1155
     Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val
25               370                 375                 380

     tac gcc gac agc ttc gtg gtg aag ggc gac gac gtg aga cag atc gcc     1203
     Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala
             385                 390                 395
30
     cct ggc cag acc ggc gtg atc gcc gac tac aat tac aag ctg ccc gac     1251
     Pro Gly Gln Thr Gly Val Ile Ala Asp Tyr As n Tyr Lys Leu Pro Asp
         400                 405                 410

35   gac ttc atg ggc tgc gtg ctg gcc tgg aac acc aga aac atc gac gcc     1299
     Asp Phe Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala
     415                 420                 425                 430

     acc tcc acc ggc aac tac aac tac aag tac cgc tac ctg agg cac ggc     1347
40   Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly
                     435                 440                 445

     aag ctg aga ccc ttc gag cgg gac atc agc aac gtg ccc ttc agc cct     1395
     Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro
45               450                 455                 460

     gac ggc aag ccc tgc acc ccc cct gcc ctg aac tgc tac tgg ccc ctg     1443
     Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu
             465                 470                 475
50
     aac gac tac ggc ttc tac acc acc acc ggc  atc ggc tac cag cct tac     1491
     Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr
         480                 485                 490

55   aga gtg gtg gtg ctg agc ttc gag ctg ctg aac gcc cct gcc acc gtg     1539
     Arg Val Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val
     495                 500                 505                 510

     tgc ggc ccc aag ctg agc acc gac ctg atc aag aac cag tgc gtg aac     1587
60   Cys Gly Pro Lys Leu Ser Thr Asp Leu Il e Lys Asn Gln Cys Val Asn
                     515                 520                 525

     ttc aac ttc aac ggc ctg acc ggc acc ggc gtg ctg acc cct agc agc     1635
```

```
Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser
            530                 535                 540

aag agg ttc cag ccc ttc cag cag ttc ggc agg gac gtg agc gat ttc    1683
Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe
545                 550                 555

acc gac agc gtg agg gat cct aag acc agc gag atc ctg gac atc agc    1731
Thr Asp Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser
560                 565                 570

cct tgc agc ttc ggc ggc gtg agc gtg atc acc ccc ggc acc aac gcc    1779
Pro Cys Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala
575                 580                 585                 590

agc tcc gag gtg gcc gtg ctg tac cag  gac gtg aac tgc acc gac gtg    1827
Ser Ser Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val
            595                 600                 605

agc acc gcc atc cac gcc gac cag ctg acc ccc gcc tgg aga atc tac    187 5
Ser Thr Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr
            610                 615                 620

agc acc ggc aac aac gtg ttc cag acc cag gcc ggc tgc ctg atc ggc    1923
Ser Thr Gly Asn Asn Val Phe Gln Th r Gln Ala Gly Cys Leu Ile Gly
625                 630                 635

gcc gag cac gtg gac acc agc tac gag tgc gac atc ccc atc gga gcc    1971
Ala Glu His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala
640                 645                 650

ggc atc tgc gcc agc tac cac acc gtg agc ctg ctg aga agc acc agc    2019
Gly Ile Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser
655                 660                 665                 670

cag aag agc atc gtg gcc tac acc atg agc ctg ggc gcc gac agc agc    2067
Gln Lys Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser
            675                 680                 685

atc gcc tac agc aac aac acc atc gcc atc ccc acc aac ttc agc atc    2115
Ile Ala Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile
            690                 695                 700

agc atc acc acc gag gtg atg ccc  gtg agc atg gcc aag acc agc gtg    2163
Ser Ile Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val
705                 710                 715

gac tgc aac atg tac atc tgc ggc gac agc acc gag tgc gcc aac ctg     2211
Asp Cys Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu
720                 725                 730

ctg ctg cag tac ggc agc ttc tgc acc cag ctg aac aga gcc ctg agc    2259
Leu Leu Gln Tyr Gly Ser Phe Cy s Thr Gln Leu Asn Arg Ala Leu Ser
735                 740                 745                 750

ggc atc gcc gcc gag cag gac aga aac acc agg gag gtg ttc gcc cag    2307
Gly Ile Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln
            755                 760                 765

gtg aag cag atg tat aag acc ccc acc ctg aag tac ttc ggc ggc ttc    2355
Val Lys Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe
            770                 775                 780
```

```
aac ttc agc cag atc ctg ccc gat cct ctg aag ccc acc aag cgg agc     2403
Asn Phe Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser
        785                 790                 795

ttc atc gag gac ctg ctg ttc aac aag gtg acc ctg gcc gac gcc ggc     2451
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
    800                 805                 810

ttt atg aag cag tac ggc gag tgc ctg ggc gat atc aac gcc agg gac     2499
Phe Met Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp
815                 820                 825                 830

ctg atc tgc gcc cag aag ttc aat ggc ctg acc gtg ctg ccc ccc ctg     2547
Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
                835                 840                 845

ctg acc gac gac atg atc gcc gcc tac aca gcc gcc ctg gtg agc ggc     2595
Leu Thr Asp Asp Met Ile Al a Ala Tyr Thr Ala Ala Leu Val Ser Gly
            850                 855                 860

acc gcc acc gcc ggc tgg acc ttt ggc gcc gga gcc gcc ctg cag atc     2643
Thr Ala Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Il e
        865                 870                 875

ccc ttc gcc atg cag atg gcc tac cgg ttc aat ggc atc ggc gtg acc     2691
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
    880                 8 85                890

cag aac gtg ctg tac gag aac cag aag cag atc gcc aac cag ttc aac     2739
Gln Asn Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn
895                 900                 905                 9 10

aag gcc atc agc cag atc cag gag agc ctg acc acc aca agc acc gcc     2787
Lys Ala Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala
                915                 920                 925

ctg ggc aag ctg cag gac gtg gtg aac cag aac gcc cag gcc ctg aat     2835
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
            930                 935                 940

acc ctg gtg aag cag ctg agc agc aac ttc ggc gcc atc agc tcc gtg     2883
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
        945                 950                 955

ctg aac gac atc ctg agc cgg ctg gac aag gtg gag gcc gag gtg cag     2931
Leu Asn Asp Ile Leu Se r Arg Leu Asp Lys Val Glu Ala Glu Val Gln
    960                 965                 970

atc gac aga ctg atc acc ggc aga ctg cag agc ctg cag acc tac gtg     2979
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Ty r Val
975                 980                 985                 990

acc cag cag ctg atc aga gcc gcc gag atc aga gcc agc gcc aac ctg     3027
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
                995                 1000                1005

gcc gcc acc aag atg agc gag tgc gtg ctg ggc cag agc aag aga         3072
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
            1010                1015                102 0

gtg gac ttc tgc ggc aag ggc tac cac ctg atg agc ttc ccc cag         3117
Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
            1025                1030                1035
```

```
gcc gct ccc cac  ggc gtg gtg ttc ctg  cac gtg acc tac gtg  cct      3162
Ala Ala Pro His  Gly Val Val Phe Leu  His Val Thr Tyr Val  Pro
                1040                 1045                 1050

agc cag gag agg  aat ttc acc acc gcc  cct gcc atc tgc c ac  gag     3207
Ser Gln Glu Arg  Asn Phe Thr Thr Ala  Pro Ala Ile Cys His  Glu
                1055                 1060                 1065

ggc aag gcc tac  ttc ccc aga gag ggc  gtg ttc gtg ttc aat  ggc     3252
Gly Lys Ala Tyr  Phe Pro Arg Glu Gly  Val Phe Val Phe Asn  Gly
                1070                 1075                 1080

acc agc tgg ttc  atc acc cag cgg aac  ttc ttc agc ccc cag  atc     3297
Thr Ser Trp Phe  Ile Thr Gln Arg Asn  Phe Phe Ser Pro  Gln  Ile
                1085                 1090                 1095

atc aca acc gac  aac acc ttc gtg agc  ggc aac tgc gac gtg  gtg     3342
Ile Thr Thr Asp  Asn Thr Phe Val Ser  Gly Asn Cys Asp Val  Val
                1100                 1105                 1110

atc ggc atc att  aac aat acc gtg tac  gac ccc ctg cag ccc  gag     3387
Ile Gly Ile Ile  Asn Asn Thr Val Tyr  Asp Pro Leu Gln Pro  Glu
                1115                 1120                 1125

ctg gat agc ttc  aag gag gag ctg gac  aag tac ttc aag aac  cac     3432
Leu Asp Ser Phe  Lys Glu Glu Leu Asp  Lys Tyr Phe Lys Asn  His
                1130                 1135                 1140

acc agc ccc gat  gtg gac ttc ggc gac  atc agc ggc atc aat  gcc     3477
Thr Ser Pro Asp  Val Asp Phe Gly Asp  Ile Ser Gly Ile Asn  Ala
                1145                 1150                 1155

agc gtg gtg aac  atc cag aag gag atc  gac cgg ctg a ac gag  gtg     3522
Ser Val Val Asn  Ile Gln Lys Glu Ile  Asp Arg Leu Asn Glu  Val
                1160                 1165                 1170

gcc aag aac ctg  aac gag agc ctg atc  gac ctg cag gag ctg  ggc     3567
Ala Lys Asn Leu  Asn Glu Ser Leu Ile  Asp Leu Gln Glu Leu  Gly
                1175                 1180                 1185

aag tac gag cag  tac atc aag tgg ccc  tgg tac gtg tgg ctg  ggc     3612
Lys Tyr Glu Gln  Tyr Ile Lys Trp Pro  Trp Tyr Val  Trp Leu  Gly
                1190                 1195                 1200

ttc atc gcc ggc  ctg atc gcc atc gtg  atg gtg acc atc ctg  ctg     3657
Phe Ile Ala Gly  Leu Ile Ala Ile Val  Met Val Thr Ile Leu  Leu
                1205                 1210                 1215

tgc tgc atg acc  agc tgc tgc tcc tgc  ctg aag ggc gcc tgc  agc     3702
Cys Cys Met Thr  Ser Cys Cys Ser Cys  Leu Lys Gly Ala Cys  Ser
                1220                 1225                 1230

tgt ggc agc tgc  tgc aag ttc gac gag  gac gat agc gag ccc  gtg     3747
Cys Gly Ser Cys  Cys Lys Phe Asp Glu  Asp Asp Ser Glu Pro  Val
                1235                 1240                 1245

ctg aag ggc gtg  aag ctg cac tac acc  tga tgaattctcg ag           3789
Leu Lys Gly Val  Lys Leu His Tyr Thr
                1250                 1255
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<210> 463

<211> 1255

<212> PRT

<213> Artificial sequence

<220>

<223> Codon-optimized sequence of S protein of SARS -CoV stra in Frankfurt 1

<400> 463

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
260 265 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335

Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
405 410 415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
420 425 430

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu

435 440 445

Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
450 455 460

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465 470 475 480

Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
485 490 495

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510

Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575

Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685

```
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690                 695                 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705                 710                 715                 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
                725                 730                 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740                 745                 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
        755                 760                 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770                 775                 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785                 790                 795                 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
                805                 810                 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp  Leu Ile
            820                 825                 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
        835                 840                 845

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val  Ser Gly Thr Ala
850                 855                 860

Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865                 870                 875                 880

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly  Ile Gly Val Thr Gln Asn
                885                 890                 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
            900                 905                 910

Ile Ser Gln Ile Gln Glu Ser Leu  Thr Thr Thr Ser Thr Ala Leu Gly
        915                 920                 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
930                 935                 940
```

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Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945                 950                 955                 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
                965                 970                 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
            980                 985                 990

Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
        995                 1000                1005

Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
    1010                1015                1020

Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
    1025                1030                1035

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
    1040                1045                1050

Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
    1055                1060                1065

Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
    1070                1075                1080

Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
    1085                1090                1095

Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
    1100                1105                1110

Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
    1115                1120                1125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
    1130                1135                1140

Pro Asp Val Asp Phe Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
    1145                1150                115 5

Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
    1160                1165                1170

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
    1175                1180                 1185
```

Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
1190 1195 1200

Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
1205 1210 1215

Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
1220 1225 1230

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
1235 1240 1245

Gly Val Lys Leu His Tyr Thr
1250 1255

<210> 464

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primer XhoISpikeRevCOG

<400> 464
gttcctcgag gggccacttg atgtactgc 29

<210> 465

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Primer SpikeCOG seq 1

<400> 465
ccaggtgaag cagatgta 18

<210> 466

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Primer KpnINCFor

<400> 466
cttggtaccg ccaccatgtc tgataatgga cc 32

<210> 467

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer XbaINCRev

<400> 467
gttctctaga tgcctgagtt gaatcagc 28

<210> 468

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide

<400> 468

Arg Ser Ala Pro Arg Ile Thr Phe Gly
1 5

<210> 469

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide primer EcoRIspikeFor318

<400> 469
cctggaattc tccatggcca acatcaccaa cc 32

<210> 470

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide primer XbaIspikeRev510

<400> 470
gaagggccct ctagacacgg tggcagg 27

<210> 471

<211> 1350

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03 -006

<220>

<221> CDS

<222> (1)..(1350)

<223>

<400> 471

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gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg        48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agc ggc tac        96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30

cct atg cac tgg gtc cgc cag gcg ccc ggg aag ggg ctg gag tgg gtg       144
Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
gca gtt ata tca tat gac gga agt aat aaa tac tat gca  gac tcc gtg      192
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat      240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

ctg caa atg aac agc ctg aga gct gag gac aca gct gtg tat tac tgt      288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  Tyr Tyr Cys
                85                  90                  95

gct aaa gac ggc agc ccc cgc acc ccc agc ttc gat tac tgg ggc cag      336
Ala Lys Asp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtg acc gtc tcc agc gct agc acc aag ggc ccc agc gtg      384
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca gcc gcc      432
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc      480
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

tgg aac agc ggc gcc ttg acc agc ggc gtg cac acc  ttc ccc gcc gtg      528
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc gtg ccc      576
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

agc agc agc ctg ggc acc cag acc tac atc tgc aac gtg aac cac aag      624
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  Val Asn His Lys
        195                 200                 205

ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag agc tgc gac      672
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

aag acc cac acc tgc ccc ccc tgc cct gcc ccc gag ctg ctg ggc gga      720
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc atg atc      768
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc cac gag      816
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

gac ccc gag gtg aag ttc aac tgg tac gtg gac  ggc gtg gag gtg cac      864
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc tac cgg      912
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
```

```
gtg gtg agc gtg ctc acc gtg ctg cac cag gac tgg ctg aac ggc aag      960
Val Val Ser Val Leu Thr Val Leu His Gln Asp  Trp Leu Asn Gly Lys
305                 310                 315                 320

gag tac aag tgc aag gtg agc aac aag gcc ctg cct gcc ccc atc gag     1008
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

aag acc atc agc aag gcc aag ggc cag ccc cgg gag ccc cag gtg tac     1056
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

acc ctg ccc ccc agc cgg gag gag atg acc aag aac cag gtg tcc ctc     1104
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag tgg     1152
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

gag agc aac ggc cag ccc gag aac aac tac  aag acc acc ccc cct gtg     1200
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

ctg gac agc gac ggc agc ttc ttc ctg tac agc aag ctc acc gtg gac     1248
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

aag agc cgg tgg cag cag ggc aac gtg ttc agc tgc agc gtg atg cac     1296
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  Ser Cys Ser Val Met His
            420                 425                 430

gag gcc ctg cac aac cac tac acc cag aag agc ctg agc ctg agc ccc     1344
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

ggc aag                                                            1350
Gly Lys
    450
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<210> 472

<211> 450

<212> PRT

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03-006

<400> 472

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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 Ser Gly Tyr
```

```
                20                  25                  30

    Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 5           35                  40                  45

    Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
        50                  55                  60
10
    Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    65                  70                  75                  80

15  Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                    85                  90                  95

20  Ala Lys Asp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr Trp Gly Gln
                100                 105                 110

    Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
25          115                 120                 125

    Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
        130                 135                 140
30
    Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
    145                 150                 155                 160

35  Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  Val
                    165                 170                 175

40  Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
                180                 185                 190

    Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  Asn His Lys
45          195                 200                 205

    Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
        210                 215                 220
50
    Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  Glu Leu Leu Gly Gly
    225                 230                 235                 240

55  Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                    245                 250                 255

60  Ser Arg Thr Pro Glu Val Thr Cys Val  Val Val Asp Val Ser His Glu
                260                 265                 270
```

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 473

<211> 1335

<212> DNA

<213> Artificial sequence

<220>

<223> IgG heavy chain of 03 -015

<220>

<221> CDS

<222> (1)..(1335)

<223>

<400> 473

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gag gtg cag ctg gtg gag tct ggg gga ggt gtg gta cgg cct  ggg ggg       48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1               5                   10                  15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt gat gat tat       96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

ggc atg agc tgg gtc cgc caa gct cca ggg aag ggg ctg gag tgg gtc      144
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

tct ggt att aat tgg aat ggt ggt agc aca ggt tat gca gac tct gtg      192
Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
    50                  55                  60

aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat      240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

ctg caa atg aac agt ctg aga gcc gag gac acg gcc gtg tat tac tgt      288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gca aga ggt ttg tct ctt cgt cct tgg ggc cag ggc acc ctg gtg acc      336
Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

gtc tcc agc gct agc acc aag ggc ccc agc gtg ttc ccc  ctg gcc ccc      384
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

agc agc aag agc acc agc ggc ggc aca gcc gcc ctg ggc tgc ctg gtg      432
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

aag gac tac ttc ccc gag ccc gtg acc gtg agc tgg aac agc ggc gcc      480
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

ttg acc agc ggc gtg cac acc ttc ccc gcc gtg ctg cag agc agc ggc      528
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

ctg tac agc ctg agc agc gtg gtg acc gtg ccc agc agc agc ctg ggc      576
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

acc cag acc tac atc tgc aac gtg aac cac aag ccc agc aac acc aag      624
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205
```

```
gtg gac aaa cgc gtg gag ccc aag agc tgc gac aag acc cac acc tgc      672
Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

ccc ccc tgc cct gcc ccc gag ctg ctg ggc gga ccc  tcc gtg ttc ctg      720
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

ttc ccc ccc aag ccc aag gac acc ctc atg atc agc cgg acc ccc gag      768
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

gtg acc tgc gtg gtg gtg gac gtg agc cac gag gac ccc gag gtg aag      816
Val Thr Cys Val Val Val Asp Val Ser His Glu As p Pro Glu Val Lys
            260                 265                 270

ttc aac tgg tac gtg gac ggc gtg gag gtg cac aac gcc aag acc aag      864
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

ccc cgg gag gag cag tac aac agc acc tac cgg gtg gtg agc gtg ctc      912
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 3 00

acc gtg ctg cac cag gac tgg ctg aac ggc aag gag tac aag tgc aag      960
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

gtg agc aac aag gcc ctg cct gcc ccc atc gag aag acc atc agc aag     1008
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

gcc aag ggc cag ccc cgg gag ccc cag gtg tac  acc ctg ccc ccc agc     1056
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

cgg gag gag atg acc aag aac cag gtg tcc ctc acc tgt ctg gtg aag     1104
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aac ggc cag     1152
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Tr p Glu Ser Asn Gly Gln
    370                 375                 380

ccc gag aac aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc     1200
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

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Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

cag ggc aac gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac     1296
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

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35 40 45

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys

195 200 205

Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
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Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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1               5                  10                  15

gac aga gtc acc atc act tgc cgg gcg agt cag ggc att agc aat tat       96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
            20                  25                  30

tta gcc tgg tat cag cag aaa cca ggg aaa gtt cct aag ctc ctg atc      144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45

tat gct gca tcc act ttg caa tca ggg gtc cca tct cgg ttc agt ggc      192
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct      240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

gaa gat gtt ggg gtt tat tac tgc cag cag agg ttc cgc acg ccg gtc      288
Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Arg Phe Arg Thr Pro Val
                85                  90                  95

acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgg acc gtg gcc gct      336
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

ccc agc gtg ttc atc ttc ccc ccc tcc gac gag cag ctg aag agc ggc      384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

acc gcc agc gtg gtg tgc ctg ctg aac aac ttc tac ccc cgg gag gcc      432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

aag gtg cag tgg aag gtg gac aac gcc ctg cag agc ggc aac agc cag      480
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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

agc acc ctc acc ctg agc aag gcc gac tac gag aag cac aag gtg tac 576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

gcc tgc gag gtg acc cac cag ggc ctg agc agc ccc gtg acc aag agc 624
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35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Arg Phe Arg Thr Pro Val
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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
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Phe Asn Arg Gly Glu Cys
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Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
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agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144
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          35                  40                  45

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 5       50                  55                  60

     agc tca gga aac aca gct tcc ttg acc atc act ggg g ct cag gcg gaa      240
     Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
     65                  70                  75                  80
10
     gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac cat      288
     Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
                 85                  90                  95

15   gtg gta ttc ggc gga ggg acc aag ctt acc gtg ctg ggc cag ccc aag      336
     Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  Gly Gln Pro Lys
             100                 105                 110

     gcc gct ccc agc gtg acc ctg ttc ccc ccc tcc tcc gag gag ctg cag      384
20   Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
         115                 120                 125

     gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc tac cct ggc      432
     Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
25       130                 135                 140

     gcc gtg acc gtg gcc tgg aag gcc gac agc agc ccc gtg aag gcc ggc      480
     Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
     145                 150                 155                 160
30
     gtg gag acc acc acc ccc agc aag cag agc aac aac aag tac gcc gcc      528
     Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
                 165                 170                 175

35   agc agc tac ctg agc ctc acc ccc gag cag tgg a ag agc cac cgg agc      576
     Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
             180                 185                 190

     tac agc tgc cag gtg acc cac gag ggc agc acc gtg gag aag acc gtg      624
40   Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
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     gcc ccc acc gag tgc agc                                          642
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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
                85                  90                  95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
            100                 105                 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
        115                 120                 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
    130                 135                 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145                 150                 155                 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
                165                 170                 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
            180                 185                 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
        195                 200                 205

Ala Pro Thr Glu Cys Ser
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CLAIMS

1. A binding molecule capable of specifically binding to a SARS-CoV.

2. A binding molecule according to claim 1, which is a human binding molecule.

3. A binding molecule according to claim 1 or 2, wherein the binding molecule comprises at least a CDR3 region comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300 and SEQ ID NO:301.

4. A binding molecule according to any one of the claims 1 - 3, wherein the binding molecule comprises a heavy chain comprising the amino acid sequence selected from the group consisting of SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:303, SEQ ID NO:307, SEQ ID NO:311, SEQ ID NO:315, SEQ ID NO:319, SEQ ID NO:323, SEQ ID NO:327, SEQ ID NO:331, SEQ ID NO:335, SEQ ID NO:339, SEQ ID NO:343, SEQ ID NO:347, SEQ ID NO:351, SEQ ID NO:355, SEQ ID NO:359, SEQ ID NO:363, SEQ ID NO:367, SEQ ID NO:371, SEQ ID NO:375, SEQ ID NO:379, SEQ ID NO:383, SEQ ID NO:387, SEQ ID

NO:391, SEQ ID NO:395, SEQ ID NO:399, SEQ ID NO:403, SEQ ID NO:407, SEQ ID NO:411, SEQ ID NO:415, SEQ ID NO:419, SEQ ID NO:423, SEQ ID NO:427, SEQ ID NO:431, SEQ ID NO:435, SEQ ID NO:439, SEQ ID NO:443, SEQ ID NO:447, SEQ ID NO:451, SEQ ID NO:455 and SEQ ID NO:459.

5. A functional variant of a binding molecule according to any one of the claims 1 - 4, wherein the functional variant is capable of competing for specifically binding to a SARS-CoV.

6. A binding molecule according to any one of the claims 1 - 4 or a functional variant according to claim 5, characterized in that the antibody or functional variant has SARS-CoV neutralizing activity.

7. An immunoconjugate comprising a binding molecule according to any one of the claims 1 - 4 or 6 or a functional variant according to claim 5 or 6, the immunoconjugate further comprising at least one tag.

8. An immunoconjugate according to claim 7, wherein the tag is selected from the group consisting of a radioactive substance, an enzyme and combinations thereof.

9. A nucleic acid molecule encoding a binding molecule according to any one of the claims 1 - 4 or 6 or a functional variant according to claim 5 or 6.

10. A vector comprising at least one nucleic acid molecule according to claim 9.

11. A host comprising at least one vector according to claim 10.

12. A host according to claim 11, wherein the host is a cell derived from a human cell.

13. A method of producing a binding molecule according to any one of the claims 1 - 4 or 6 or a functional variant according to claim 5 or 6, wherein the method comprises the steps of:

a) culturing a host according to claim 11 or 12 under conditions conducive to the expression of the binding molecule or functional variant, and optionally,

b) recovering the expressed binding molecule or functional variant.

14. A binding molecule or functional variant thereof as obtainable by the method according to claim 13.

15. A composition comprising a binding molecule according to any one of the claims 1 - 4 or 6, a functional variant according to claim 5 or 6, an immunoconjugate according to claim 7 or 8, or a binding molecule or functional variant thereof according to claim 14.

16. A composition comprising a nucleic acid molecule according to claim 9.

17. A pharmaceutical composition comprising a binding molecule according to any one of the claims 1 - 4 or 6, a functional variant according to claim 5 or 6, an

immunoconjugate according to claim 7 or 8, a binding molecule or functional variant thereof according to claim 14, or a composition according to claim 15 or 16, the pharmaceutical composition further comprising at least one pharmaceutically acceptable excipient.

18. A pharmaceutical composition according to claim 17 further comprising at least one other therapeutic agent.

19. A binding molecule according to any one of the claims 1 - 4 or 6, a functional variant according to claim 5 or 6, an immunoconjugate according to claim 7 or 8, a binding molecule or functional variant thereof according to claim 14, a composition according to claim 15 or 16, or a pharmaceutical composition according to claim 17 or 18 for use as a medicament.

20. A binding molecule according to any one of the claims 1 - 4 or 6, a functional variant according to claim 5 or 6, an immunoconjugate according to claim 7 or 8, a binding molecule or functional variant thereof according to claim 14, a composition according to claim 15 or 16, or a pharmaceutical composition according to claim 17 or 18 for use in the diagnosis, prophylaxis, treatment, or combination thereof, of a condition resulting from a SARS-CoV.

21. Use of a binding molecule according to any one of the claims 1 - 4 or 6, a functional variant according to claim 5 or 6, an immunoconjugate according to claim 7 or 8, a binding molecule or functional variant thereof according to claim 14, a composition according to claim 15 or 16, or a pharmaceutical composition according to claim 17 or 18 in the

preparation of a medicament for the diagnosis, prophylaxis, treatment, or combination thereof, of a condition resulting from a SARS-CoV.

22. A kit comprising a binding molecule according to any one of the claims 1 - 4 or 6, a functional variant according to claim 5 or 6, an immunoconjugate according to claim 7 or 8, a nucleic acid molecule according to claim 9, a vector according to claim 10, a host according to claim 11 or 12, a binding molecule or functional variant thereof according to claim 14, a composition according to claim 15 or 16, a pharmaceutical composition according to claim 17 or 18, or a combination thereof.

23. A method of identifying a binding molecule specifically binding to a SARS-CoV or a nucleic acid molecule encoding a binding molecule specifically binding to a SARS-CoV, wherein the method comprises the steps of:

a) contacting a phage library of binding molecules with a SARS-CoV or a fragment thereof,

b) selecting at least once for a phage binding to the SARS-CoV or the fragment thereof, and

c) separating and recovering the phage binding to the SARS-CoV or the fragment thereof.

24. A method according to claim 23, wherein the phage library of binding molecules is prepared from RNA isolated from cells obtained from a subject that has been vaccinated or exposed to a SARS-CoV.

25. A method according to claim 23 or 24, wherein the phage library of binding molecules is a scFv phage library.

26. A method according to any of the claims 23 - 25, wherein the subject is a human subject which has recovered from SARS-CoV.

27. A method of obtaining a binding molecule specifically binding to a SARS-CoV or a nucleic acid molecule encoding a binding molecule specifically binding to a SARS-CoV, wherein the method comprises the steps of:

a) performing the method according to any of the claims 23 - 26, and

b) isolating from the recovered phage the binding molecule and/or the nucleic acid molecule encoding the binding molecule.

28. A phage library of binding molecules, characterized in that the library is prepared from RNA isolated from cells obtained from a subject that has been vaccinated or exposed to a SARS-CoV.

29. A phage library of binding molecules according to claim 28, characterized in that the library is a scFv phage library.

30. A phage library of binding molecules according to claim 28 or 29, characterized in that the subject is a human subject which has recovered from SARS-CoV.

31. A method of detecting a SARS-CoV in a sample, wherein the method comprises the steps of:

a) contacting a sample with a diagnostically effective amount of a binding molecule according to any one of

the claims 1 - 4, 6 or 14 or a functional variant according to claim 5, 6 or 14 or an immunoconjugate according to claim 7 or 8, and

b) determining whether the binding molecule, functional variant, or immunoconjugate specifically binds to a molecule of the sample.

32. A method according to claim 31, wherein the sample is a sample from a human subject potentially infected with a SARS-CoV.

33. A method of screening a binding molecule or a functional variant of a binding molecule for specific binding to the same epitope of a SARS-CoV as the epitope bound by the binding molecule according to any one of the claims 1 - 4, 6 or 14, wherein the method comprises the steps of:

a) contacting a binding molecule or a functional variant to be screened, a binding molecule according to any one of the claims 1 - 4, 6 or 14 and a SARS-CoV or fragments thereof,

b) measure if the binding molecule or functional variant to be screened is capable of competing for specifically binding to the SARS-CoV with the binding molecule according to any one of the claims 1 - 4, 6 or 14.

34. A method of identifying a binding molecule potentially having neutralizing activity against SARS-CoV, wherein the method comprises the steps of:

a) contacting a collection of binding molecules on the surface of replicable genetic packages with the SARS-CoV under conditions conducive to binding,

b) separating and recovering binding molecules that bind to the SARS-CoV from binding molecules that do not bind,

c) isolating at least one recovered binding molecule,

d) verifying if the binding molecule isolated has neutralizing activity against the SARS-CoV,

characterized in that the SARS-CoV in step a is inactivated.

35. A method according to claim 34, characterized in that the inactivation is performed by gamma- or UV-irradiation.

36. A method according to claim 34 or 35, characterized in that the replicable genetic package is selected from the group consisting of a phage particle, a bacterium, a yeast, a fungus, a spore of a microorganism and a ribosome.

37. A method according to any of the claims 34 - 36, characterized in that the binding molecule is a human binding molecule.

38. A method according to any of the claims 34 - 37, characterized in that the binding molecule is a single chain Fv.

39. A method according to any of the claims 34 - 38, characterized in that the inactivated SARS-CoV is purified before being inactivated.

40. A method according to any of the claims 34 - 39, characterized in that the inactivated SARS-CoV in step a is immobilized.

41. A binding molecule obtainable by the method according to any of the claims 34 - 40, the binding molecule having neutralizing activity against the SARS-CoV.

42. A pharmaceutical composition comprising a binding molecule according to claim 41, the pharmaceutical composition further comprising at least one pharmaceutically acceptable excipient.

43. A pharmaceutical composition according to claim 42 further comprising at least one other therapeutic agent.

44. A binding molecule according to claim 41 or a pharmaceutical composition according to claim 42 or 43 for use as a medicament.

45. A binding molecule according to claim 41 or a pharmaceutical composition according to claim 42 or 43 for use in the diagnosis, prophylaxis, treatment, or combination thereof of a condition resulting from SARS-CoV.