

TITLE OF THE INVENTION

Binding molecules against SARS-coronavirus and uses thereof

FIELD OF THE INVENTION

5 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.

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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., 15 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 20 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

25 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 30 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
5 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.

10 Figure 3 shows the construction of the bivalent scFv expression vector pPICZbiFVH. In figure 3A the vector pPICZ00B 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.

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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-
20 016, 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
25 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
30 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
5 (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,
10 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
15 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.

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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
25 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
30 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 fluorescence 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.

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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.

15 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.

25 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.

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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.

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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.

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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.

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20 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.

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DESCRIPTION OF THE INVENTION

Herebelow follow definitions of terms as used in the invention

DEFINITIONS

5

Amino acid sequence

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

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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
5 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
10 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.

15 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
20 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 engineered by
25 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
30 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
5 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
10 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
15 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
20 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
25 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

30 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
5 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.

10 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
15 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,
20 as present on the proteins as denatured, e.g., by solubilization in SDS. Epitopes may also consist of posttranslational modifications of proteins.

Deletion

25 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.

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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
5 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
10 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
15 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

20 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
25 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
30 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.

10 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), 15 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 20 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 25 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 30 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
5 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
10 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
15 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
20 herein.

Human

The term "human", when applied to binding molecules as defined herein, refers to molecules that are either directly derived
25 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
30 include binding molecules having variable and constant regions derived from human germline immunoglobulin sequences based on variable or constant regions either or not occurring 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
5 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
10 template exactly or with minor modifications. Semisynthetic molecules based on human sequences are also considered to be human as used herein.

Insertion

15 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.

20

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,
25 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
30 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.

20 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 occurring

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.

10 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
5 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
10 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
15 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
20 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
25 sequence should be understood as being "under the control of" the promoter.

Pharmaceutically acceptable excipient

By "pharmaceutically acceptable excipient" is meant any inert
30 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.

5

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
10 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
15 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
20 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
25 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.

30 Substitutions

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

5 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.

10

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
15 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 from infection with SARS-CoV might also be in need of treatment. Prevention encompasses inhibiting or
20 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

25 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
30 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.

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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.

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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

5 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

10 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

15 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

20 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

25 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

30 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
5 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
10 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
15 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
20 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).
25 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
30 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

5 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 $0.2 \cdot 10^{-4}$ M, $1.0 \cdot 10^{-5}$ M, $1.0 \cdot 10^{-6}$ M, $1.0 \cdot 10^{-7}$ M, preferably
10 lower than $1.0 \cdot 10^{-8}$ M, more preferably lower than $1.0 \cdot 10^{-9}$ M, more preferably lower than $1.0 \cdot 10^{-10}$ M, even more preferably lower than $1.0 \cdot 10^{-11}$ M, and in particular lower than $1.0 \cdot 10^{-12}$ M. The affinity constants can vary for antibody isotypes. For example, affinity binding for an IgM isotype refers to a
15 binding affinity of at least about $1.0 \cdot 10^{-7}$ 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
20 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
25 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
30 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 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 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
5 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
10 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
15 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
20 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
25 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
30 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
5 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
10 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
15 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
20 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
25 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
30 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 preferred embodiment the binding
5 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
10 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
15 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
20 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
25 of phosphatidylinositol, 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,
30 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 particular 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.

5 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
10 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
15 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,
20 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
25 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),
30 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-galactopyranoside (PNPG), 3', 3'-diaminobenzidine (DAB), 3-amino-9-ethylcarbazole (AEC), 4-chloro-1-naphthol (CN), 5-bromo-4-chloro-3-indolyl-phosphate (BCIP), ABTS, BlueGal, 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 , ^3H , 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
5 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-
10 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.

15 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
20 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
25 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
30 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
5 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
10 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
15 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
20 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
25 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
30 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
5 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
10 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
15 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
20 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
25 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
30 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

5 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

10 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

15 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

20 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

25 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

30 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

5 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

10 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

15 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

20 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

25 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

30 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 ϕ , 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, phytorepovirus, plant rhabdovirus, potexvirus, potyvirus, sobemovirus, tenuivirus, tobamovirus, tobnavirus, 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, vesicular 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.

5 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

10 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

15 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

20 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

25 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*.

30 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
5 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
10 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
15 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
20 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
25 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 upstream or downstream as well as descendants from ancestors of
30 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
5 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
10 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
15 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
20 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
25 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
30 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.

10 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.

25 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

5 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.

10 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.

15 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)
20 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
25 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
30 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

5 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

10 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

15 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

20 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

25 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

30 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

5 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-

10 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

15 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

20 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

25 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

30 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 Mabstrat™ process. Mabstrat™ 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
5 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,
10 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
15 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
20 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
25 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 alkanolic acids, hydroxy alkanolic acids, aromatic
30 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
5 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
10 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 salts as described above), detergents (e.g., SDS) and/or other suitable components.

15 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
20 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,
25 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
30 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, 5 cidofovir, D4T, ddC, ddI, d4T, delavirdine, didanosine, efavirenz, famciclovir, fialuridine, foscarnet, FTC, ganciclovir, GG167, idoxuridine, indinavir, interferon alpha, lamivudine, lobucavir, loviride, nelfinavir, nevirapine, 10 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 15 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 20 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.

25 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 30 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
5 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
10 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
15 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.

20 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
25 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,
30 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
5 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
10 categories include, but are not limited to, bolus, buccal, epidermal, epidural, inhalation, intra-abdominal, intra-arterial, intra-articular, intrabronchial, intracapsular, intracardiac, intracartilaginous, intracavitary, intracelical, intracelebellar, intracerebronventricular, intracolic,
15 intracervical, intradermal, intragastric, intrahepatic, intramedullary, intramuscular, intramyocardial, intranasal, intra-ocular intra-orbital, intra-osteal, intrapelvic, intrapericardiac, intraperitoneal, intraplaque, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal,
20 intraretinal, intraspinal, intrasternal, intrasynovial, intrathecal, intrathoracic, intratumoral, intra-uterine, intravenous, intraventricular, intravesical, rectal, spinal, subarachnoid, subcapsular, subcutaneous, subcuticular, sublingual, topical, transdermal, transmucosal, transtracheal,
25 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, dispersible powders or granules, emulsions, hard capsules,
30 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 vegetable 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 paraffin; 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),
5 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
10 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
15 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
20 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
25 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
30 *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 administered 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
5 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
10 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
15 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
20 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
25 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
30 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

5 (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

10 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 disintegrate into antigenic components such as proteins, (poly)peptides or other antigenic fragments. Preferably, the

15 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

20 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,

25 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

30 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
5 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
10 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
15 molecules, functional variants or immunoconjugates of the invention.

Furthermore, 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
20 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.
25 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
30 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

5 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
10 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.

15 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
20 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
25 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
30 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
5 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
10 ("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
15 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.
20 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
25 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
30 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.

5 In yet a further aspect 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
10 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
15 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
20 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,
25 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
30 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 described 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 excipients 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 cytopathic 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
5 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
10 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
15 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
20 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
25 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-
30 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
5 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,
10 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,
15 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 μ l (approximately 10^{13} cfu)
20 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
25 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.

30 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

5 *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
10 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,
15 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
20 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-
25 016, 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
30 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

5 *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
10 of Methods for Expression of Recombinant Proteins Using pPICZ and pPICZ α in Pichia pastoris (Version F)". The bivalent scFv expression vector pPicZbiFVH (see figure 3B) was constructed from the vector pPICZ μ B (see figure 3A) (Invitrogen) following standard molecular biology techniques known to a person
15 skilled in the art. Three modifications were introduced in the pPICZ μ B (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.
- 20 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
25 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 #
30 204414) was transformed with 5-10 μ g 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
5 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
10 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
15 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
20 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
25 purification by the addition of 1 M Na₂HPO₄ 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
30 AKTApurime FPLC-system (Pharmacia). A 5 ml HiTrap chelating column (Pharmacia) was charged with NiSO₄ and equilibrated according to the manufacturers instructions. Conditioned

supernatant was loaded directly onto the column and washed extensively in equilibration buffer (20 mM Na₂PO₄ 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
5 of 250 mM imidazole pH 8.5. The column was then washed in 20 mM Tris-HCl pH 8, then briefly in 20 mM Na₂PO₄ 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.
10 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,
15 pyBi03-009C02, pyBi03-010C02, pyBi03-012C02, pyBi03-013C02, pyBi03-014C02, pyBi03-015C02, respectively.

Example 5

*Construction of fully human immunoglobulin molecules (human
20 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
25 restriction sites and/or sequences for expression in the IgG expression vectors pSyn-C03-HC_μ1 (see SEQ ID No:110) and pSyn-C05-C_μ (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
30 products cloned into vector pSyn-C05-C_μ. 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-HCp1 and nucleotide sequences were verified according to standard techniques known to the skilled person in the art.

5H-B

acctgtcttgaattctccatggccgaggtgcagctggtggagtctg

10 sy3H-A

gcccttggtgctagcgctggagacggtcaccagggtgccctggcccc

5K-I

acctgtctcgagttttccatggctgacatccagatgacccagtctccatcctcc

15

sy3K-C

gggaccaaggtggagatcaaacggaccgtggccgccccccagc

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 4×10^3 TCID₅₀/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 $\geq 1:10$ 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 TCID₅₀/25 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.

5 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, pyBi03-10 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 15 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 20 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 25 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 30 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 TCID₅₀/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 TCID₅₀/25 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 2×10^3 TCID₅₀/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 TCID₅₀/50 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 1×10^4 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 TCID₅₀ 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 Frankfurt-1 strain of SARS-CoV. The cells were observed daily for any cytopathic 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 acetone 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

5 *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
10 cells which were infected with O.I. moi SARS-CoV strain Frankfurt 1 was harvested as soon as cytopathic 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
15 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
20 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
25 UV-irradiated at 4°C for 15 minutes (UV-B radiation 280-350 nm; μ max 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
30 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
5 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
10 (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
15 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
20 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

25 *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
30 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 performed 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,
5 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
10 (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
15 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
20 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
25 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-XCXXXXXXXXXXXXCX-minicard). If other cysteines besides the cysteines at position-2 and
30 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
5 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 H₂O 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 H₂O for
10 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
15 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
20 subsequently, after washing the peroxidase substrate 2,2'-azino-di-3-ethylbenzthiazoline sulfonate (ABTS) and 2 µl/ml 3% H₂O₂ 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
25 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,
30 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. Strikingly, 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*.
5 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
10 above peptides or parts thereof are useful in the detection of SARS-CoV in general.

Example 12

*Selection of single-chain phage antibodies specifically
15 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
20 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
25 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
30 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).

5 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-
10 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.

15 DNA encoding for the N-terminal 565 amino acids (portion called S565) was cloned as a *KpnI*-*BamHI* 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).

20 DNA encoding for the N-terminal 826 amino acids (portion called S826) was cloned as *KpnI*-*EcoRV* 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).

25 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: *XhoI*SpikeRevCOG 5'-
gttcctcgaggggccacttgatgtactgc-3' (SEQ ID NO:464) and SpikeCOG
30 seq 1 5'-ccaggtgaagcagatgta-3' (SEQ ID NO:465). The resulting fragment is cloned as *BstEII*-*XhoI* fragment together with a *KpnI*-*BstEII* fragment derived from the codon-optimized S

protein cDNA (alternatively, a restriction site other than *BstEII*, 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
5 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: *EcoRI*SpikeFor318 5'-cctggaattctccatggccaacatcaccaacc-3' (SEQ ID NO:469) and
10 *XbaI*SpikeRev510 5'-gaagggccctctagacacggtggcagg-3' (SEQ ID NO:470). The resulting fragment was digested with *EcoRI*-*XbaI* and cloned into pHAVT20/myc His A to yield pHAVT20/myc-His A S318-510. In this vector expression of fragment S318-510 fused
15 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 *KpnI*INCF 5'-cttggtagccgcccaccatgtctgataatggacc-3' (SEQ ID NO:466) and
20 *XbaI*INCFRev 5'-gttctctagatgcctgagttgaatcagc-3' (SEQ ID NO:467) and cloned as *KpnI*-*XbaI* 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
25 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
30 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 H₂SO₄ 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. Cells were washed three times, incubated for 45 minutes with biotinylated goat anti-human IgG followed by a 10 minute incubation with streptavidin-conjugated phycoerythrin. 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).

- 5 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

- 10 *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 ($\sim 5 \times 10^6$) 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/ μ l) and 2 μ l SuperscriptTMIII MMLV reverse transcriptase (200 U/ μ l) 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
5 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 μ l with DEPC treated ultrapure water. The OD_{260nm} of a 50 times diluted solution (in 10 mM Tris buffer) of the
10 dilution of the obtained cDNA products gave a value of 0.1.

5 to 10 μ l 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
15 reaction mixtures contained, besides the diluted cDNA products, 25 pmol sense primer and 25 pmol anti-sense primer in a final volume of 50 μ l of 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 2.5 mM MgCl₂, 250 μ M dNTPs and 1.25 units Taq polymerase. In a heated-lid thermal cycler having a temperature of 96°C,
20 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
25 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
30 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 MgCl₂, 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
5 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
10 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 HuCp2 5'-
TGAACATTCTGTAGGGGCCACTG-3' (see SEQ ID NO:159) or HuCp7 5'-
15 AGAGCATTCTGCAGGGGCCACTG-3' (see SEQ ID NO:160) (the HuCp2 and HuCp7 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
20 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
25 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
30 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
5 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
10 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
15 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
20 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
25 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
30 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 10×10^6 .

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
10 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
15 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
20 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
25 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
30 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.

5 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
15 obtained.

Example 15

Validation of the SARS-CoV specific single-chain phage antibodies derived from the naïve and immune phage display library
20

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
25 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-
30

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
5 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

10 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,
15 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,
20 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
25 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
30 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 TCID₅₀) of the SARS-CoV strain SCV-P4(5688) (obtained from patient 5688, see above). Antibody

5 concentrations used were extrapolated from the concentration of antibody needed to neutralize 100TCID₅₀ of virus in a volume of 100 μ l (*i.e.* 6.25 μ g/ml; see *in vitro* neutralization data in Example 7) and multiplied by twenty (*i.e.* 0.13 mg/ml for 1000TCID₅₀, 1.3 mg/ml for 10,000TCID₅₀). The virus/antibody

10 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-

15 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

20 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 μ l of the working solution was added to 2.46 ml

25 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

30 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 μ l 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
5 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 TCID₅₀/ml. The
10 starting solution was thawed at 37°C and 100 μ l of this solution was added to 900 μ l PBS and mixed well. The working solution thus obtained had a concentration of 10^6 TCID₅₀/ml.

To obtain a high dose SARS-CoV solution 200 μ l working solution was added to 1.8 ml PBS and mixed well (high dose
15 SARS-CoV solution, 100,000 TCID₅₀/ml). To obtain a low dose SARS-CoV solution 200 μ l 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
20 dose SARS-CoV solution, 2,000 TCID₅₀/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.

- 25 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 TCID₅₀/ml; final concentration of monoclonal antibody 03-014 0.13 mg/ml; total volume 5.4 ml).
- 30 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

TCID₅₀/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
5 well (final concentration of SARS-CoV was 1,000 TCID₅₀/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
10 mixed well (final concentration of SARS-CoV was 10,000 TCID₅₀/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
15 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
20 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
25 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 anaesthetized by means of light
30 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 intratracheally

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-
5 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
10 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
15 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
20 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
25 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
30 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 anaesthetized 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
5 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 μ l of the virus stock was added to 900 μ l PBS (at room temperature) to obtain a working virus stock of 10^6 TCID₅₀/ml. To obtain the
10 final solution containing the challenge dose of 10^4 TCID₅₀ per 3 ml challenge dose, 100 μ l 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
15 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
20 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; $p \leq 0.001$). The data were compared using the Students's T-test, differences were considered significant at p-value less than 0.05.

25 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
30 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 μ g/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
5 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),
10 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-
15 014 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
20 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
25 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
30 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.

30 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
5 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
10 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
15 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,
20 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 *EcoRI*-*XbaI*) fragment was recloned in *EcoRI*-*XbaI* cut pHAVT20/myc-His A. The resulting
25 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
30 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.

5 110 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.

10 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

15 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

20 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

25 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.

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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

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10

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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 nucleotide sequence	SEQ ID NO of amino acid sequence	HCDR3	V _H - germline	V _L - germline
SC03-001	46	47	HREFRHVFDY	V _H 3 V _H 3-38	V _K I DPK9 (02/012)
SC03-002	48	49	YYSRSLKAFDY	V _H 3 DP29 (V _H 3-72)	V _K I DPK9 (02/012)
SC03-003	50	51	RSYFRRFDY	V _H 3 DP47 (V _H 3-23)	V _K I DPK9 (02/012)
SC03-004	89	90	DGSRFPAREFDY	V _H 3 (V _H 3- 73)	V _K I DPK9 (02/012)
SC03-005	52	53	GGGRPYNPFDY	V _H 3 V _H 3-38	V _K I DPK9 (02/012)
SC03-006	54	55	DGSPRTPSFDY	V _H 3 DP49 (V _H 3-30)	V _K I DPK4 (A20)
SC03-007	56	57	GYWTSLTGFDY	V _H 3 DP49 (V _H 3-30)	V _K I DPK9 (02/012)
SC03-008	58	59	RVRPRRFDY	V _H 3 DP47 (V _H 3-23)	V _K I DPK9 (02/012)
SC03-009	60	61	GLFMVTTYAFDY	V _H 3 DP47 (V _H 3-23)	V _K I DPK9 (02/012)
SC03-010	62	63	GGGLPYLSFDY	V _H 3 V _H 3-38	V _K I DPK9 (02/012)
SC03-012	64	65	MFRKSSFDS	V _H 1 DP14 (V _H 1-18)	V _L III DPL16 (2- 13, 31)
SC03-013	66	67	GLTPLYFDY	V _H 3 DP29 (V _H 3-72)	V _K I DPK9 (02/012)
SC03-014	68	69	GISPFYFDY	V _H 3 DP29 (V _H 3-72)	V _K I DPK9 (02/012)
SC03-015	70	71	GLSLRP	V _H 3 DP32 (V _H 3-20)	V _L III DPL16 (2- 13, 31)
SC03-016	91	92	YGSAYRPPFDY	V _H 3 (V _H 3- 49)	V _K I DPK9 (02/012)
SC03-017	93	94	SRSAGFFDY	V _H 4 DP66 (V _H 4-61)	V _K III (L6)
SC03-018	95	96	FNPFTSFDY	V _H 3 DP47 (V _H 3-23)	V _K I 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

5 + 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
NGPQSNQRSAPRIIT	1.6	0.3
GPQSNQRSAPRIITNG	3.2	0.3
PQSNQRSAPRIITEGG	3.3	4.7
QSNQRSAPRIITEGGP	2.9	4.1
SNQRSAPRIITEGGPI	3.3	2.2
NQRSAPRIITEGGPIID	2.9	1.4
QRSAPRIITEGGPIIDS	2.6	3.9
RSAPRIITEGGPIIDSI	2.5	1.6
SAPRIITEGGPIIDSDI	1.4	0.6
APRIITEGGPIIDSDIN	2.3	0.5
PRITEGGPIIDSDIDNN	1.6	0.3
RITFEGGPIIDSDIDNNQ	0.5	0.2
ITFEGGPIIDSDIDNNQ	1.2	0.3
TFGGPIIDSDIDNNQNG	0.1	0.2
FGGPIIDSDIDNNQNGG	0.1	0.2
GGPIDSDIDNNQNGGR	0.1	0.2
GPIIDSDIDNNQNGGRN	0.2	0.2
PTDSDIDNNQNGGRNG	0.1	0.2
TDSDIDNNQNGGRNGA	0.2	0.2
DSDIDNNQNGGRNGAR	0.2	0.3
STDIDNNQNGGRNGARP	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
TALTQHGKEELRFP	0.1	0.3
ALTQHGKEELRFP	0.2	0.2
LTQHGKEELRFP	0.1	0.2
TQHGKEELRFP	0.1	0.2
QHGKEELRFP	0.1	0.2
HGKEELRFP	0.1	0.2
GKEELRFP	0.1	0.3
KEELRFP	0.1	0.3
EELRFP	0.1	0.3
ELRFP	0.1	0.2
LRFP	0.1	0.2
RFP	0.1	0.2
FPR	0.1	0.2
PRG	0.1	0.2
RG	0.1	0.2
GQ	0.1	0.2
QGV	0.1	0.1
GV	0.1	0.2
VP	0.1	0.2
PINT	0.1	0.2
INT	0.1	0.2
NT	0.1	0.3
TNS	0.1	0.2
NS	0.1	0.2
SG	0.1	0.3
GP	0.1	0.3
PDD	0.1	0.3
DD	0.1	0.3
DQ	0.1	0.3
QIG	0.1	0.2
IG	0.1	0.2
GY	0.1	0.2
YY	0.1	0.2
YR	0.1	0.3
YRR	0.1	0.2
YRRR	0.1	0.3
YRRRA	0.1	0.2
YRRRAT	0.1	0.2
YRRRATR	0.1	0.3
YRRRATRR	0.1	0.3
YRRRATRRV	0.1	0.3
YRRRATRRVR	0.1	0.3
YRRRATRRVRG	0.1	0.3
YRRRATRRVRGG	0.1	0.2
YRRRATRRVRGGD	0.1	0.2
YRRRATRRVRGGDG	0.1	0.2
YRRRATRRVRGGDGK	0.1	0.2

YRRATRRVRGGDGKM	0.1	0.2
RRATRRVRGGDGKMK	0.1	0.2
RATRRVRGGDGKMKE	0.1	0.2
ATRRVRGGDGKMKEL	0.1	0.2
TRRRVRGGDGKMKELS	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
GKMKELSPRWYFYLL	0.1	0.3
KMKELSPRWYFYLLG	0.1	0.2
MKELSPRWYFYLLGT	0.1	0.2
KELSPRWYFYLLGTG	0.1	0.3
ELSPRWYFYLLGTGP	0.1	0.2
LSPRWYFYLLGTGPE	0.1	0.2
SPRWYFYLLGTGPEA	0.1	0.2
PRWYFYLLGTGPEAS	0.1	0.2
RWYFYLLGTGPEASL	0.1	0.2
WYFYLLGTGPEASLP	0.1	0.2
YFYLLGTGPEASLPY	0.1	0.2
FYLLGTGPEASLPYG	0.1	0.2
YYLGTGPEASLPYGA	0.1	0.2
YLGTPPEASLPYGAN	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
ASLPYGANKEGIVVW	0.1	0.3
SLPYGANKEGIVVVA	0.1	0.2
LPYGANKEGIVVWAT	0.1	0.2
PYGANKEGIVVWATE	0.1	0.2
YGANKEGIVVWATEG	0.1	0.2
GANKEGIVVWATEGA	0.1	0.2
ANKEGIVVWATEGAL	0.1	0.2
NKEGIVVWATEGALN	0.1	0.2
KEGIVVWATEGALNT	0.1	0.2
EGIVVWATEGALNTP	0.1	0.2
GIVVWATEGALNTPK	0.1	0.2
IVVWATEGALNTPKD	0.1	0.2
VVWATEGALNTPKDH	0.1	0.3
WVATEGALNTPKDH	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
AEGRGGSQASSRSS	0.1	0.2
EGSRGGSQASSRSSS	0.1	0.2
GSRGGSQASSRSSSR	0.1	0.2
SRGGSQASSRSSSRs	0.1	0.2
RGGGSQASSRSSSRsR	0.1	0.1
GGsQASSRSSSRsRG	0.1	0.2

GSQASSRSSRSRGN	0.1	0.2
SQASSRSSRSRGNS	0.1	0.2
QASSRSSRSRGNSR	0.1	0.2
ASSRSSRSRGNSRN	0.1	0.2
SSRSSRSRGNSRNS	0.1	0.2
SRSSRSRGNSRNST	0.1	0.2
RSSRSRGNSRNSTP	0.1	0.2
SSRSRGNSRNSTPG	0.1	0.2
SSRSRGNSRNSTPGS	0.1	0.2
SRSRGNNSRNSTPGSS	0.1	0.2
RSRGNSRNSTPGSSR	0.1	0.2
SRGNNSRNSTPGSSRG	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
SRGNNSPARMASGGGE	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

DRLNQLESKVSQKGGQ	0.1	0.3
RLNQLESKVSQKGGQ	0.1	0.2
LNQLESKVSQKGGQQ	0.1	0.3
NQLESKVSQKGGQQQ	0.1	0.3
QLESKVSQKGGQQQG	0.1	0.3
LESKVSQKGGQQQGGQ	0.1	0.3
ESKVSQKGGQQQGGQT	0.1	0.2
SKVSQKGGQQQGGQTV	0.1	0.2
KVSQKGGQQQGGQTVT	0.1	0.2
VSQKGGQQQGGQTVTK	0.1	0.3
SGKGGQQQGGQTVTKK	0.1	0.2
GKGGQQQGGQTVTKKS	0.1	0.2
KGQQQGGQTVTKKSA	0.1	0.2
GQQQGGQTVTKKSAA	0.1	0.2
QQQGGQTVTKKSAAE	0.1	0.2
QQGGQTVTKKSAAEA	0.1	0.2
QGGQTVTKKSAAEAS	0.1	0.2
QGQTVTKKSAAEASK	0.1	0.2
GQTVTKKSAAEASKK	0.1	0.2
QTVTKKSAAEASKKP	0.1	0.2
TVTKKSAAEASKKPR	0.1	0.2
VTTKKSAAEASKKPRQ	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
DYKHWPQIAQFAPSAS	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
EVTTPSGTWLTYHGAI	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
WLTYPHGAIKLDDKDP	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
DPQFKDNVILLNKH	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

FPPTPKKDKKKKTD	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
MDDFSRQLQNSMSGAS	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. ($\mu\text{g/ml}$)	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+

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

-: No CPE

+: CPE $\leq$ 50%

2+: CPE 50-90%

5 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
 5 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 CAGRTGCAGCTGGTGCA 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 CAGCCGGCCATGGCCAGSTG 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

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	GACGGTGACCGTGGTCCC-3'	
--	-----------------------	--

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

Primer name	Primer nucleotide sequence	SEQ ID NO
HuVp1A	5'-CAGTCTGTGCTGACT CAGCCACC-3'	SEQ ID NO:161
HuVp1B	5'-CAGTCTGTGYTGACG CAGCCGCC-3'	SEQ ID NO:162
HuVp1C	5'-CAGTCTGTCGTGACG CAGCCGCC-3'	SEQ ID NO:163
HuVp2	5'-CARTCTGCCCTGACT CAGCCT-3'	SEQ ID NO:164
HuVp3A	5'-TCCTATGWGCTGACT CAGCCACC-3'	SEQ ID NO:165
HuVp3B	5'-TCTTCTGAGCTGACT CAGGACCC-3'	SEQ ID NO:166
HuVp4	5'-CACGTTATACTGACT CAACCGCC-3'	SEQ ID NO:167
HuVp5	5'-CAGGCTGTGCTGACT CAGCCGTC-3'	SEQ ID NO:168
HuVp6	5'-AATTTTATGCTGACT CAGCCCCA-3'	SEQ ID NO:169
HuVp7/8	5'-CAGRCTGTGGTGACY CAGGAGCC-3'	SEQ ID NO:170
HuVp9	5'-CWGCCTGTGCTGACT CAGCCMCC-3'	SEQ ID NO:171

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

Primer name	Primer nucleotide sequence	SEQ ID NO
HuV μ 1B	5'-GACATCCAGWTGACCC AGTCTCC-3'	SEQ ID NO:172
HuV μ 2	5'-GATGTTGTGATGACT CAGTCTCC-3'	SEQ ID NO:173
HuV μ 3	5'-GAAATTGTGWTGACR CAGTCTCC-3'	SEQ ID NO:174
HuV μ 4	5'-GATATTGTGATGACC CACACTCC-3'	SEQ ID NO:175
HuV μ 5	5'-GAAACGACACTCACG CAGTCTCC-3'	SEQ ID NO:176
HuV μ 6	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
HuJ μ 1	5'-ACCTAGGACGGTGACC TTGGTCCC-3'	SEQ ID NO:178
HuJ μ 2/3	5'-ACCTAGGACGGTCAG CTTGGTCCC-3'	SEQ ID NO:179
HuJ μ 4/5	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	
HuJ μ 1	5'-ACGTTTGATTCCAC CTTGGTCCC-3'	SEQ ID NO:181
HuJ μ 2	5'-ACGTTTGATCTCCAG CTTGGTCCC-3'	SEQ ID NO:182
HuJ μ 3	5'-ACGTTTGATATCCAC TTTGGTCCC-3'	SEQ ID NO:183
HuJ μ 4	5'-ACGTTTGATCTCCAC CTTGGTCCC-3'	SEQ ID NO:184
HuJ μ 5	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
HuV μ 1B-SalI	5'-TGAGCACACAGGTCG ACGGACATCCAGWTGACC CAGTCTCC-3'	SEQ ID NO:186
HuV μ 2-SalI	5'-TGAGCACACAGGTCG ACGGATGTTGTGATGACT CAGTCTCC-3'	SEQ ID NO:187
HuV μ 3B-SalI	5'-TGAGCACACAGGTCG ACGGAAATTGTGWTGACR CAGTCTCC-3'	SEQ ID NO:188

HuVp4B-SalI	5'-TGAGCACACAGGTCG ACGGATATTGTGATGACC CACACTCC-3'	SEQ ID NO:189
HuVp5-SalI	5'-TGAGCACACAGGTCGACG GAAACGACACTCACGCAGTCT CC-3'	SEQ ID NO:190
HuVp6-SalI	5'-TGAGCACACAGGTCG ACGGAAATTGTGCTGACT CAGTCTCC-3'	SEQ ID NO:191
HuJp1-NotI	5'-GAGTCATTCTCGACTTGC GGCCGCACGTTTGATTTCAC CTTGGTCCC-3'	SEQ ID NO:192
HuJp2-NotI	5'-GAGTCATTCTCGACT TGCGGCCGCACGTTTGAT CTCCAGCTTGGTCCC-3'	SEQ ID NO:193
HuJp3-NotI	5'-GAGTCATTCTCGACTTGC GGCCGCACGTTTGATATCCAC TTTGGTCCC-3'	SEQ ID NO:194
HuJp4-NotI	5'-GAGTCATTCTCGACT TGCGGCCGCACGTTTGAT CTCCACCTTGGTCCC-3'	SEQ ID NO:195
HuJp5-NotI	5'-GAGTCATTCTCGACTTGC GGCCGCACGTTTAATCTCCAG TCGTGTCCC-3'	SEQ ID NO:196
HuVp1A-SalI	5'-TGAGCACACAGGTCGACG CAGTCTGTGCTGACTCAGCCA CC-3'	SEQ ID NO:197
HuVp1B-SalI	5'-TGAGCACACAGGTCGACG CAGTCTGTGYTGACGCAGCCG CC-3'	SEQ ID NO:198
HuVp1C-SalI	5'-TGAGCACACAGGTCGACG	SEQ ID NO:199

	CAGTCTGTCGTGACGCAGCCG CC-3'	
HuVp2-SalI	5'-TGAGCACACAGGTCGACG CARTCTGCCCTGACTCAGCCT- 3'	SEQ ID NO:200
HuVp3A-SalI	5'-TGAGCACACAGGTCGACG TCCTATGWGCTGACTCAGCCA CC-3'	SEQ ID NO:201
HuVp3B-SalI	5'-TGAGCACACAGGTCGACG TCTTCTGAGCTGACTCAGGAC CC-3'	SEQ ID NO:202
HuVp4-SalI	5'-TGAGCACACAGGTCGACG CACGTTATACTGACTCAACCG CC-3'	SEQ ID NO:203
HuVp5-SalI	5'-TGAGCACACAGGTCGACG CAGGCTGTGCTGACTCAGCCG TC-3'	SEQ ID NO:204
HuVp6-SalI	5'-TGAGCACACAGGTCGACG AATTTTATGCTGACTCAGCCC CA-3'	SEQ ID NO:205
HuVp7/8-SalI	5'-TGAGCACACAGGTCGACG CAGRCTGTGGTGACYCAGGAG CC-3'	SEQ ID NO:206
HuVp9-SalI	5'-TGAGCACACAGGTCGACG CWGCCTGTGCTGACTCAGCCM CC-3'	SEQ ID NO:207
HuJp1-NotI	5'-GAGTCATTCTCGACTTGC GGCCGCACCTAGGACGGTGAC CTTGGTCCC-3'	SEQ ID NO:208
HuJp2/3-NotI	5'-GAGTCATTCTCGACTTGC GGCCGCACCTAGGACGGTCAG	SEQ ID NO:209

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	CTTGGTCCC-3'	
HuJp4/5-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		
Vp1A/Jl1-3	5	6	5
Vp1B/Jl1-3			
Vp1C/Jl1-3			
Vp2/Jl1-3	5	7	5
Vp3A/Jl1-3	9	8	9
Vp3B/Jl1-3			
Vp4/Jl1-3	3	9	5
Vp5/Jl1-3	1		
Vp6/Jl1-3	1		
Vp7/8/Jl1-3	3	10	6
Vp9/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

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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.

5 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.

10

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 nucleotide sequence	SEQ ID NO of amino acid sequence	HCDR3	V _H -germline	V _L -germline
sc03-019	211	212	FPGGTRSRGYMDV (SEQ ID NO:291)	V _H 3-30.3 (DP-46)	V _K III (L6)
sc03-020	213	214	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _K IV (B3- DPK24)
sc03-021	215	216	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _K IV (B3- DPK24)
sc03-022	217	218	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _K IV (B3- DPK24)
sc03-023	219	220	RVEVVEYQLLRPRYKSWFDP (SEQ ID NO:293)	V _H 4-34 (DP-63)	V _L II (2a2- V1-04)
sc03-024	221	222	KSAGSNAFDI (SEQ ID NO:294)	V _H 7-04.1 (DP-21)	V _L I (1b- V1-19)
sc03-025	223	224	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-026	225	226	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-027	227	228	TTNRAFDI	V _H 3-64	V _K IV (B3-

			(SEQ ID NO:295)		DPK24)
sc03-029	229	230	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-030	231	232	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-031	233	234	ESGGGYDNHFDY (SEQ ID NO:296)	V _H 1-69 (DP-10)	V _L 1 (1c- V1-16)
sc03-032	235	236	DGWDLTGSFLGYGMDV (SEQ ID NO:297)	V _H 1-e (DP-88)	V _L 1 (1c- V1-16)
sc03-033	237	238	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _R IV (B3- DPK24)
sc03-034	239	240	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _R IV (B3- DPK24)
sc03-035	241	242	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _R IV (B3- DPK24)
sc03-036	243	244	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _R IV (B3- DPK24)
sc03-037	245	246	DAHRGFGMDV (SEQ ID NO:298)	V _H 3-53 (DP-42)	V _L 3 (31- V2-13)
sc03-038	247	248	DAHRGFGMDV (SEQ ID NO:298)	V _H 3-53 (DP-42)	V _L 3 (31- V2-13)
sc03-039	249	250	GSKWNDVGGGDY (SEQ ID NO:299)	V _H 3-23 (DP-47)	V _L 6 (6A- V1-22)
sc03-040	251	252	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-041	253	254	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-042	255	256	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-043	257	258	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-044	259	260	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-045	261	262	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)
sc03-046	263	264	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _R IV (B3- DPK24)

sc03-047	265	266	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-048	267	268	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-049	269	270	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-050	271	272	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-051	273	274	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _K IV (B3- DPK24)
sc03-052	275	276	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _K IV (B3- DPK24)
sc03-053	277	278	GTGYLRSYHGMDV (SEQ ID NO:300)	V _H 1-03 (DP-25)	V _K II (A19/A03- DPK15)
sc03-054	279	280	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K IV (B3- DPK24)
sc03-055	281	282	RVEVVEYQLLRPRYKSWFDP (SEQ ID NO:293)	V _H 4-34 (DP-63)	V _L 1 (1b- V1-19)
sc03-056	283	284	GSGISTPMDV (SEQ ID NO:292)	V _H 5-51 (DP-73)	V _K IV (B3- DPK24)
sc03-057	285	286	PDIVVAGHSPPHYTMDV (SEQ ID NO:301)	V _H 1-69 (DP-10)	V _K I L11- DPK3
sc03-058	287	288	TTNRAFDI (SEQ ID NO:295)	V _H 3-64	V _K VI A14- DPK25
sc03-059	289	290	FPGGTRSRGYMDV (SEQ ID NO:291)	V _H 1-46 (DP-7)	V _K III (L6)

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

Group	Animals /group	Challenge (intratracheal) *	Split ^b	Sampling (days) ^c							
				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 sacrifice

c S means swabs; LT means lung tissue after sacrifice

5

Table 20: Scheme for tissue and fluid sampling

Group	No/Group	Challenge/ mAb	Sampling (days)						
			-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

10

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 Sin3765V Sin845 Sin847 Sin849 Sin852 Sin3725V Sin842 Sin846 Sin848 Sin850	AY559083 AY559084 AY559093 AY559095 AY559086 AY559082 AY559087 AY559081 AY559094 AY559085 AY559096
R426G	Shanghai LY	AY322205S3

N437D		
Y436H	GZ-C	AY394979
Y442S	Sinol-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.

- 5 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 TCID ₅₀
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

10 indicated

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SEQUENCE LISTING

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Ter Meulen, Jan H.
De Kruif, Cornelis A.
10 Van den Brink, Edward N.
Goudsmit, Jaap
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20 Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr
1 5 10

```

25  <210>  10
    <211>   9
    <212>  PRT
30  <213>  Artificial sequence

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35  <220>
    <223>  HCDR3 of SC03 -012
    <400>  10
40  Met Phe Arg Lys Ser Ser Phe Asp Ser
    1           5

```

45	<210>	11
	<211>	9
	<212>	PRT
50	<213>	Artificial sequence

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55  <220>
    <223>  HCDR3 of SC03 -013
    <400>  11
60  Gly Leu Thr Pro Leu Tyr Phe Asp Tyr
    1              5

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162

5 <210> 12
<211> 9
<212> PRT
<213> Artificial sequence
10
<220>
<223> HCDR3 of SC03 -014
15 <400> 12
Gly Ile Ser Pro Phe Tyr Phe Asp Tyr
1 5
20
<210> 13
<211> 6
25 <212> PRT
<213> Artificial sequence
30
<220>
<223> HCDR3 of SC03 -015
35 <400> 13
Gly Leu Ser Leu Arg Pro
1 5
40
<210> 14
<211> 354
45 <212> DNA
<213> Artificial sequence
50
<220>
<223> Variable heavy chain of SC03 -001
55 <220>
<221> CDS
60 <222> (1)..(354)
<223>

163

<400> 14
 atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aa g cct 48
 5 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
 10 Gly Gly Ser Leu Arg Leu 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
 15 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
 20 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
 25 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
 30 gca aga cac cgg ttc 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
 35
 <210> 15
 <211> 118
 40 <212> PRT
 <213> Artificial sequence
 45
 <220>
 <223> Variable heavy chain of SC03-001
 50
 <400> 15
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
 1 5 10 15
 55 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 60 Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

164

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

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

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

15 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

20 <210> 16
 <211> 372
 25 <212> DNA
 <213> Artificial sequence

30 <220>
 <223> Variable heavy chain of SC03 -002
 35 <220>
 <221> CDS
 40 <222> (1)..(372)
 <223>

45 <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

50 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

55 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

60 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

165

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
 5 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
 10 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
 15
 <210> 17
 <211> 124
 20 <212> PRT
 <213> Artificial sequence
 25
 <220>
 <223> Variable heavy chain of SC03 -002
 30
 <400> 17
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
 1 5 10 15
 35 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 40 Gly Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 45 Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
 50 55 60
 50 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
 55 Val Tyr Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp
 100 105 110
 60 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
 115 120

166

<210> 18
 <211> 360
 5 <212> DNA
 <213> Artificial sequence
 10
 <220>
 <223> Variable heavy chain of SC03 -003
 15 <220>
 <221> CDS
 20 <222> (1)..(360)
 <223>
 25
 <400> 18
 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
 30 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
 35 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
 40 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
 45 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
 50 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
 55 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
 60 ggc acc ctg gtg acc gtg ctc gag 360
 Gly Thr Leu Val Thr Val Leu Glu
 115 120
 <210> 19
 <211> 120

167

<212> PRT
 <213> Artificial sequence
 5
 <220>
 <223> Variable heavy chain of SC03 -003
 10
 <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
 25 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
 30 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 35 85 90 95
 Tyr Cys Ala Arg Arg Ser Tyr Phe Arg Arg Phe Asp Tyr Trp Gly Gln
 100 105 110
 40 Gly Thr Leu Val Thr Val Leu Glu
 115 120
 45 <210> 20
 <211> 360
 <212> DNA
 50 <213> Artificial sequence
 55 <220>
 <223> Variable heavy chain of SC03 -005
 <220>
 60 <221> CDS

168

<222> (1) .. (360)

<223>

5

<400> 20

	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 Gly Gly Gly Leu Ile Gln Pro	
10	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	
15	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	
20	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
25	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
30	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	336
	Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly Gln	
	100 105 110	
35	ggc acc ctg gtg acc gtg ctc gag	360
	Gly Thr Leu Val Thr Val Leu Glu	
	115 120	

40

<210> 21

<211> 120

45

<212> PRT

<213> Artificial sequence

50

<220>

<223> Variable heavy chain of SC03 -005

55

<400> 21

	Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro
	1 5 10 15
60	Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
	20 25 30

169

Gly Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 35 40 45
 5 Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 20 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
 25 <210> 22
 <211> 366
 30 <212> DNA
 <213> Artificial sequence
 35 <220>
 <223> Variable heavy chain of SC03 -006
 40 <220>
 <221> CDS
 <222> (1)..(366)
 45 <223>
 50 <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 P ro
 1 5 10 15
 55 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
 60 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

170

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Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
50      55      60
5  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 ctg caa atg aac agc ctg aga gct gag gac aca gct gt g tat      288
10  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
15  Tyr Cys Ala Lys Asp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr Trp
   100      105      110

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

20  <210> 23
   <211> 122
25  <212> PRT
   <213> Artificial sequence

30  <220>
   <223> Variable heavy chain of SC03 -006
35  <400> 23

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

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

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

50  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 Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
   65      70      75      80

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

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

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171

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

5 <210> 24
 <211> 366

10 <212> DNA
 <213> Artificial sequence

15 <220>
 <223> Variable heavy chain of SC03 -007

20 <220>
 <221> CDS
 <222> (1)..(366)

25 <223>

30 <400> 24
 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 Leu Val Gln Pro
 1 5 10 15

35 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

40 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

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

50 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

55 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

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

172

<210> 25
 <211> 122
 5 <212> PRT
 <213> Artificial sequence
 10
 <220>
 <223> Variable heavy chain of SC03 -007
 15 <400> 25
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 20 Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 25 Asp Tyr Arg Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 30 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
 35 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95
 40 Tyr Cys Ala Arg Gly Tyr Trp Thr Ser Leu Thr Gly Phe Asp Tyr Trp
 100 105 110
 45 Gly Gln Gly Thr Leu Val Thr Val Leu Glu
 115 120
 50 <210> 26
 <211> 360
 <212> DNA
 55 <213> Artificial sequence
 <220>
 60 <223> Variable heavy chain of SC03 -008

173

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<220>
<221> CDS
5 <222> (1)..(360)
<223>

10 <400> 26
    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

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

20    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

25    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

35    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

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

45 <210> 27
    <211> 120
    <212> PRT
50 <213> Artificial sequence

55 <220>
    <223> Variable heavy chain of SC03 -008
    <400> 27
60 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
    1          5          10          15

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174

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 5 Ser Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 10 Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
 50 55 60
 15 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 20 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
 25 Gly Thr Leu Val Thr Val Leu Glu
 115 120
 30 <210> 28
 <211> 369
 <212> DNA
 35 <213> Artificial sequence

 40 <220>
 <223> Variable heavy chain of SC03-009
 <220>
 45 <221> CDS
 <222> (1)..(369)
 50 <223>

 <400> 28
 55 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
 60 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

175

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      Asp Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
      35          40          45
5    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
    10  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 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

    20  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

25  <210> 29
    <211> 123
    <212> PRT
30  <213> Artificial sequence

35  <220>
    <223> Variable heavy chain of SC03 -009
    <400> 29
40  Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
    1          5          10          15

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

50  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

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

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

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176

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

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

10 <210> 30
 <211> 360
 <212> DNA
 15 <213> Artificial sequence

20 <220>
 <223> Variable heavy chain of SC03-010
 <220>

25 <221> CDS
 <222> (1)..(360)
 30 <223>

<400> 30

35 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

40 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

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

50 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

55 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

60 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

177

Gly Thr Leu Val Thr Val Leu Glu
 115 120

5 <210> 31
 <211> 120
 <212> PRT
 10 <213> Artificial sequence

15 <220>
 <223> Variable heavy chain of SC03 -010
 <400> 31

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

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

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

35 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

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

45 Ala Lys Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr Trp Gly Gln
 100 105 110

50 Gly Thr Leu Val Thr Val Leu Glu
 115 120

<210> 32
 55 <211> 360
 <212> DNA
 <213> Artificial sequence
 60

178

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<220>
<223> Variable heavy chain of SC03 -012
5  <220>
    <221> CDS
    <222> (1)..(360)
10 <223>

15 <400> 32
    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

20 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

25 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

35 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

40 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

50 <210> 33
    <211> 120
    <212> PRT
55 <213> Artificial sequence

60 <220>
    <223> Variable heavy chain of SC03 -012
    <400> 33

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179

Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15
 5 Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 20 25 30
 10 Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 35 40 45
 15 Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln
 50 55 60
 20 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
 25 Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly Gln
 100 105 110
 30 Gly Thr Leu Val Thr Val Ser Arg
 115 120
 35 <210> 34
 <211> 366
 <212> DNA
 40 <213> Artificial sequence
 45 <220>
 <223> Variable heavy chain of SC03 -013
 <220>
 50 <221> CDS
 <222> (1)..(366)
 <223>
 55
 <400> 34
 atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct 48
 60 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

180

	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
				20					25					30			
5	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				
10	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					
15	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	
						70					75				80		
20	aac	tca	ctg	tat	ctg	caa	atg	aac	agc	ctg	aaa	acc	gag	gac	acg	gcc	288
	Asn	Ser	Leu	Tyr		85					90				95		
25	gtg	tat	tac	tgt	gca	aag	ggg	ttg	act	cct	ttg	tac	ttt	gac	tac	tg	336
	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Leu	Thr	Pro	Leu	Tyr	Phe	Asp	Tyr	Trp	
				100				105						110			
30	ggc	caa	ggt	acc	ctg	gtc	acc	gtc	tcg	agt							366
	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
			115					120									
35	<210>	35															
40	<211>	122															
	<212>	PRT															
45	<213>	Artificial sequence															
50	<220>																
55	<223>	Variable heavy chain of SC03 -013															
60	<400>	35															
65	Met	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	
	1				5					10				15			
70	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
				20					25					30			
75	Asp	His	Tyr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	
			35					40					45				
80	Trp	Val	Gly	Arg	Thr	Arg	Asn	Lys	Ala	Asn	Ser	Tyr	Thr	Thr	Glu	Tyr	
		50					55					60					
85	Ala	Ala	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	
	65					70					75				80		

181

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

5 Val Tyr Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr Trp
 100 105 110

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

<210> 36

15 <211> 366

<212> DNA

20 <213> Artificial sequence

<220>

25 <223> Variable heavy chain of SC03 -014

<220>

30 <221> CDS

<222> (1)..(366)

<223>

35

<400> 36

40 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 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
 45 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

50 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

55 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

60 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

182

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

5 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

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

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

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

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

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

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

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

<210> 38
 <211> 351
 <212> DNA

183

<213> Artificial sequence

5 <220>

<223> Variable heavy chain of SC03 -015

<220>

10

<221> CDS

<222> (1)..(351)

15 <223>

<400> 38

20	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	

25	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	

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	

35	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	

40	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	

40	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	

45	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	

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

<210> 39

55 <211> 117

<212> PRT

60 <213> Artificial sequence

184

<220>

<223> Variable heavy chain of SC03 -015

5 <400> 39

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

10

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

15

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

20

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

25

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

30

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

35

Val Thr Val Ser Arg
 115

40

<210> 40

<211> 318

<212> DNA

45

<213> Artificial sequence

<220>

50

<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

55

<220>

<221> CDS

60

<222> (1)..(318)

<223>

185

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<400> 40
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  Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
  1 5 10 15

10 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

15 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

20 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

25 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

30 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

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

<210> 41
35 <211> 106
    <212> PRT
40 <213> Artificial sequence

<220>
45 <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

50 <400> 41
  Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
  1 5 10 15

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

60 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

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186

	50		55		60	
5	Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp					
	65		70		75	80
10	Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe					
		85		90		95
15	Gly Gln Gly Thr Lys Val Glu Ile Lys Arg					
		100		105		
20	<210> 42					
	<211> 324					
25	<212> DNA					
	<213> Artificial sequence					
30	<220>					
	<223> Variable light chain of SC03 -006					
35	<221> CDS					
	<222> (1)..(324)					
40	<223>					
45	<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					
50	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					
55	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					
60	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					
65	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					
70	gaa gat gtt ggg gtt tat ta c tgc cag cag agg ttc cgc acg ccg gtc					288
	Glu Asp Val Gly Val Tyr Tyr Cys Gln Arg Phe Arg Thr Pro Val					
	85 90 95					

187

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

324

5

<210> 43

<211> 108

10

<212> PRT

<213> Artificial sequence

15

<220>

<223> Variable light chain of SC03-006

20

<400> 43

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

25

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

30

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

35

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

40

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

45

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

50

<210> 44

<211> 324

55

<212> DNA

<213> Artificial sequence

60

<220>

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

188

<220>
 <221> CDS
 5 <222> (1)..(324)
 <223>
 10
 <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
 15 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 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
 25 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
 30 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
 35 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
 40 100 105
 <210> 45
 <211> 108
 45 <212> PRT
 <213> Artificial sequence
 50
 <220>
 <223> Variable light chain of SC03 -012 and SC03-015
 55 <400> 45
 Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
 1 5 10 15
 60 Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 20 25 30

189

5 Trp Tyr Gln Gln Lys Pro Gly 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
 10 Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
 65 70 75 80
 15 Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val
 85 90 95
 20 Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105
 <210> 46
 25 <211> 729
 <212> DNA
 <213> Artificial sequence
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 <220>
 35 <223> SC03-001
 <220>
 <221> CDS
 40 <222> (1)..(729)
 <223>
 45
 <400> 46
 tcc atg gct gag gtg 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
 50 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
 55 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
 60 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 A la Asp Ser
 50 55 60

190

	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	
5	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	
10	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	
15	acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc gga acc ggc	384
	Thr Leu Val Thr Val Leu Glu Gly Thr Gly Ser Gly Gly Thr Gly	
	115 120 125	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	gcg gcc gca	729
	Ala Ala Ala	
60	<210> 47	
	<211> 243	
	<212> PRT	
	<213> Artificial sequence	
65	<220>	
	<223> SC03-001	

191

<400> 47

5 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
 10 Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 15 Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
 50 55 60
 20 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
 25 Cys Ala Arg His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 30 Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly Thr Gly
 115 120 125
 35 Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser
 130 135 140
 40 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
 45 Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
 180 185 190
 50 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 195 200 205
 55 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln S er Tyr
 210 215 220
 60 Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 225 230 235 240
 Ala Ala Ala

192

5 <210> 48
 <211> 747
 <212> DNA
 10 <213> Artificial sequence

 <220>
 15 <223> SC03-002
 <220>
 20 <221> CDS
 <222> (1)..(747)
 <223>
 25

 <400> 48
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 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
 35 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
 40 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
 45 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
 50 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
 55 100 105 110
 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
 60 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

193

5 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
 10 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
 15 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
 20 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
 25 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
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 50 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 55 Ser Gly Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 60 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

	194															
	65				70				75				80			
5	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr
					85					90					95	
10	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr	Ser	Arg	Ser	Leu	Lys	Ala	Phe
				100					105					110		
15	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Leu	Glu	Gly	Thr	Gly
			115					120					125			
20	Gly	Ser	Gly	Gly	Thr	Gly	Ser	Gly	Thr	Gly	Thr	Ser	Glu	Leu	Thr	Gln
		130					135					140				
25	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
	145					150					155					160
30	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln
					165					170					175	
35	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu
				180				185						190		
40	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
			195					200					205			
45	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr
	210					215						220				
50	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr
	225					230					235					240
55	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala							
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	1 5 10 15	
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	
20	agc agc tac ccg atg aac tgg gtc cgc cag gog 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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	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	
75	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	

196

	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					
5	225	230	235		240	
	aaa cgt gcg gcc gca					735
	Lys Arg Ala Ala Ala					
		245				
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25						
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	Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe					
		20	25		30	
35						
	Ser Ser Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu					
		35	40		45	
40						
	Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala					
		50	55		60	
45						
	Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn					
	65	70	75		80	
50						
	Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val					
		85	90		95	
55						
	Tyr Tyr Cys Ala Arg Arg Ser Tyr Phe Arg Arg Phe Asp Tyr Trp Gly					
		100	105		110	
60						
	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	

197

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

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

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

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

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

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

25 Lys Arg Ala Ala Ala
    245

30 <210> 52
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    <212> DNA
35 <213> Artificial sequence

40 <220>
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    <220>

45 <221> CDS
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    <223>

50

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    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
60 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

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198

	35	40	45	
5	gag tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser 50 55 60			192
10	agg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 65 70 75 80			240
15	tat ctt caa atg aac aac ctg aga gct gag gac acg gcc gtg tat tac Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr 85 90 95			288
20	tgt gca aaa ggc ggc ggc cgc ccg tac aac ccc ttc gat tac tgg ggc Cys Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly 100 105 110			336
25	cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc gga Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Ser Gly Gly 115 120 125			384
30	acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc tcc Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser 130 135 140			432
35	ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt Leu Ser Ala Ser Val Gly As p Arg Val Thr Ile Thr Cys Arg Ala Ser 145 150 155 160			480
40	cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg aaa Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Ly s 165 170 175			528
45	gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg gtc Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val 180 185 190			576
50	cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr 195 200 205			624
55	atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln 210 215 220			672
60	agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag atc Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile 225 230 235 240			720
	aaa cgt gcg gcc gca Lys Arg Ala Ala Ala 245			735
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199

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5 <223> SC03-005

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 15 20 25 30
 Ser Gly Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45
 20 Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
 50 55 60
 25 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
 30 85 90 95
 Cys Ala Lys Gly Gly Gly Arg Pro Tyr Asn Pro Phe Asp Tyr Trp Gly
 35 100 105 110
 Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
 115 120 125
 40 Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
 130 135 140
 45 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
 50 165 170 175
 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
 55 180 185 190
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205
 60 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

200

Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 225 230 235 240
 5 Lys Arg Ala Ala Ala
 245
 10 <210> 54
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 <212> DNA
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 40 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
 45 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
 55 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
 60 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

201

	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Leu	Glu	Gly	Thr	Gly	Gly	Ser	
			115					120						125			
5	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					
10	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		
15	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		
20	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			
25	act	ttg	caa	tca	ggg	gtc	cca	tct	cgg	ttc	agt	gg	c	agt	gga	tct	624
	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
			195				200					205					
30	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					
35	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	
	225					230					235				240		
40	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								
45	<210>	55															
50	<211>	251															
	<212>	PRT															
	<213>	Artificial sequence															
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	1				5					10					15		
60	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				

202

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
 50 55 60
 5 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75 80
 10 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 85 90 95
 15 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
 20 Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
 130 135 140
 25 Thr Gln Ser Pro His Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
 145 150 155 160
 30 Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr
 165 170 175
 35 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 Ser Gly Ser Gly Ser Gly
 195 200 205
 40 Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Gly
 210 215 220
 45 Val Tyr Tyr Cys Gln Gln Arg Phe Arg Thr Pro Val Thr Phe Gly Gln
 225 230 235 240
 50 Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala
 245 250
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 55 <211> 741
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 60 <213> Artificial sequence

203

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5 <220>

<221> CDS

10 <222> (1)..(741)

<223>

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20 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

25 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

30 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

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

40 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

45 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

50 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

55 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

60 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

55 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

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

204

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      ggc 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

5    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

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      <212> PRT
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25

      <220>
30    <223> SC03-007
      <400> 57

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      20                                25                                30
40

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

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

50    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

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

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

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205

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 130 135 140
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 145 150 155 160
 10 Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
 165 170 175
 15 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
 180 185 190
 20 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205
 25 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
 30 Glu Ile Lys Arg Ala Ala Ala
 245
 35 <210> 58
 <211> 735
 <212> DNA
 40 <213> Artificial sequence
 45 <220>
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 50 <221> CDS
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 55 <223>
 60 <400> 58
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 Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
 1 5 10 15

206

	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	
5	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	
10	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	
15	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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	aaa cgt gcg gcc gca	735
	Lys Arg Ala Ala Ala	
	245	
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207

<211> 245

<212> PRT

5 <213> Artificial sequence

<220>

10 <223> SC03-008

<400> 59

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1 5 10 15

20 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

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

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

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

40 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

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

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

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

60 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

208

195 200 205

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

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

15 Lys Arg Ala Ala Ala
 245

20 <210> 60
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 <212> DNA
 <213> Artificial sequence

25 <220>
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30 <220>
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 <222> (1)..(744)

35 <223>

40 <400> 60
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 Ser Met Ala Glu Val Gln Ieu Val Glu Ser Gly Gly Gly Val Val Gln
 1 5 10 15

45 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 Ph e Thr Phe
 20 25 30

50 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

55 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

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

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

209

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
 5 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
 10 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 Leu Thr Gln Ser
 130 135 140
 15 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
 20 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
 25 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
 30 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
 35 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
 40 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
 45 <211> 248
 <212> PRT
 50 <213> Artificial sequence
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 55 <223> SC03-009
 <400> 61
 60 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

210

	20	25	30
5	Ser Asp Tyr Pro Met Asn Trp Val Arg Gln Ala Pr o Gly Lys Gly Leu 35 40 45		
10	Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala 50 55 60		
15	Asp Ser Val Lys Gly Arg Phe Thr Ile Se r Arg Asp Asn Ser Lys Asn 65 70 75 80		
20	Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 85 90 95		
25	Tyr Tyr Cys Ala Lys Gly Leu Ph e Met Val Thr Thr Tyr Ala Phe Asp 100 105 110		
30	Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly 115 120 125		
35	Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser 130 135 140		
40	Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys 145 150 155 160		
45	Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys 165 170 175		
50	Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln 180 185 190		
55	Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 195 200 205		
60	Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr 210 215 220		
65	Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys 225 230 235 240		
70	Val Glu Ile Lys Arg Ala Ala Ala 245		
75	<210> 62		
80	<211> 735		

211

<212> DNA

<213> Artificial sequence

5

<220>

<223> SC03-010

<220>

<221> CDS

<222> (1) .. (735)

<223>

20

<400> 62

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

25

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	

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	

35

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	

40

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

45

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	

50

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 A sp Tyr Trp Gly	
100 105 110	

55

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	

60

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	

65

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	

70

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	

212

	165	170	175		
5	gcc cct aag ctc ctg atc tat gct gca tcc agt tt g caa agt ggg gtc Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val	180	185	190	576
10	cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	195	200	205	624
15	atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln	210	215	220	672
20	agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag atc Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	225	230	235	720
25	aaa cgt gcg gcc goa Lys Arg Ala Ala Ala	245			735
30	<210> 63 <211> 245 <212> PRT <213> Artificial sequence				
35	<220> <223> SC03-010 <400> 63				
40	Ser Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln 1 5 10 15				
45	Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe 20 25 30				
50	Ser Gly Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45				
55	Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser 50 55 60				
60	Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 65 70 75 80				
65	Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr 85 90 95				

213

Cys Ala Lys Gly Gly Gly Leu Pro Tyr Leu Ser Phe Asp Tyr Trp Gly
 100 105 110

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

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

15 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

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

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

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

35 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

40 <210> 64
 <211> 741

45 <212> DNA
 <213> Artificial sequence

50 <220>
 <223> SC03-012

55 <220>
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 <222> (1)..(741)

60 <223>

214

	<400> 64	
5	gcc atg gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 1 5 10 15	48
10	cct ggg gcc tca gtg aag gtc tcc tgc a ag gct tct ggt tac acc ttt Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 20 25 30	96
15	acc agc tat ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 35 40 45	144
	gag tgg atg gga tgg atc agc gct tac aat ggt aac aca aac tat gca Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala 50 55 60	192
20	cag aag ctc cag ggc aga gtc acc atg acc aca gac aca tcc acg agc Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser 65 70 75 80	240
25	aca gcc tac atg gag ctg agc agc ctg aga tct gac gac acg gcc gtg Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val 85 90 95	288
30	tat tac tgt gca agg atg ttt agg aag agt tcc ttt gac tcc tgg ggc Tyr Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly 100 105 110	336
35	caa ggt acc ctg gtc acc gtc tcg aga ggt gga ggc ggt tca ggc gga Gln Gly Thr Leu Val Thr Val Ser Arg Gly Gly Gly Ser Gly Gly 115 120 125	384
	ggt ggc tct ggc ggt ggc gga tcg t ct gag ctg act cag gac cct gct Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala 130 135 140	432
40	gtg tct gtg gcc ttg gga cag aca gtc agg atc aca tgc caa gga gac Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp 145 150 155 160	480
45	agc ctc aga agc tat tat gca agc tgg tac cag cag aag cca gga cag Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln 165 170 175	528
50	gcc cct gta ctt gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile 180 185 190	576
55	cca gac cga ttc tct ggc tcc agc tca gga aac aca gct tcc ttg acc Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr 195 200 205	624
	atc act ggg gct cag gcg gaa gat gag gct gac tat tac tgt aac tcc Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser 210 215 220	672
60	cgg gac agc agt ggt aac cat gtg gta ttc ggc gga ggg acc aag ctg Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu 225 230 235 240	720

215

741

acc gtc cta ggt gcg gcc gca
 Thr Val Leu Gly Ala Ala Ala
 245

5
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 <211> 247
 10 <212> PRT
 <213> Artificial sequence
 15
 <220>
 <223> SC03-012
 20 <400> 65
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 1 5 10 15
 25 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 20 25 30
 30 Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45
 35 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
 40 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
 85 90 95
 45 Tyr Tyr Cys Ala Arg Met Phe Arg Lys Ser Ser Phe Asp Ser Trp Gly
 100 105 110
 50 Gln Gly Thr Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 55 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
 60 Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

216

[illegible]

217

	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	
5	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	
10	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	
15	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 Ser	
	115 120 125	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	aag gtg gag atc aaa cgt gcg gcc gca	747
	Lys Val Glu Ile Lys Arg Ala Ala Ala	
	245	
60	<210> 67	
	<211> 249	
	<212> PRT	
	<213> Artificial sequence	
	<220>	
	<223> SC03-013	

218

<400> 67

5 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
 10 Ser Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 15 Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
 50 55 60
 20 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
 25 Ala Val Tyr Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr
 100 105 110
 30 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125
 35 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln
 130 135 140
 40 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
 45 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
 180 185 190
 50 Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205
 55 Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 210 215 220
 60 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

219

245

5 <210> 68
 <211> 747
 <212> DNA
 10 <213> Artificial sequence

 15 <220>
 <223> SC03-014
 <220>
 20 <221> CDS
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 <223>
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 30 <400> 68
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 Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10 15

 35 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 2 5 30

 40 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

 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

 50 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

 55 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

 60 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

 65 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

 70 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

220

5 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
 10 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
 15 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
 20 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
 25 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
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 35 <212> PRT
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 45 <400> 69
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 1 5 10 15
 50 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 55 Ser Asp His Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 60 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

221

	65		70		75		80									
5	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr
				85					90					95		
10	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Ile	Ser	Pro	Phe	Tyr	Phe	Asp	Tyr
				100					105					110		
15	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
			115					120					125			
20	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Glu	Leu	Thr	Gln
			130				135					140				
25	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
					145		150				155					160
30	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln
				165						170					175	
35	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu
				180					185					190		
40	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
			195					200					205			
45	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr
			210				215					220				
50	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr
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55	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala							
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222

<221> CDS

<222> (1) .. (732)

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<400> 70

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15	cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 20 25 30	96
20	gat gat tat ggc atg agc tgg gtc cgc caa gct cca ggg aag ggg ctg Asp Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45	144
25	gag tgg gtc tct ggt att aat tgg aat ggt ggt agc aca ggt ta t gca Glu Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala 50 55 60	192
30	gac tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn 65 70 75 80	240
35	tcc ctg tat ctg caa atg aac agt ctg aga gcc gag gac acg gcc gtg Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr A la Val 85 90 95	288
40	tat tac tgt gca aga ggt ttg tct ctt cgt cct tgg ggc caa ggt acc Tyr Tyr Cys Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr 100 105 110	336
45	ctg gtc acc gtc tgg aga ggt gga ggc ggt tca ggc gga ggt ggc tct Leu Val Thr Val Ser Arg Gly Gly Gly Ser Gly Gly Gly Ser 115 120 125	384
50	ggc ggt ggc gga tgg tct gag ctg act cag gac cct gct gtg tct gtg Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val 130 135 140	432
55	gcc ttg gga cag aca gtc agg atc aca tgc caa gga gac agc ctc aga Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg 145 150 155 160	480
60	agc tat tat gca agc tgg tac cag cag aag cca gga cag gc c cct gta Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val 165 170 175	528
65	ctt gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc cca gac cga Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg 180 185 190	576
70	ttc tct ggc tcc agc tca gga aac aca gct tcc ttg acc atc act ggg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr I le Thr Gly 195 200 205	624
75	gct cag gcg gaa gat gag gct gac tat tac tgt aac tcc cgg gac agc Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser	672

223

	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			
5	225	230	235	240
	ggt gcg gcc gca			732
	Gly Ala Ala Ala			
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		20	25	30
35				
	Asp Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
		35	40	45
40				
	Glu Trp Val Ser Gly Ile Asn T rp Asn Gly Gly Ser Thr Gly Tyr Ala			
		50	55	60
45				
	Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn			
		65	70	75
50				
	Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val			
		85	90	95
55				
	Tyr Tyr Cys Ala Arg Gly Leu Ser Leu Arg Pro Trp Gly Gln Gly Thr			
		100	105	110
60				
	Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
		115	120	125
60				
	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

5 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
10 180 185 190

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

20 Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
225 230 235 240

25 Gly Ala Ala Ala

<210> 72

<211> 55

<212> DNA

35 <213> Artificial sequence

<220>

40 <223> 5' cloning site of pPicZalphaB

<400> 72

45 tctctcgaga aaagagagggc tgaagctgca ggaattcaagc tggcccagcc ggccg 55

<210> 73

<211> 55

<212> DNA

<213> Artificial sequence

55

<220>

60 <223> 5' cloning site of pPicZEVH

<400> 73

tctctcgaga aaagagccat ggaagctgca ggaattcacg tggcccagcc ggccg 55

225

<210> 74
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5 <212> DNA
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15 <400> 74
gcgggcgcgc caaagccaag taccacacca gggttttcat gtccaccatg tccaggctct 60
ggcggtggcgc caatcgatag cggctttcta ga 92
20
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<211> 11
25 <212> PRT
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35 <400> 75
Asp Gly Ser Arg Phe Pro Ala Arg Phe Asp Tyr
1 5 10
40
<210> 76
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45 <212> PRT
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<220>
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55 <400> 76
Tyr Gly Ser Ala Tyr Arg Pro Pro Phe Asp Tyr
1 5 10
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<210> 77

226

<211> 9
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10 <223> HCDR3 of SC03 -017
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15 Ser Arg Ser Ala Gly Phe Phe Asp Tyr
1 5

<210> 78
20 <211> 9
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25 <213> Artificial sequence

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30 <223> HCDR3 of SC03 -018
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35 Phe Asn Pro Phe Thr Ser Phe Asp Tyr
1 5

<210> 79
40 <211> 372
<212> DNA
45 <213> Artificial sequence

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<223>
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<400> 79

227

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

5 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

10 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

15 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

20 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

25 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

30 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

35 <210> 80
 <211> 124
 <212> PRT

40 <213> Artificial sequence

45 <220>
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 <400> 80

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

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

60 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

228

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5      Ala Val Ser 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

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

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

      <210> 81
20     <211> 372
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      <220>
30     <223> Variable heavy chain of SC03 -016

      <400> 81
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      agactctccc gtgcagcctc tggattcacc tttagcaact accccatgcg ctgggtccgc 120
      caggcgcccg ggaaggggct ggagtgggta ggtttcat ta gaaacaaagc taatgggtggg 180
40     acaacagaat agaccacgtc tgtgagaggc agattcacia tctcaagaga tgattccaaa 240
      agcatcacct atctgcaaat gaacagcctg agagccgagg acacagccgt gtattactgt 300
45     gctaaatacg gcagcgccca cgcgccgccc ttgcattact gggggccaggg caccctgggtg 360
      accgtgctcg ag 372

      <210> 82
50     <211> 125
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55     <213> Artificial sequence

      <220>
60     <223> Variable heavy chain of SC03 -016

      <400> 82

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229

Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 5 Pro Gly Gly Ser Leu Arg Leu Ser Arg Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 10 Ser Asn Tyr Pro Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 15 Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu
 50 55 60
 20 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
 25 Ala Val Tyr Tyr Cys Ala Lys Tyr Gly Ser Ala Tyr Arg Pro Pro Phe
 100 105 110
 30 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu
 115 120 125
 35 <210> 83
 <211> 363
 <212> DNA
 40 <213> Artificial sequence
 45 <220>
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 50 <221> CDS
 <222> (1) .. (363)
 <223>
 55 <400> 83
 atg gcc cag gtg cag ctg cag gag tcg ggc gca gga ctg ttg aag cct 48
 60 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					
5	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							
10	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								
15	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				
20	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					
25	tat	tac	tgt	gca	aag	tct	cgt	tct	gct	ggt	ttc	ttt	gac	tac	tgg	ggc		336	
	Tyr	Tyr	Cys	Ala	Lys	Ser	Arg	Ser	Ala	Gly	Phe	Phe	Asp	Tyr	Trp	Gly			
				100				105					110						
30	caa	ggt	acc	ctg	gtc	acc	gtc	tcg	agt									363	
	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser										
			115					120											
35	<210>	84																	
40	<211>	121																	
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45	<213>	Artificial sequence																	
50	<220>																		
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	<400>	84																	
55	Met	Ala	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	A	la	Gly	Leu	Leu	Lys	Pro		
	1				5					10						15			
60	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Val	Ser			
				20				25						30					
65	Ser	Gly	Ser	Tyr	Tyr	Trp	Ser	Trp	I le	Arg	Gln	Pro	Pro	Gly	Lys	Gly			
			35					40				45							
70	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn			
			50				55				60								
75	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn			
	65					70			</										

231

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 85 90 95

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

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

15 <210> 85
 <211> 360
 <212> DNA
 20 <213> Artificial sequence

25 <220>
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 <220>

30 <221> CDS
 <222> (1)..(360)
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40 <400> 85
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 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15

45 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

50 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

55 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

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

65 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

232

Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly Gln
 100 105 110

5 ggt acc ctg gtc acc gtc tcg agt 360
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

10 <210> 86
 <211> 120
 <212> PRT

15 <213> Artificial sequence

20 <220>
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 <400> 86

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

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

35 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

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

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

50 Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly Gln
 100 105 110

55 Gly Thr Leu Val Thr Val Ser Ser
 115 120

60 <210> 87
 <211> 324
 <212> DNA

233

<213> Artificial sequence

5 <220>

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<220>

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<221> CDS

<222> (1)..(324)

15 <223>

<400> 87

20 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

25 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

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

35 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

40 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

40 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

45 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

50 <210> 88

<211> 108

<212> PRT

55 <213> Artificial sequence

<220>

60

<223> Variable light chain of SC03-017

<400> 88

234

Glu Ile Glu Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 5 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30
 10 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 15 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 20 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
 25 Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105
 30 <210> 89
 <211> 747
 <212> DNA
 35 <213> Artificial sequence
 40 <220>
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 45 <221> CDS
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 50 <223>
 <400> 89
 55 tcc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag 48
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 1 5 10 15
 60 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

235

	Ser	Asp	Tyr	Leu	Met	Asn	Tr p	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	35						40					45					
5	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					
10	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	
15	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		
20	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	
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25	gat	tac	tgg	ggc	cag	ggc	acc	ctg	gtg	acc	gtg	ctc	gag	ggg	acc	gga	384
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	Gly	Ser	Gly	Gly	Thr	Gly	Ser	Gly	Thr	Gly	Thr	Ser	Glu	Leu	Thr	Gln	
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	Ser	Pro	Ser	Ser	Leu	Se r	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
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	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gl n	Gln	
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45	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	
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	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
			195					200					205				
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	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	
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 35 40 45

25 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

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

35 Ala Val Tyr Tyr Cys Ala Lys Asp Gly Ser Arg Phe Pro Ala Arg Phe
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40 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
 115 120 125

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

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

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

60 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

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	cgccaggcg cccggaagg gctggagtgg gtaggtttca ttagaataaa agctaattgt		180	
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 35 40 45

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 50 55 60

Gln Thr Thr Ser Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
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25 Lys Ser Ile Thr Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
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30 Ala Val Tyr Tyr Cys Ala Lys Tyr Gly Ser Ala Tyr Arg Pro Pro Phe
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35 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
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Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
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45 Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
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50 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
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55 Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205

60 Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
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Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr

239

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	35 40 45				
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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 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala				
	85 90 95				
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	Val Tyr Tyr Cys Ala Lys Ser Arg Ser Ala Gly Phe Phe Asp Tyr Trp				
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	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly				
	115 120 125				

240

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

20   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
      195                      200                      205

    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
      210                      215                      220

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    Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys
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241

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20	Gly 115	Gln Gly Thr Leu Val	Thr Val Ser Ser Gly	Gly Gly Gly Ser	Gly 125
25	Gly 130	Gly Gly Ser Gly Gly	Gly Gly Ser Glu Ile	Glu Leu Thr Gln	Ser 140
30	Pro 145	Ala Thr Leu Ser Leu	Ser Pro Gly Glu Arg	Ala Thr Leu Ser	Cys 160
35	Arg 165	Ala Ser Gln Ser Val	Ser Ser Tyr Leu Ala	Trp Tyr Gln Gln	Lys 175
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50	Thr 210	Leu Thr Ile Ser Ser	Leu Glu Pro Glu Asp	Phe Ala Val Tyr	Tyr 220
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 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
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 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
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 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
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 Tyr Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly
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 165 170 175
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 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
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243

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45	Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala			
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50	Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn			
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55	Tyr Tyr Cys Ala Lys Phe Asn Pro Phe Thr Ser Phe Asp Tyr Trp Gly			
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60	Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly			
	115 120 125			

244

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 145 150 155 160

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 180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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20 Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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249

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250

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30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	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	
75	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	

259

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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
    5      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

10    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

15    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

20    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

25    <210> 117

    <211> 446

30    <212> PRT

    <213> Artificial sequence

35    <220>

    <223> IgG heavy chain sequence 03 -001

40    <400> 117

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

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

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

55    Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
    50      55      60

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

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260

	85	90	95
5	His Arg Phe Arg His Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val 100	10 5	110
10	Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala 115	120	125
15	Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu 130	13 5	140
20	Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly 145	150	155 160
25	Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser 16 5	170	175
30	Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu 180	185	190
35	Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr 19 5	200	205
40	Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr 210	215	220
45	Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe 225	230	235 240
50	Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 245	250	255
55	Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val 260	265	270
60	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

261

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

5 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

10 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380

15 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

20 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

25 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

30 <210> 118
 <211> 1356
 <212> DNA
 35 <213> Artificial sequence

40 <220>
 <223> IgG heavy chain sequence of 03 -002
 <220>

45 <221> CDS
 <222> (1)..(1356)
 <223>

50

<400> 118
 gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtc aag cct ggg ggg 48
 55 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
 60 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

262

	35	40	45	
5	ggc cgt act aga aac aaa gct aac agt tac acc aca gaa tac gcc gcg Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala	55	60	192
10	tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca aag aac tca Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser	65	75	240
15	ctg tat ctg caa atg aac agc c tg aaa acc gag gac acg gcc gtg tat Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr	85	90	288
20	tac tgt gct aga tac tac tcc cgc tcc ctc aag gcc ttc gat tac tgg Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp Tyr Trp	100	105	336
25	ggc cag ggc acc ctg gtg acc gtc tcc agc gct agc acc aag ggc ccc Gly Gln Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	115	120	384
30	agc gtg ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	130	135	432
35	gcc gcc ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	145	150	480
40	gtg agc tgg aac agc ggc gcc ttg acc agc ggc gtg cac acc ttc ccc Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	165	170	528
45	gcc gtg ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	180	185	576
50	gtg ccc agc agc agc ctg ggc acc cag acc tac atc tgc aac gtg aac Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn	195	200	624
55	cac aag ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag a gc His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser	210	215	672
60	tgc gac aag acc cac acc tgc ccc ccc tgc cct gcc ccc gag ctg ctg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	225	230	720
65	ggc gga ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	245	250	768
70	atg atc agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	260	265	816
75	cac gag gac ccc gag gtg aag ttc aac tgg tac gtg gac ggc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	275	280	864
80	gtg cac aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc			912

263

	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr		
	290						295					300						
5	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			
10	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			
15	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				
20	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					
25	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							
30	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			
35	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				
40	gtg	gac	aag	agc	cgg	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					
45	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						
50	agc	ccc	ggc	aag														1356
	Ser	Pro	Gly	Lys														
				450														
55	<210>	119																
	<211>	452																
	<212>	PRT																
60	<213>	Artificial sequence																
55	<220>																	
	<223>	IgG heavy chain sequence of 03 -002																
	<400>	119																
60	Glu	Val	Gln	Ieu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly		
	1				5					10					15			

264

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
 20 25 30
 5 Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 10 Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala
 50 55 60
 15 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
 20 Tyr Cys Ala Arg Tyr Tyr Ser Arg Ser Leu Lys Ala Phe Asp Tyr Trp
 100 105 110
 25 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 30 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 35 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
 40 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 45 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 50 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220
 55 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
 60 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

265

5 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

 10 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

 15 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

 20 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

 25 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

 30 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

 35 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

 40 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

 45 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

 50 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

 55 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

 60 Ser Pro Gly Lys
 450

 <210> 120
 <211> 1353
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> IgG heavy chain sequence 03-009

266

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<220>
<221> CDS
5 <222> (1)..(1353)
<223>

10
<400> 120
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
15 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 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

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267

5	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	
10	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	
15	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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	tgg gag agc aac ggc cag ccc 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	
65	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	
70	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	
75	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	
80	ccc ggc aag	1353
	Pro Gly Lys	

268

450

5 <210> 121
 <211> 451
 <212> PRT
 10 <213> Artificial sequence

 15 <220>
 <223> IgG heavy chain sequence 03 -009
 <400> 121
 20 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 25 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 30 Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 35 Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 40 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 45 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 50 Ala Lys Gly Leu Phe Met Val Thr Thr Tyr Ala Phe Asp Tyr Trp Gly
 100 105 110
 55 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 60 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 55 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 60 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

269

	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
				180					185					190			
5	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
				195				200					205				
10	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	
		210					215					220					
15	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
	225					230					235					240	
20	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
					245					250						255	
25	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
				260					265					270			
30	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
			275					280					285				
35	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
		290					295					300					
40	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
	305					310					315					320	
45	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
					325					330					335		
50	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
				340					345					350			
55	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	
			355					360					365				
60	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
	370						375					380					
65	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
	385					390					395					400	
70	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
					405					410					415		
75	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
				420					425					430			

270

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

5 Pro Gly Lys
 450

10 <210> 122
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 15 <213> Artificial sequence

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<400> 122

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 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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40 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

45 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

50 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

55 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

60 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

60 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

271

	Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val	
	115 120 125	
5	ttc ccc ctg gcc ccc agc agc aag agc acc agc gcc gcc aca gc c gcc Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala	432
	130 135 140	
10	ctg gcc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser	480
	145 150 155 160	
15	tgg aac agc gcc gcc ttg acc agc gcc gtg cac acc ttc ccc gcc gtg Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro A la Val	528
	165 170 175	
20	ctg cag agc agc gcc ctg tac agc ctg agc agc gtg gtg acc gtg ccc Leu Gln Ser Ser Gly Leu Tyr Ser Ser Val Val Thr Val Pro	576
	180 185 190	
25	agc agc agc ctg gcc acc cag acc tac atc tgc aac gtg aac cac aag Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys	624
	195 200 205	
30	ccc agc aac acc aag gtg gac aaa cgc gtg gag ccc aag agc tgc gac Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp	672
	210 215 220	
35	aag acc cac acc tgc ccc ccc tgc cct gcc ccc gag .ctg ctg gcc gga Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly	720
	225 230 235 240	
40	ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ct c atg atc Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile	768
	245 250 255	
45	agc cgg acc ccc gag gtg acc tgc gtg gtg gtg gac gtg agc cac gag Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu	816
	260 265 270	
50	gac ccc gag gtg aag ttc aac tgg tac gtg gac gcc gtg gag gtg cac Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val G lu Val His	864
	275 280 285	
55	aac gcc aag acc aag ccc cgg gag gag cag tac aac agc acc tac cgg Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg	912
	290 295 300	
60	gtg gtg agc gtg ctc acc gtg ctg cac cag gac tgg ctg aac gcc aag Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys	960
	305 310 315 320	
65	gag tac aag tgc aag gtg agc aac aag gcc ctg cct gcc ccc atc gag Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu	1008
	325 330 335	
70	aag acc atc agc aag gcc aag gcc cag ccc cgg gag ccc cag gtg tac Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr	1056
	340 345 350	
75	acc ctg ccc ccc agc cgg gag gag atg acc aag aac ca g gtg tcc ctc Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu	1104
	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					
5	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	
10	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		
15	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		
20	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	
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	Gly	Lys															
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	1				5					10					15		
45	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Ph	e	Ser	Asp	His
				20					25						30		
50	Tyr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
			35					40						45			
55	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	
60	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Ly	s	Thr	Glu	Asp	Thr	Ala	Val	Tyr
					85						90					95	

273

Tyr Cys Ala Lys Gly Leu Thr Pro Leu Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110
 5
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 10
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 15
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 20
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 25
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 30
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 35
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 40
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 45
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 50
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 55
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 60
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 65
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 70
 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

274

	340	345	350	
5	Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu			
	355	3 60	365	
10	Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp			
	370	375	380	
15	Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val			
	385	3 90	395	400
20	Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp			
	405	410	415	
25	Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His			
	420	425	430	
30	Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro			
	435	440	445	
35	Gly Lys			
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	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
	1 5 10 15			
70	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			

275

5	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	
10	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	
15	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	
20	ctg tat ctg caa atg aac agc ctg aaa acc gag gac acg gcc gtg t at	288
	Ieu Tyr Ieu Gln Met Asn Ser Ieu Lys Thr Glu Asp Thr Ala Val Tyr	
	85 90 95	
25	tac tgt gca agg ggg att tgg cgg 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	
30	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	
35	ttc ccc ctg gcc ccc agc agc aag agc acc agc ggc ggc aca gcc gcc	432
	Phe Pro Ieu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala	
	130 135 140	
40	ctg ggc tgc ctg gtg aag gac tac ttc ccc gag ccc gtg acc gtg agc	480
	Ieu Gly Cys Ieu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser	
	145 150 155 160	
45	tgg aac agc ggc gcc ttg acc agc ggc gtg cac acc ttc ccc gcc gtg	528
	Trp Asn Ser Gly Ala Ieu Thr Ser Gly Val His Thr Phe Pro Ala Val	
	165 170 175	
50	ctg cag agc agc ggc ctg tac agc ctg agc agc gtg gtg acc gtg ccc	576
	Leu Gln Ser Ser Gly Ieu Tyr Ser Leu Ser Ser Val Val Thr Val Pro	
	180 185 190	
55	agc agc agc ctg ggc acc cag acc tac atc tgc aac gtg aac c ac aag	624
	Ser Ser Ser Ieu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys	
	195 200 205	
60	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	
65	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	
70	ccc tcc gtg ttc ctg ttc ccc ccc aag ccc aag gac acc ctc atg atc	768
	Pro Ser Val Phe Ieu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile	
	245 250 255	
75	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	
80	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	

276

	275	280	285	
	aac gcc aag acc a ag ccc cgg gag gag cag tac aac agc acc tac cgg			912
5	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 a ac ggc aag			960
	Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys			
10	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
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			
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	ggc aag			1350
45	Gly Lys			
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	<210> 125			
50	<211> 450			
	<212> PRT			
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	<400> 125			

277

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 5 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
 20 25 30
 10 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
 15 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
 65 70 75 80
 20 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 25 Tyr Cys Ala Arg Gly Ile Ser Pro Phe Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110
 30 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
 35 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 40 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 45 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 50 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
 55 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 60 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

278

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 5 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 10 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 15 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 20 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
 25 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 30 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 35 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 40 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
 45 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu S er Pro
 435 440 445
 50 Gly Lys
 450
 55 <210> 126
 <211> 1344
 <212> DNA
 60 <213> Artificial sequence

279

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5 <220>
 <221> CDS
 <222> (1) .. (1344)
 10 <223>

15 <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

20 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

25 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

30 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

35 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

40 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

45 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

50 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

55 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

60 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

280

	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				
5	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					
10	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		
15	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		
20	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			
25	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				
30	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					
35	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	
					310					315					320		
40	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		
45	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				
50	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	
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	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
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282

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283

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285

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286

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288

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316

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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 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 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 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

318

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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

5  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

10 <210> 216
    <211> 254
    <212> PRT
15 <213> Artificial sequence

20 <220>
    <223> SC03-021
    <400> 216

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

30 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
   20                25                30

35 Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
   35                40                45

40 Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
   50                55                60

45 Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
   65                70                75                80

50 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
   85                90                95

55 Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
  100                105                110

60 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

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

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319

5 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
 10 Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205
 15 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
 210 215 220
 20 Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro
 225 230 235 240
 25 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 245 250
 <210> 217
 <211> 762
 30 <212> DNA
 <213> Artificial sequence
 35 <220>
 <223> SC03-022
 40 <220>
 <221> CDS
 45 <222> (1)..(762)
 <223>
 50 <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
 55 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
 60 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

320

	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	
5	cgc 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 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	
20	ggc caa ggc 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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act cgc tac	720
	Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr	
	225 230 235 240	
60	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	
55	<210> 218	
	<211> 254	
	<212> PRT	
60	<213> Artificial sequence	

321

<220>

<223> SC03-022

5 <400> 218

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

10 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
 20 25 30

15 Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Tyr Gly Leu
 35 40 45

20 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

25 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
 85 90 95

30 Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
 100 105 110

35 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
 115 120 125

40 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

45 Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Ile Asn Lys Asn Tyr
 165 170 175

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

55 Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205

60 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

322

[illegible]

323

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    gtc tgc 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

5    ggg tgc 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

10   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

15   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

25   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

30   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

35   cta ggt gcg gcc      780
    Leu Gly Ala Ala
      260

40   <210> 220
      <211> 260
      <212> PRT

45   <213> Artificial sequence

    <220>
50   <223> SC03-023
      <400> 220

55   Ala Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
      1                      5                      10                      15

60   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

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324

	35	40	45
5	Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro 50 55 60		
10	Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln 65 70 75 80		
15	Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr 85 90 95		
20	Tyr Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro 100 105 110		
25	Arg Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr 115 120 125		
30	Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr G ly 130 135 140		
35	Gly Ser Thr Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser 145 150 155 160		
40	Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Ser Ser S er Thr Val 165 170 175		
45	Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 180 185 190		
50	Pro Lys Leu Met Ile Tyr Asp Val Ser Lys Arg P ro Ser Gly Val Ser 195 200 205		
55	Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 210 215 220		
60	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		

325

<212> DNA

<213> Artificial sequence

5

<220>

<223> SC03-024

10

<220>

<221> CDS

15 <222> (1)..(753)

<223>

20

<400> 221

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

25

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

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

35

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

40

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

45

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

50

ggc caa ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc 384
 Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
 115 120 125

55

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

60

cag 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
 145 150 155 160

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

326

165 170 1 75
 5 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
 10 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
 15 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
 20 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
 25 <210> 222
 <211> 251
 <212> PRT
 30 <213> Artificial sequence
 35 <220>
 <223> SC03-024
 <400> 222
 40 Ala Met Ala Gln Val Gln Leu Val Glu Ser Gly Ser Glu Leu Lys Ile
 1 5 10 15
 45 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Thr Gly Tyr Thr Phe
 20 25 30
 50 Thr Arg Tyr Ser Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45
 55 Glu Trp Val Gly Trp Ile Asn Thr Gln Thr Gly Asn Ser Asn Tyr Gly
 50 55 60
 60 Gln Ala Phe Ser Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
 65 70 75 80
 60 Thr Ala Tyr Leu Gln Ile Ser Ser Leu Gln Ala Glu Asp Thr Ala Thr
 85 90 95

327

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

5  Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
      115      120      125

10 Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Gln Ser Val Val Thr Gln
     130      135      140

15 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

20 Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn Asn Lys
     180      185      190

25 Arg Pro Ser Gly Ile Pro Asn Arg Phe Ser Gly Ser Lys Ser Gly Thr
     195      200      205

30 Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp
     210      215      220

35 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

40 <210> 223
    <211> 756

45 <212> DNA
    <213> Artificial sequence

50 <220>
    <223> SC03-025

55 <220>
    <221> CDS
    <222> (1)..(756)

60 <223>

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328

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<400> 223
5 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

10 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

15 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

15 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

20 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

25 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

30 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

35 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

35 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

40 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

45 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

50 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

55 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

55 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

60 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

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329

756

ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc
 Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250

5
 <210> 224
 <211> 252
 10 <212> PRT
 <213> Artificial sequence
 15
 <220>
 <223> SC03-025
 20 <400> 224
 Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 25 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 30 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 35 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 40 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
 45 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 50 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 55 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
 130 135 140
 60 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

330

5 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
 10 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 15 Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Ile Pro Tyr Ala Phe
 225 230 235 240
 20 Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250
 <210> 225
 25 <211> 756
 <212> DNA
 <213> Artificial sequence
 30
 <220>
 35 <223> SC03-026
 <220>
 <221> CDS
 40 <222> (1)..(756)
 <223>
 45
 <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
 50 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
 55 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
 60 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

331

	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	
5	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	
10	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	
15	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	
20	ggc agc ggc act ggc ggc 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	
25	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 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	
35	tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac t gg	576
	Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp	
	180 185 190	
40	gca tct acc cgg gaa tcc ggc gtc cct gac cga ttc agt ggc agc ggc	624
	Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
	195 200 205	
45	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 ggc acc aag gtg gag atc aaa cgt gcg gcc	756
	Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala	
	245 250	
60	<210> 226	
	<211> 252	
	<212> PRT	
	<213> Artificial sequence	
	<220>	
	<223> SC03-026	

332

<400> 226

Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 5 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 10 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 15 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 20 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
 25 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 30 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 35 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140
 40 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
 45 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 50 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 55 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 60 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

333

245

250

5 <210> 227
 <211> 756
 <212> DNA
 10 <213> Artificial sequence

 15 <220>
 <223> SC03-027
 <220>
 20 <221> CDS
 <222> (1)..(756)
 <223>
 25

 30 <400> 227
 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

 35 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

 40 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

 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

 50 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

 55 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

 60 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

 65 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

334

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
 5 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
 10 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
 15 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
 20 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
 25 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
 30 <210> 228
 <211> 252
 35 <212> PRT
 <213> Artificial sequence
 40 <220>
 <223> SC03-027
 45 <400> 228
 Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 50 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala A la Ser Gly Phe Thr Phe
 20 25 30
 55 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 60 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
5	Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val 85		90	95
10	Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln 100		105	110
15	Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr 115		120	125
20	Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro 130		135	140
25	Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys 145	150	155	160
30	Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala 165		170	175
35	Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp 180		185	190
40	Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly 195	200	205	
45	Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp 210	215	220	
50	Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe 225	230	235	240
55	Gly Gln Gly Thr Lys Val Asp Ile Lys Arg Ala Ala 245		250	
	<210>	229		
	<211>	756		
	<212>	DNA		
	<213>	Artificial sequence		
	<220>			
60	<223>	SC03-029		
	<220>			

336

<221> CDS

<222> (1)..(756)

5 <223>

<400> 229

10	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	
15	cgc 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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	ggg aca atg gtc acc gtc tgc 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	
50	ggc agc ggc act ggc ggg tgc 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	
55	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	
60	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	
65	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	
70	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	
75	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	

337

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
 5 225 230 235 240
 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
 10 245 250
 <210> 230
 <211> 252
 15 <212> PRT
 <213> Artificial sequence
 20
 <220>
 <223> SC03-029
 25 <400> 230
 Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 30 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 35 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 40 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 45 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
 50 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 55 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 60 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140

338

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

5 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
 165 170 175

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

15 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

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

25 Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250

<210> 231

30 <211> 756

<212> DNA

35 <213> Artificial sequence

<220>

40 <223> SC03-030

<220>

45 <221> CDS

<222> (1)..(756)

<223>

50

<400> 231

55 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
 60 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

339

	35	40	45	
5	gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr A la 50 55 60			192
10	aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75 80			240
	acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val 85 90 95			288
15	tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln 100 105 110			336
20	ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr 115 120 125			384
25	ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag tc t cca Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro 130 135 140			432
30	gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys 145 150 155 160			480
	tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr L eu Ala 165 170 175			528
35	tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp 180 185 190			576
40	gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly 195 200 205			624
45	tct ggg aca gat ttt act ctc acc atc agc agt ctg cag gct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp 210 215 220			672
50	gtg gca gtt tat ta c tgt cag caa tat tat agt act cct ctg acg ttc Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe 225 230 235 240			720
	ggc caa ggg acc aag gtg gaa atc aaa cgt gcg gcc Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala 245 250			756
55	<210> 232			
	<211> 252			
60	<212> PRT			
	<213> Artificial sequence			

340

<220>

5 <223> SC03-030

<400> 232

10 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
 15 20 25 30
 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 20 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 25 Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75 80
 30 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
 35 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 40 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140
 45 Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
 145 150 155 160
 50 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
 55 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 60 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220

341

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

5 Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250

10 <210> 233

<211> 759

<212> DNA

15 <213> Artificial sequence

20 <220>

<223> SC03-031

<220>

25 <221> CDS

<222> (1)..(759)

30 <223>

<400> 233
35 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
40 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
45 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
50 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
55 Thr Gly Asn Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
85 90 95
tat tac tgt gcg aga gaa tcg ggt ggt ggc tac gat aac cac ttt gac 336
60 Tyr Tyr Cys Ala Arg Glu Ser 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

342

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Thr Gly Gly
 115 120 125
 5 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
 10 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
 15 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
 20 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
 25 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
 30 ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag gat gag 720
 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
 Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Thr Gly Gly Val
 225 230 235 240
 35 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
 40 <212> PRT
 <213> Artificial sequence
 45
 <220>
 <223> SC03-031
 50 <400> 234
 Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Asp Val Lys Lys
 1 5 10 15
 55 Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Gly Thr Phe
 20 25 30
 60 Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45

343

Glu Trp Met Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
 50 55 60

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

10 Thr Gly Asn Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 85 90 95

15 Tyr Tyr Cys Ala Arg Glu Ser Gly Gly Gly Tyr Asp Asn His Phe Asp
 100 105 110

20 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

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

30 Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ser Asn Thr Val Asn Trp
 165 170 175

35 Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val Ile Tyr Ala Asn
 180 185 190

40 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

45 Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Thr Gly Gly Val
 225 230 235 240

50 Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Ser Ala Ala
 245 2 50

55 <210> 235
 <211> 771
 <212> DNA

60 <213> Artificial sequence

344

<220>
 <223> SC03-032
 5 <220>
 <221> CDS
 <222> (1)..(771)
 10 <223>

15 <400> 235
 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

20 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

25 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

30 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

35 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

40 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

45 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

50 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

55 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

60 act gta agc tgg tac cag cag gtt cca ggg acg gcc ccc aag etc etc 576
 Thr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
 180 185 190

345

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        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

5      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

10     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

20

    <210> 236

    <211> 257
25     <212> PRT
        <213> Artificial sequence

30

    <220>

    <221> misc_feature
35     <222> (204)..(204)
        <223> The 'Xaa' at location 204 stands for Pro, or Leu.

40     <220>

    <221> misc_feature
        <222> (218)..(218)
45     <223> The 'Xaa' at location 218 stands for Leu.
        <220>

50     <221> misc_feature
        <222> (240)..(240)
        <223> The 'Xaa' at location 240 stands for Met, or Leu.

55     <220>
        <223> SC03-032

60     <400> 236

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

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346

5 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
 20 25 30
 10 Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45
 15 Glu Trp Met Gly Lys Ile Ile Pro Ile Leu Gly Lys Val Thr Tyr Ala
 50 55 60
 20 Gln Lys Phe Gln Ala Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75 80
 25 Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 85 90 95
 30 Phe Tyr Cys Ala Arg Asp Gly Trp Asp Leu Thr Gly Ser Phe Leu Gly
 100 105 110
 35 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125
 40 Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr
 130 135 140
 45 Gln Ser Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 145 150 155 160
 50 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 165 170 175
 55 Thr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
 180 185 190
 60 Ile Tyr Arg Asn Asn Gln Arg Pro Pro Gly Val Xaa Asp Arg Phe Ser
 195 200 205
 65 Gly Ser Lys Ser Gly Thr Ser Ala Ser Xaa Ala Ile Ser Gly Leu Gln
 210 215 220
 70 Ser Asp Asp Glu Ala Phe Tyr Tyr Cys Ala Ala Trp Asp Gly Ser Xaa
 225 230 235 240
 75 Asn Gly Leu Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
 245 250 255
 Ala

347

5 <210> 237
 <211> 765
 <212> DNA
 10 <213> Artificial sequence

 15 <220>
 <223> SC03-033
 <220>
 20 <221> CDS
 <222> (1)..(765)
 <223>
 25

 <400> 237
 30 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 Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
 35 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
 40 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
 55 100 105 110

 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
 60 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

348

5 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

10 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

15 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

20 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

25 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

30 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

35 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

40 <210> 238
 <211> 255

45 <212> PRT
 <213> Artificial sequence

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

55 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
 20 25 30

60 Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 35 40 45

65 Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
 50 55 60

70 Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn

349

	65		70		75		80	
5	Thr	Ala	Tyr	Leu	Gln	Trp	Ala	Ile
				85			90	95
10	Tyr	Tyr	Cys	Ala	Gly	Gly	Ser	Trp
				100			105	110
15	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
				115			120	125
20	Gly	Thr	Gly	Ser	Gly	Thr	Gly	Ser
				130			135	140
25	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser
					145		150	155
30	Cys	Lys	Thr	Ser	His	Asn	Ile	Phe
					165		170	175
35	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro
				180			185	190
40	Tyr	Trp	Ala	Ser	Thr	Arg	Ala	Ser
				195			200	205
45	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser
				210			215	220
50	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys
					225		230	235
55	Tyr	Ser	Phe	Gly	Gln	Gly	Thr	Lys
				245			250	255
60	<210> 239							
	<211> 762							
	<212> DNA							
	<213> Artificial sequence							
	<220>							
	<223> SC03-034							
	<220>							

350

<221> CDS

<222> (1)..(762)

5 <223>

<400> 239

10	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	
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	
20	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	
25	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	
30	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	
35	acc gcc tac ctg cag tgg agc agc ctg aag gcc tgc gac acc gcc ata	288
	Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile	
	85 90 95	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	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	
75	agc ggg tct ggg aca gat 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	

351

	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			
5	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	
10				
	<210> 240			
	<211> 254			
15	<212> PRT			
	<213> Artificial sequence			
20				
	<220>			
	<223> SC03-034			
25				
	<400> 240			
	Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
	1	5	10	15
30				
	Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe			
		20	25	30
35				
	Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu			
		35	40	45
40				
	Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser			
		50	55	60
45				
	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
50				
	Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp			
		100	105	110
55				
	Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly			
		115	120	125
60				
	Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln			
		130	135	140

352

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

5 Cys Lys Ser Ser Gln Ser Ile Leu Asn Arg Ser Asn Asn Lys Asn Tyr
 165 170 175

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

15 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

20 Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
 225 230 235 240

25 Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
 245 250

30 <210> 241
 <211> 765
 <212> DNA

35 <213> Artificial sequence

40 <220>
 <223> SC03-035
 <220>

45 <221> CDS
 <222> (1)..(765)
 <223>

50 <400> 241
 gcc atg gcc gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag 48
 55 Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10 15

60 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

353

	35	40	45	
5	gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser	55	60	192
10	cgc tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn	65	70 75 80	240
15	acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile	85	90 95	288
20	tat tac tgt cgc ggg ggt tgc ggg att tct acc c ct atg gac gtc tgg Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp	100	105 110	336
25	ggc caa ggg acc acg gtc acc gtc tgc agc ggt acg ggc ggt tca ggc Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly	115	120 125	384
30	gga acc ggc agc ggc act ggc ggg tgc acg gac atc cag atg acc cag Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln	130	135 140	432
35	tct cca gac tcc ctg gct gtg tct ctg ggc gag agy gcc acc atc aac Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn	145	150 155 160	480
40	tgc aag tcc agt cag agt gtt tta tac agc tcc aac aat aag aac tac Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr	165	170 175	528
45	tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile	180	185 190	576
50	tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly	195	200 205	624
55	agc ggg tct ggg aca gat ttc act ctc acc a tc agc agc ctg cag gct Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala	210	215 220	672
60	gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccc ctg Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu	225	230 235 240	720
65	tac agt ttt ggc cag ggg acc aag gtg gag atc aaa cct gcg gcc Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Pro Ala Ala	245	250 255	765
70	<210> 242			
75	<211> 255			
80	<212> PRT			
85	<213> Artificial sequence			

354

<220>

5 <223> SC03-035

<400> 242

10 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
 15 20 25 30
 Ile Thr Tyr Trp Ile Gly Trp Val Arg Gl n Met Pro Gly Lys Gly Leu
 35 40 45
 20 Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
 50 55 60
 25 Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn
 65 70 75 80
 30 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
 35 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
 115 120 125
 40 Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln
 130 135 140
 45 Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
 145 150 155 160
 50 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
 55 Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205
 60 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
 210 215 220

355

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu
 225 230 235 240

5 Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Pro Ala Ala
 245 250 255

10 <210> 243
 <211> 759
 <212> DNA
 15 <213> Artificial sequence

20 <220>
 <223> SC03-036
 <220>
 25 <221> CDS
 <222> (1)..(759)
 30 <223>

<400> 243
 35 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

40 cgg 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

cgg 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

55 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

60 tat tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg 336
 Tyr Tyr Cys Ala 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

356

	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Thr	Gly	Gly	Ser	Gly	
			115					120					125				
5	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					
10	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	
							150					155				160	
15	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		
20	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			
25	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				
30	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					
35	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	
						230					235				240		
40	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								
45	<210>	244															
50	<211>	253															
55	<212>	PRT															
60	<213>	Artificial sequence															
65	<220>																
70	<223>	SC03-036															
75	<400>	244															
80	Ala	Met	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Thr	Glu	Val	Lys	Lys	
	1				5					10					15		
85	Pro	Gly	Glu	Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Gly	Phe	
				20					25					30			
90	Ile	Thr	Tyr	Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	
			35				40						45				

357

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
 50 55 60
 5 Pro Ser Phe Gln Gly Gln Val Thr Ile Ser A la Asp Lys Ser Ile Asn
 65 70 75 80
 10 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile
 85 90 95
 15 Tyr Tyr Cys Ala Gly Gly Ser Gly I le Ser Thr Pro Met Asp Val Trp
 100 105 110
 20 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
 25 Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
 145 150 155 160
 30 Cys Lys Ser Ser Gln Ser Val Leu His Ser Pro Asn Asn Lys Asn Tyr
 165 170 175
 35 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 180 185 190
 40 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
 45 Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Asn Ser
 225 230 235 240
 50 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250
 55 <210> 245
 <211> 744
 <212> DNA
 60 <213> Artificial sequence

358

<220>

<223> SC03-037

5 <220>

<221> CDS

10 <222> (1)..(744)

<223>

15 <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

20 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

25 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

30 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

35 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

40 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

45 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

50 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

55 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

60 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

55 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

60 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

359

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

5 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

10 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 Val Phe Gly Gly Gly Thr
 225 230 235 240

15 aag ctg acc gtc cta ggt gcg gcc 744
 Lys Leu Thr Val Leu Gly Ala Ala
 245

<210> 246

20 <211> 248

<212> PRT

25 <213> Artificial sequence

<220>

30 <223> SC03-037

<400> 246

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

40 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

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

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

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

60 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

360

5 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
 10 Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro
 165 170 175
 15 Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
 180 185 190
 20 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
 25 Asn Gly Arg Asp Ser Ser Gly Asn His Trp Val Phe Gly Gly Gly Thr
 225 230 235 240
 30 Lys Leu Thr Val Leu Gly Ala Ala
 245
 35 <210> 247
 <211> 744
 <212> DNA
 40 <213> Artificial sequence
 45 <220>
 <223> SC03-038
 <220>
 50 <221> CDS
 <222> (1)..(744)
 55 <223>
 60 <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

361

	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	
5	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	
10	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	
15	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	
20	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	
25	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	
30	cag ggg acc acg gtc acc gtc tgc 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	
35	acc ggc agc ggc act ggc ggg tgc 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	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	aag ctg acc gtc cta ggt gcg gcc	744
	Lys Leu Thr Val Leu Gly Ala Ala	
	245	
	<210> 248	

362

<211> 248

<212> PRT

5 <213> Artificial sequence

<220>

10 <223> SC03-038

<400> 248

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

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

25 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

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

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

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

45 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

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

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

60 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

363

	195	200	205	
5	Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys 210 215 220			
10	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			
15	<210> 249			
	<211> 759			
20	<212> DNA			
	<213> Artificial sequence			
25	<220>			
	<223> SC03-039			
30	<220>			
	<221> CDS			
	<222> (1)..(759)			
35	<223>			
40	<400> 249			
	gcc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag Ala Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln 1 5 10 15			48
45	cct ggg ggg tcc ctg aga ctc tcc tgt g ca gcc tct gga ttc acc ttt Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 20 25 30			96
50	agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45			144
55	gag tgg gtc tca gtt att tat agc ggt ggt act agt aca tac tat gca Glu Trp Val Ser Val Ile Tyr Ser Gly Gly Thr Ser Thr Tyr Tyr Ala 50 55 60			192
60	gac tcc gtg aag ggc cgg ttc acc atc tcc aga gat aat tcc aag aac Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75 80			240
	aca ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 85 90 95			288

364

	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	
5	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	
10	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	
15	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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	<210> 250	
55	<211> 253	
	<212> PRT	
	<213> Artificial sequence	
60	<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	

365

	20	25	30
5	Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45		
10	Glu Trp Val Ser Val Ile Tyr Ser Gly Gly Thr Ser Thr Tyr Tyr Ala 50 55 60		
15	Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75 80		
20	Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 85 90 95		
25	Tyr Phe Cys Ala Lys Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp 100 105 110		
30	Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Thr Gly Gl y 115 120 125		
35	Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asn Phe Met Leu 130 135 140		
40	Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys Thr Va l Thr Ile 145 150 155 160		
45	Ser Cys Ala Gly Ser Ser Gly Ser Ile Ala Ser Asn Tyr Val Gln Trp 165 170 175		
50	Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Va l Ile Tyr Glu Asp 180 185 190		
55	Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Asp 195 200 205		
60	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		

366

<212> DNA

<213> Artificial sequence

5

<220>

<223> SC03-040

10

<220>

<221> CDS

15

<222> (1)..(756)

<223>

20

<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

25

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

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

35

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

40

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

45

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

50

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

55

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

60

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

367

	165	170	175			
5	tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp	180	185	190	576	
10	gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	195	200	205	624	
15	tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp	210	215	220	672	
20	gtg gca gtt tat tac tgt cag caa tat tat agt agt ccg tac agt ttt Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Ser Pro Tyr Ser Phe	225	230	235	240	720
25	ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala	245	250		756	
30	<210> 252 <211> 252 <212> PRT <213> Artificial sequence					
35	<220> <223> SC03-040 <400> 252					
40	Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln 1 5 10 15					
45	Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 20 25 30					
50	Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45					
55	Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala 50 55 60					
60	Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75 80					
65	Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val 85 90 95					

368

Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 5 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 10 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140
 15 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
 20 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 25 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 30 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 35 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
 40 <210> 253
 <211> 756
 45 <212> DNA
 <213> Artificial sequence
 50 <220>
 <223> SC03-041
 55 <220>
 <221> CDS
 <222> (1)..(756)
 60 <223>

369

<400> 253
 gcc atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag 48
 5 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
 10 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
 15 Glu Tyr Val Ser Gly Ile Ser Ser Asn 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
 20 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
 25 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
 30 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
 35 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 cgg acc acc atc aac tgc aag 480
 40 Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Thr 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
 45 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
 50 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
 55 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
 60 Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
 225 230 235 240

370

ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc
 Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250

756

5
 <210> 254
 <211> 252
 10 <212> PRT
 <213> Artificial sequence
 15
 <220>
 <223> SC03-041
 20 <400> 254
 Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 25 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 30 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 35 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
 40 Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
 85 90 95
 45 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 50 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 55 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
 60 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
 165 170 175

371

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 5
 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 10
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 15
 Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe
 225 230 235 240
 20
 Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250
 <210> 255
 25 <211> 756
 <212> DNA
 <213> Artificial sequence
 30
 <220>
 35 <223> SC03-042
 <220>
 <221> misc_feature
 40 <222> (153)..(154)
 <223> n can be a, g, c or t
 45
 <220>
 <221> CDS
 50 <222> (1)..(756)
 <223>
 55
 <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
 60 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

372

	20	25	30	
5	agc agt tat gct atg cac tgg gtc cgc cag gct cca ggg aag gga ctg Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45	144		
10	gaa tat gtn tca ggt att agt agt aat ggg ggt agc aca tat tat gca Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala 50 55 60	192		
15	aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75 80	240		
20	acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val 85 90 95	288		
25	tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln 100 105 110	336		
30	ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Ser Gly Gly Thr 115 120 125	384		
35	ggc agc ggc act ggc ggc tcg acg gat gtt gtg atg a ct cag tct cca Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln Ser Pro 130 135 140	432		
40	gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys 145 150 155 160	480		
45	tcc agc cag agt gtt tta tac agc tcc aac gat aag aac tac tta gct Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asp Lys Asn Tyr Leu Ala 165 170 175	528		
50	tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp 180 185 190	576		
55	gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agc ggc agc ggg Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly 195 200 205	624		
60	tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp 210 215 220	672		
65	gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac agt ttt Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe 225 230 235 240	720		
70	ggc cag ggg acc aag ctg gag atc aaa cgt gcg g cc Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala 245 250	756		
75	<210> 256			
80	<211> 252			

373

<212> PRT

<213> Artificial sequence

5

<220>

<223> SC03-042

10

<220>

<221> misc_feature

15

<222> (153)..(154)

<223> n can be a, g, c or t

<400> 256

20

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

25

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

30

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

35

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

40

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

45

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

50

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

55

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

60

Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asp Lys Asn Tyr Leu Ala
 165 170 175

374

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

5

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

10

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

15

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

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Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250

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50

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

55

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

60

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

375

	Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	
	65 70 75 80	
5	acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val	288
	85 90 95	
10	tat tac tgt gcg aga act act aat cgg gct ttt gat atc tgg ggc caa Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln	336
	100 105 110	
15	ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Ser Gly Gly Thr	384
	115 120 125	
20	ggc agc ggc act ggc ggg tcg acg gac atc cag ttg acc cag tct cca Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro	432
	130 135 140	
25	gac tcc ctg gct gtg tct ctg ggc gag agg g cc acc atc aac tgc aag Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys	480
	145 150 155 160	
30	tcc agc cag agt gtt tta tac agg tcc aac aat aag aac tac tta gct Ser Ser Gln Ser Val Leu Tyr Arg Ser Asn Asn Lys Asn Tyr Leu Ala	528
	165 170 175	
35	tgg tac cag cag aag cca gga cag cct cct aag ctg ctc att tac tgg Trp Tyr Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp	576
	180 185 190	
40	gca tct acc cgt gaa tcc ggg gtc tct gag cga ttc agt ggc agc ggg Ala Ser Thr Arg Glu Ser Gly Val Ser Glu Arg Phe Ser Gly Ser Gly	624
	195 200 205	
45	tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp	672
	210 215 220	
50	gtg gca gtt tat tac tgt cag caa tat tat agt acc ccg tac agt ttt Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe	720
	225 230 235 240	
55	ggc cag ggg acc aag ctg gag atc aaa cgt gcg gcc Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala	756
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376

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 10 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 15 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr r Tyr Tyr Ala
 50 55 60
 20 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 a Glu Asp Met Ala Val
 85 90 95
 25 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 30 Gly Thr Met Val Thr Val Ser Ser Gl y Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 35 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
 130 135 140
 40 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
 45 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 50 Ala Ser Thr Arg Glu Ser Gly Val Ser Glu Arg Phe Ser Gly Ser Gly
 195 200 205
 55 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 60 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
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377

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 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
 35 20 25 30
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 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 40 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
 45 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
 50 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
 55 100 105 110
 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
 60 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

378

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	Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys	
	145 150 155 160	
5	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	
10	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	
15	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	
20	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	
25	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	
30	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	
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60	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	

379

5 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
 10 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 15 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140
 20 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
 25 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 30 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Arg Gly Ser Gly
 195 200 205
 35 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 40 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
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 50 <212> DNA
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   1          5          10          15
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
20 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
25 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
30 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
35 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
40 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
45 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
50 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
55 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
60 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
65 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
70 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
75 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

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381

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
 5 225 230 235 240
 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
 10
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 <211> 252
 15 <212> PRT
 <213> Artificial sequence
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 25 <400> 262
 Ala Met Ala Gln Leu Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 30 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30
 35 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 40 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 45 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
 50 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 55 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 60 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
 130 135 140

382

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

5 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
 165 170 175

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

15 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

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

25 Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Ala Ala
 245 250

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35 <213> Artificial sequence

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<400> 263
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cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
 60 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

383

	35	40	45	
5	gaa tat gtt tca ggt att agt agt aat ggg ggt agc aca tat tat gca Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala	55	60	192
10	aac tct gtg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	65	70 75 80	240
15	acg ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg gct gtg Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val	85	90 95	288
20	tat tac tgt gcg aga act act aat cgg gc t ttt gat atc tgg ggc caa Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln	100	105 110	336
25	ggg aca atg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc gga acc Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr	115	120 125	384
30	ggc agc ggc act ggc ggg tcg acg gat gtt gtg atg act cag tct cca Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln Ser Pro	130	135 140	432
35	gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys	145	150 155 160	480
40	tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac tta gct Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala	165	170 175	528
45	tgg tac cag cag aaa cca ggg cag cct cct aag ctg ctc att tac tgg Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp	180	185 190	576
50	gca tct acc cgg gaa tcc ggg gtc cct gac agg ttc agt ggc agc ggg Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	195	200 205	624
55	tct ggg aca gac ttc agt ctc acc at c agc agc ctg cag gct gaa gat Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp	210	215 220	672
60	gtg gcg gtt tat tac tgt cag caa tat tac agt cct ccg tac act ttt Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Pro Pro Tyr Thr Phe	225	230 235 240	7 20
	ggc ccg ggg acc aag gtg gaa atc aaa cgt gcg gcc Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Ala Ala	245	250	756
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384

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 15 20 25 30
 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 20 Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 25 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
 30 85 90 95
 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 35 100 105 110
 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 40 Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln Ser Pro
 130 135 140
 45 Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
 145 150 155 160
 50 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
 55 180 185 190
 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 60 Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220

385

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

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 245 250

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cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 96
 40 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
 45 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
 50 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
 55 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
 60 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 tgg agc ggt acg ggc ggt tca ggc gga acc 384

386

	Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr	
	115 120 125	
5	ggc agc ggc act ggc ggg tgc acg gat gtt gtg atg act cag tct cca Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val Met Thr Gln Ser Pro	432
	130 135 140	
10	gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac tgc aag Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys	480
	145 150 155 160	
15	tcc agc cag agt gtt tta tat agc tcc aac aat aag aac tac tta gct Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala	528
	165 170 175	
20	tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp	576
	180 185 190	
25	gca tct acc cgg gaa tcc ggg gtc c ct gac cga ttc agt ggc agc ggg Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	624
	195 200 205	
30	tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp	672
	210 215 220	
35	gtg gca gtt tat tac tgt cag caa tat tat agt act cct ctc act ttc Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe	720
	225 230 235 240	
40	ggc gga ggg acc aag gtg gaa atc aaa cgt gcg gcc Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala	756
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	Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
	35 40 45	

387

Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala
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 5 Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75 80
 10 Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val
 85 90 95
 15 Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 20 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
 25 Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
 145 150 155 160
 30 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
 165 170 175
 35 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 40 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
 45 Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu Thr Phe
 225 230 235 240
 50 Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 245 250
 <210> 267
 55 <211> 756
 <212> DNA
 60 <213> Artificial sequence

388

<220>

<223> SC03-048

5 <220>

<221> CDS

10 <222> (1)..(756)

<223>

15 <400> 267
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Ala Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln
1 5 10 15

20 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

25 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

30 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

35 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

40 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

45 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

50 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

55 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

60 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

389

	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	
5	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	
10	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	
15	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	
20	<211> 252	
	<212> PRT	
25	<213> Artificial sequence	
	<220>	
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	<400> 268	
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40	Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
	20 25 30	
45	Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
	35 40 45	
50	Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala	
	50 55 60	
55	Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	
	65 70 75 80	
60	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	

390

5 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
 10 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
 165 170 175
 15 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 20 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser G ly
 195 200 205
 25 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
 30 Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 245 250
 35 <210> 269
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 40 <213> Artificial sequence
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 55 <223>
 60 <400> 269
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 1 5 10 15

391

	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	
5	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	
10	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	
15	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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	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

392

<211> 252

<212> PRT

5 <213> Artificial sequence

<220>

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<223> SC03-049

<400> 270

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

25 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

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

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

40 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

45 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro
130 135 140

50 Ser Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
145 150 155 160

55 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
165 170 175

60 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

393

	195	200	205		
5	Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp	210	215	220	
10	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		
15	<210> 271				
	<211> 756				
20	<212> DNA				
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25	<220>				
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30	<220>				
	<221> CDS				
	<222> (1)..(756)				
35	<223>				
40	<400> 271				
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	Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln	1	5	10	15
45	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	
50	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	
55	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	
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	

394

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
 5 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
 10 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
 15 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
 20 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
 25 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 Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 30 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
 35 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
 40 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> 272
 45 <211> 252
 <212> PRT
 <213> Artificial sequence
 50
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 55 <223> SC03-050
 <400> 272
 Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln
 60 1 5 10 15
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

395

	20	25	30
5	Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45		
10	Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala 50 55 60		
15	Asn Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75 80		
20	Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val 85 90 95		
25	Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln 100 105 110		
30	Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr 115 120 125		
35	Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro 130 135 140		
40	Ser Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys 145 150 155 160		
45	Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala 165 170 175		
50	Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp 180 185 190		
55	Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly 195 200 205		
60	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		

396

<212> DNA

<213> Artificial sequence

5

<220>

<223> SC03-051

10

<220>

<221> CDS

15

<222> (1)..(762)

<223>

20

<400> 2 73

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

25

cgc 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

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

35

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

40

cgc 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

45

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

50

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

55

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

60

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

397

	165	170	175			
5	tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctt ctc att Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile	180	185	190	576	
10	tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly	195	200	205	624	
15	agc ggg tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala	210	215	220	672	
20	gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr	225	230	235	240	720
25	act ttt ggc cag ggg acc a ag gtg gaa atc aaa cgt gcg gcc Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala	245	250		762	
30	<210> 274 <211> 254 <212> PRT <213> Artificial sequence					
35	<220> <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					
45	Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe 20 25 30					
50	Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu 35 40 45					
55	Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser 50 55 60					
60	Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn 65 70 75 80					
65	Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile 85 90 95					

398

Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
 100 105 110

5 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
 115 120 125

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

15 Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala 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

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

25 Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205

30 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
 210 215 220

35 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

40 <210> 275
 <211> 762

45 <212> DNA
 <213> Artificial sequence

50 <220>
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55 <220>
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 <222> (1) .. (762)

60 <223>

399

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15	atc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu 35 40 45	144
20	gag tgg atg ggg atc atc tat cct ggt gac tct gaa acc aga tac agc Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser 50 55 60	192
25	cgc tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn 65 70 75 80	240
30	acc acc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc gcc ata Thr Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile 85 90 95	288
35	tat tac tgt ggc ggg ggt tcg ggg att tct acc cct atg gac gtc tgg Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp 100 105 110	336
40	ggc caa ggg acc acg gtc acc gtc tcg agc ggt acg ggc ggt tca ggc Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly 115 120 125	384
45	gga acc ggc agc ggc act ggc ggg tcg acg gac atc cag atg acc cag Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln 130 135 140	432
50	tct cca gac tcc ctg gct gtg tct ctg ggc gag agg gcc acc atc aac Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn 145 150 155 160	480
55	tgc aag tcc agc cag agt gtt tta tac agc tcc aac aat aag aac tac Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr 165 170 175	528
60	tta gct tgg tac cag cag aaa cca gga cag cct cct aag ctg ctc att Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile 180 185 190	576
65	tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly 195 200 205	624
70	agc ggg tct ggg aca gat ttc act ctc acc atc agc agc ctg cag gct Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala 210 215 220	672
75	gaa gat gtg gca gtt tat tac tgt cag caa tat tat agt act ccg tac Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr 225 230 235 240	720

400

act ttt ggc cag ggg acc aag gtg gaa atc aaa cgt gcg gcc
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 245 250

762

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 <211> 254
 10 <212> PRT
 <213> Artificial sequence
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 1 5 10 15
 25 Pro Gly Glu Ser Leu Lys Val Ser Cys Lys Gly Ser Gly Tyr Gly Phe
 20 25 30
 30 Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 35 40 45
 35 Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
 50 55 60
 40 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
 45 Tyr Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp
 100 105 110
 50 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly
 115 120 125
 55 Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln
 130 135 140
 60 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

401

5 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
 10 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser L eu Gln Ala
 210 215 220
 15 Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
 225 230 235 240
 20 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys A rg Ala Ala
 245 250
 <210> 277
 25 <211> 768
 <212> DNA
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 35 <223> SC03-053
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 40 <222> (1)..(768)
 <223>
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 <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
 50 1 5 10 15
 cct ggg gcc tca gtg atg gtt tcc tgc aag gcc tct gga tac acc ttc 9 6
 Pro Gly Ala Ser Val Met Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 20 25 30
 55 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
 60 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

402

	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	
5	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	
10	tat tac tgt gcg aga ggg acc gga tat ttg cgg agc tac cac gcc atg	336
	Tyr Tyr Cys Ala Arg Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met	
	100 105 110	
15	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	
20	ggt tca gcc 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	
25	atg act cag tct cca ccc tcc ctg ccc gtc acc cct ggg gag ccg gcc	480
	Met Thr Gln Ser Pro Pro Ser Leu Pro Val Thr Pro Gly Glu Pro Ala	
	145 150 155 160	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	<210> 278	
	<211> 256	
	<212> PRT	
	<213> Artificial sequence	
	<220>	
	<223> SC03-053	

403

<400> 278

5 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
 10 Ser Asn Tyr Ala Met His Trp Val Arg Gln Gly Pro Gly Gln Arg Leu
 35 40 45
 15 Glu Trp Met Gly Trp Ile Asn Ala Asp Lys Gly Gln Thr Lys Tyr Ser
 50 55 60
 20 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
 25 Tyr Tyr Cys Ala Arg Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met
 100 105 110
 30 Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Thr Gly
 115 120 125
 35 Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Asp Val Val
 130 135 140
 40 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
 45 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
 180 185 190
 50 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 195 200 205
 55 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 210 215 220
 60 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

404

245

250

255

5 <210> 279
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 <212> DNA
 10 <213> Artificial sequence

 15 <220>
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 20 <221> CDS
 <222> (1)..(756)
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 30 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
 35 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
 40 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
 45 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
 55 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
 50 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
 55 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
 60 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	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	
	145					150					155				160		
5	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		
10	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			
15	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				
20	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					
25	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	
30	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								
35	<210>	280															
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40	<212>	PRT															
	<213>	Artificial sequence															
45	<220>																
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50	<400>	280															
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	1				5					10					15		
55	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	
				20					25					30			
60	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	

406

	65	70	75	80
5	Thr Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val	85	90	95
10	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
15	Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Leu Thr Gln Ser Pro	130	135	140
20	Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys	145	150	155
25	Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala	165	170	175
30	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
35	Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp	210	215	220
40	Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe	225	230	235
45	Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala	24 5	250	
	<210>	281		
50	<211>	780		
	<212>	DNA		
55	<213>	Artificial sequence		
	<220>			
60	<223>	SC03-055		
	<220>			

407

<221> CDS

<222> (1)..(780)

5 <223>

<400> 281

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	Ala Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys	
	1 5 10 15	
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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	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	
75	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	

408

	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
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 Ala Asp Thr Ser Ly s Asn Gln			
		65	70	75
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

409

Val Ser Ser Gly Thr Gly Gly Ser Gly Gl y Thr Gly Ser Gly Thr Gly
 130 135 140

5 Gly Ser Thr Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala
 145 150 155 160

10 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

15 His Leu Leu Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp
 195 200 205

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

25 Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp
 225 230 235 240

30 Pro Ser Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val
 245 250 255

Leu Ser Ala Ala
 260

35 <210> 283

<211> 762

40 <212> DNA

<213> Artificial sequence

45 <220>

<223> SC03-056

50 <220>

<221> CDS

55 <222> (1)..(762)

<223>

60 <400> 283

gcc atg gcc gaa gtg cag ctg gtg cag tct gga aca gag gtg aaa aag
 Ala Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys

48

410

	1	5	10	15	
	ccg ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac ggc ttt				96
5	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	
10	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	
15	ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc aac				240
	Pro Ser Phe Gln Gly Val Thr Ile Ser Ala Asp Lys Ser Ile Asn	65	70	75	80
20	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
25	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	
30	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	
35	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
40	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
45	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	
50	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	
55	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
60	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		

411

<210> 284

<211> 254

5 <212> PRT

<213> Artificial sequence

10

<220>

<223> SC03-056

15 <400> 284

Ala Met Ala Glu Val Gln Leu Val Gln S er Gly Thr Glu Val Lys Lys
 1 5 10 15

20

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe
 20 25 30

25

Ile Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 35 40 45

30

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser
 50 55 60

35

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

40

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

45

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

50

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

55

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

60

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

412

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205
 5 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
 210 215 220
 10 Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
 225 230 235 240
 15 Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 245 250
 <210> 285
 20 <211> 768
 <212> DNA
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 25
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 30 <223> SC03-057
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 35 <222> (1)..(768)
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 40
 <400> 285
 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
 45 1 5 10 15
 cct ggg tcc tgg 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
 50 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
 55 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
 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

413

	Thr	Ala	Tyr	Met	Glu	Met	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Ile	
					85					90					95		
5	tat	tac	tgt	gcg	agc	ccg	gat	ata	gta	gta	gcc	ggg	cac	gct	tcc	ccc	336
	Tyr	Tyr	Cys	Ala	Ser	Pro	Asp	Ile	Val	Val	Ala	Gly	His	Ala	Ser	Pro	
				100					105					110			
10	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				
15	tcg	agc	ggg	acg	ggc	ggg	tca	ggc	gga	acc	ggc	agc	ggc	act	ggc	ggg	432
	Ser	Thr	Gly	Thr	Gly	Gly	Ser	Gly	Gly	Thr	Gly	Ser	Gly	Thr	Gly	Gly	
				130			135						140				
20	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	
						150					155					160	
25	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		
30	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			
35	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				
40	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					
45	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	
					230						235				240		
50	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	Lys	Arg	Ala	Ala	
					245				250					255			
55	<210>	286															
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	<212>	PRT															
60	<213>	Artificial sequence															
55	<220>																
	<223>	SC03-057															
	<400>	286															
60	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

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

10 Glu Trp Met Gly Arg Ile Asn Pro Ile Leu Asn Leu Thr Asn Tyr Ala
 50 55 60

15 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

25 Pro His Tyr Thr Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
 115 120 125

30 Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly
130 135 140

35 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 Ileu Gly Trp Tyr Gln Gln Iys Pro Gly Iys Ala Pro Asn Ileu
180 185 190

45
Leu Ile Tyr Gln Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe
195 200 205

50 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
55 225 230 235 240

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
245 250 255

60

<210> 287

415

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 15 <221> CDS
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 <223>
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 <400> 287
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 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
 30 Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr P he
 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 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
 40 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
 45 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 gg c caa 336
 50 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
 55 115 120 125
 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 S er Pro
 130 135 140
 60 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

416

	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	
5	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	
10	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	
15	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	
20	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	
25	<210> 288	
	<211> 252	
30	<212> PRT	
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35	<220>	
	<223> SC03-058	
40	<400> 288	
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	1 5 10 15	
45	Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
	20 25 30	
50	Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
	35 40 45	
55	Glu Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala	
	50 55 60	
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	

417

Tyr Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 5
 Gly Thr Met Val Thr Val Ser Ser Gly Thr Gly Gly Ser Gly Gly Thr
 115 120 125
 10
 Gly Ser Gly Thr Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140
 15
 Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
 145 150 155 160
 20
 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala
 165 170 175
 25
 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 30
 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 195 200 205
 35
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 210 215 220
 40
 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
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418

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	1 5 10 15																
10	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 Val																
	20 25 30																
15	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																
20	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																
25	gca cag aag ttc cag ggc 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																
30	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																
35	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																
40	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																
45	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																
50	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																
55	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																
60	tgg tac caa cag aaa 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																
65	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																
70	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																
75	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																

419

756

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ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250
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<211> 252
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15
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25 Pro Gly Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Gly Val
    20 25 30
30 Phe Arg Asn Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
    35 40 45
35 Leu Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr
    50 55 60
40 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
45 Val Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr
    100 105 110
50 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Thr
    115 120 125
55 Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Gly Ser Thr Glu Il e
    130 135 140
60 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

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420

165

170

175

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

10 Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Ph e Ser Gly Ser Gly
 195 200 205

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

20 Phe Ala Val Tyr Tyr Cys Gln Gln Arg Se r Asn Trp Pro Pro Ala Phe
 225 230 235 240

25 Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 245 250

30 <210> 291
 <211> 13
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35 <220>
 <223> HCDR3 of SC03-019 and SC03-059
 <400> 291

40 Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met Asp Val
 1 5 10

45 <210> 292
 <211> 10
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50 <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

60 Gly Ser Gly Ile Ser Thr Pro Met Asp Val
 1 5 10

421

<210> 293
<211> 20
5 <212> PRT
<213> Artificial sequence
10
<220>
<223> HCDR3 of SC03-023 and SC03-055
15 <400> 293
Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg Tyr Lys Ser
1 5 10 15
20 Trp Phe Asp Pro
20
25 <210> 294
<211> 10
30 <212> PRT
<213> Artificial sequence
35
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40 <400> 294
Lys Ser Ala Gly Ser Asn Ala Phe Asp Ile
1 5 10
45 <210> 295
<211> 8
50 <212> PRT
<213> Artificial sequence
55
<220>
<223> HCDR3 of SC03-025, SC03-026, SC03-027, SC03-029, SC03-030, SC03-0
40, SC03-050, SC03-054 and SC03-058
60 <400> 295
Thr Thr Asn Arg Ala Phe Asp Ile

1 5

<210>	296
<211>	12
<212>	PRT

<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

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<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

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<210>	298
<211>	10
<212>	PRT

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<220>
<223> HCDR3 of SC03-037 and SC03-038
<400> 298
Asp Ala His Arg Gly Phe Gly Met Asp Val
1          5          10
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423

<210> 299
<211> 12
5 <212> PRT
<213> Artificial sequence
10
<220>
<223> HCDR3 of SC03 -039
15 <400> 299
Gly Ser Lys Trp Asn Asp Val Gly Gly Gly Asp Tyr
1 5 10
20
<210> 300
<211> 13
25 <212> PRT
<213> Artificial sequence
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<220>
<223> HCDR3 of SC03 -053
35 <400> 300
Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met Asp Val
1 5 10
40
<210> 301
<211> 17
45 <212> PRT
<213> Artificial sequence
50
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<223> HCDR3 of SC03 -057
55 <400> 301
Pro Asp Ile Val Val Ala Gly His Ser Pro Pro His Tyr Thr Met Asp
1 5 10 15
60
Val

424

<210> 302
 <211> 372
 5 <212> DNA
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 15 <220>
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 20 <222> (1)..(372)
 <223>
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 <400> 302
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 Met Ala Gln Met Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro
 1 5 10 15
 30 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
 35 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
 40 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
 45 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
 50 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
 55 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
 60 <210> 303
 <211> 124

425

<212> PRT

<213> Artificial sequence

5

<220>

<223> Variable heavy chain of SC03 -019

10

<400> 303

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

15

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

20

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

25

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

30

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

35

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

40

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

45

<210> 304

<211> 330

<212> DNA

50

<213> Artificial sequence

55

<220>

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<220>

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426

<222> (1)..(330)

<223>

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<400> 304

gaa att gtg ctc aca cag tct cca gcc acc ctg tct ttg tct cca ggg 4 8
 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 Thr Lys Val Glu Ile Lys Arg Ala Ala
 100 105 110

35

<210> 305

<211> 110

40

<212> PRT

<213> Artificial sequence

45

<220>

<223> Variable light chain of SC03 -019

50

<400> 305

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

55

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

60

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

427

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 5 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 10 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95
 15 Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 100 105 110
 <210> 306
 20 <211> 363
 <212> DNA
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 <220>
 30 <223> Variable heavy chain of SC03 -020
 <220>
 <221> CDS
 35 <222> (1)..(363)
 <223>
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 <400> 306
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 Met Ala Glu Val Gln Leu Val Gln Ser Gly Ser Glu Val Lys Lys Pro
 45 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
 50 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
 55 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
 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

428

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Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
      85                      90                      95
336
5  tac tgt gcg ggg ggt tcg ggg att tct acc cct atg gac gtc tgg ggc
   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
Gln Gly Thr Thr Val Thr Val Ser Ser
10      115                      120

<210> 307
15 <211> 121
   <212> PRT
   <213> Artificial sequence
20
   <220>
25 <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
30 1      5      10      15

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
35      20      25      30

Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
40      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
45 65      70      75      80

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
50      85                      90                      95

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
55      100                      105                      110

Gln Gly Thr Thr Val Thr Val Ser Ser
      115                      120

<210> 308
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429

<211> 348
 <212> DNA
 5 <213> Artificial sequence

 <220>
 10 <223> Variable light chain of SC03 -020
 <220>
 15 <221> CDS
 <222> (1)..(348)
 <223>
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 <400> 308
 25 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
 30 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 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

 40 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
 45 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
 50 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
 55

 <210> 309

 <211> 116
 60 <212> PRT

430

<213> Artificial sequence

5 <220>

<223> Variable light chain of SC03 -020

<400> 309

10

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

15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Lys Ile Leu His Ser
20 25 30

20

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gl n Lys Pro Gly Gln
35 40 45

25

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60Pro Asp Arg Phe Ser Gly Ser Gly Ser Gl y Thr Asp Phe Thr Leu Thr
65 70 75 80

30

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

35

Tyr Tyr Ser Thr Pro Pro Val Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

40

Lys Arg Ala Ala
115

<210> 310

45

<211> 363

<212> DNA

50

<213> Artificial sequence

<220>

55

<223> Variable heavy chain of SC03 -021

<220>

<221> CDS

60

<222> (1)..(363)

<223>

431

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<400> 310
5  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

10  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

15  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

20  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

25  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

30  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

35  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

35  caa ggg acc acg gtc acc gtc tcg agc      363
   Gln Gly Thr Thr Val Thr Val Ser Ser
           115              120

<210> 311

40 <211> 121

<212> PRT

45 <213> Artificial sequence

<220>

50 <223> Variable heavy chain of SC03 -021

<400> 311
55  Met Ala Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
   1              5              10              15

60  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

```

432

5 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
 10 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
 85 90 95
 15 Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
 100 105 110
 20 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120
 <210> 312
 25 <211> 348
 <212> DNA
 <213> Artificial sequence
 30
 <220>
 35 <223> Variable light chain of SC03 -021
 <220>
 <221> CDS
 40 <222> (1)..(348)
 <223>
 45
 <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
 50 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
 55 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
 60 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

433

```

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

5  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

10 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
15      115

<210> 313

20 <211> 116

    <212> PRT

    <213> Artificial sequence

25

    <220>

30 <223> Variable light chain of SC03 -021

    <400> 313

35 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

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

45 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val
50        55        60

50 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65          70          75          80

55 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85          90          95

60 Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100        105        110

Lys Arg Ala Ala
115

```

434

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<210> 314
5 <211> 363
  <212> DNA
  <213> Artificial sequence
10
  <220>
15 <223> Variable heavy chain of SC03 -022
  <220>
  <221> CDS
20 <222> (1)..(363)
  <223>
25
  <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
30 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
35 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
40 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
45 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
50 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
55 caa ggg acc acg gtc acc gtc tcg agc      363
  Gln Gly Thr Thr Val Thr Val Ser Ser
  115          120
60
  <210> 315

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435

<211> 121

<212> PRT

5 <213> Artificial sequence

<220>

10

<223> Variable heavy chain of SC03 -022

<400> 315

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

20 Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
20 25 30

25 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

30

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

35 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
85 90 95

40 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

45

<210> 316

<211> 348

50

<212> DNA

<213> Artificial sequence

55

<220>

<223> Variable light chain of SC03 -022

60

<220>

436

<221> CDS

<222> (1)..(348)

5 <223>

<400> 316
 10 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
 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
 20 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
 25 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
 30 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
 35 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
 40 aaa cgt gcg gcc 348
 Lys Arg Ala Ala
 115
 <210> 317
 45 <211> 116
 <212> PRT
 50 <213> Artificial sequence
 <220>
 55 <223> Variable light chain of SC03 -022
 <400> 317
 60 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

437

	20		25		30	
5	Ser Ile Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	35	40	45		
10	Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50	55	60		
15	Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	65	70	75	80	
20	Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	85	90	95		
25	Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	100	105	110		
30	Lys Arg Ala Ala	115				
35	<210> 318					
40	<211> 390					
45	<212> DNA					
50	<213> Artificial sequence					
	<220>					
	<223> Variable heavy chain of SC03 -023					
	<220>					
	<221> CDS					
	<222> (1)..(390)					
	<223>					
55	<400> 318					48
	atg gcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct					
	Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro					
	1 5 10 15					
	tgc 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					
60	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					

438

	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	
5	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	
10	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	
15	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	
20	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	
25	tcg agc	390
	Ser Ser	
	130	
30	<210> 319	
	<211> 130	
	<212> PRT	
	<213> Artificial sequence	
35	<220>	
	<223> Variable heavy chain of SC03 -023	
40	<400> 319	
45	Met Ala Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro	
	1 5 10 15	
50	Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser	
	20 25 30	
55	Gly Phe Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu	
	35 40 45	
60	Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser	
	50 55 60	
65	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	

439

	85	90	95	
5	Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg	100	105	110
10	Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val	115	120	125
	Ser Ser			
	130			
15	<210> 320			
	<211> 339			
20	<212> DNA			
	<213> Artificial sequence			
25	<220>			
	<223> Variable light chain of SC03 -023			
30	<220>			
	<221> CDS			
	<222> (1)..(339)			
35	<223>			
40	<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			
45	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			
50	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			
55	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			
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			

440

```

    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
5      gcc
    Ala                                                                339

10     <210>  321
        <211>  113

15     <212>  PRT
        <213>  Artificial sequence

20     <220>
        <223>  Variable light chain of SC03 -023

25     <400>  321

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

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

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

40     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

45     Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
          85          90          95

50     Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
          100          105          110

55     Ala

60     <210>  322
        <211>  363

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441

<212> DNA
 <213> Artificial sequence
 5
 <220>
 <223> Variable heavy chain of SC03 -024
 10
 <220>
 <221> CDS
 15 <222> (1) .. (363)
 <223>
 20
 <400> 322
 atg gcc cag gtg cag ctg gtg gag tct ggg tct gag ttg aag atc oot 48
 Met Ala Gln Val Gln Leu Val Glu Ser Gly S er Glu Leu Lys Ile Pro
 1 5 10 15
 25 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
 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
 35 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
 40 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
 45 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
 50 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
 55 caa ggg aca atg gtc acc gtc tcg agc 363
 Gln Gly Thr Met Val Thr Val Ser Ser
 115 120
 60
 <210> 323
 <211> 121
 <212> PRT
 <213> Artificial sequence

442

<220>

5 <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

40

<210> 324

<211> 339

45

<212> DNA

<213> Artificial sequence

50

<220>

<223> Variable light chain of SC03 -024

55

<220>

<221> CDS

<222> (1)..(339)

60

<223>

443

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<400> 324
5  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
10  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
15  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

20  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

25  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
30  Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
   100           105           110

   gcc
   Ala      339

35

<210> 325

<211> 113
40
<212> PRT

<213> Artificial sequence

45

<220>

<223> Variable light chain of SC03 -024
50
<400> 325

   Gln Ser Val Val Thr Gln Pro Pr o Ser Val Ser Ala Ala Pro Gly Gln
55  1           5           10           15

   Lys Ala Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
   20           25           30

60  Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
   35           40           45

```

444

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

5

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
 65 70 75 80

10

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
 85 90 95

15

Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ala
 100 105 110

20

Ala

<210> 326

<211> 357

25

<212> DNA

<213> Artificial sequence

30

<220>

<223> Variable heavy chain of SC03 -025

35

<220>

<221> CDS

40

<222> (1)..(357)

<223>

45

<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

50

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

55

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

60

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

445

```

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

5  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

10  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

15  aca atg gtc acc gtc tgc agc      357
    Thr Met Val Thr Val Ser Ser
                        115

20  <210> 327
    <211> 119
    <212> PRT
    <213> Artificial sequence

25  <220>
    <223> Variable heavy chain of SC03 -025
    <400> 327

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

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

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

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

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

60  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

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446

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<210> 328
<211> 348
5  <212> DNA
    <213> Artificial sequence
10
    <220>
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15  <220>
    <221> CDS
20  <222> (1).. (348)
    <223>

25  <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
30  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
35  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
40  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 Thr Asp Phe Thr Leu Thr
    45  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
50  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
55  aaa cgt gcg gcc      348
    Lys Arg Ala Ala
           115

60  <210> 329
    <211> 116

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447

<212> PRT

<213> Artificial sequence

5

<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

448

<222> (1)..(357)

<223>

5

<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 Leu Val Gln Pro	
10	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	
15	agt tat gcc 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	
20	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	
25	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	
30	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	
35	aca atg gtc acc gtc tgc agc	357
	Thr Met Val Thr Val Ser Ser	
	115	

40

<210> 331

<211> 119

45

<212> FRT

<213> Artificial sequence

50

<220>

<223> Variable heavy chain of SC03 -026

55

<400> 331

	Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
	1 5 10 15
60	Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
	20 25 30

449

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 5 Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
 50 55 60
 10 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 15 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 20 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
 25 <210> 332
 <211> 348
 30 <212> DNA
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 35 <220>
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 40 <220>
 <221> CDS
 <222> (1) .. (348)
 45 <223>
 50 <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
 55 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
 60 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

450

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Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50      55      60
5  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

15  aaa cgt gcg gcc 348
   Lys Arg Ala Ala
   115

20  <210> 333
   <211> 116

25  <212> PRT
   <213> Artificial sequence

30  <220>
   <223> Variable light chain of SC03 -026

35  <400> 333
   Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
   1      5      10      15

40  Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Ser
   20      25      30

45  Ser Asn Ser Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
   35      40      45

50  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

55  Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gl n
   85      90      95

60  Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
   100      105      110

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451

Lys Arg Ala Ala
115

5 <210> 334
<211> 357

10 <212> DNA
<213> Artificial sequence

15 <220>
<223> Variable heavy chain of SC03 -027

20 <220>
<221> CDS
<222> (1)..(357)
25 <223>

30 <400> 334
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

35 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

40 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

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

50 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

55 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

60 aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

452

<210> 335
 <211> 119
 5 <212> PRT
 <213> Artificial sequence

 10 <220>
 <223> Variable heavy chain of SC03 -027
 15 <400> 335
 Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 20 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 25 Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 30 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
 35 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 40 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 45 Thr Met Val Thr Val Ser Ser
 115
 50 <210> 336
 <211> 348
 <212> DNA
 55 <213> Artificial sequence

 60 <220>
 <223> Variable light chain of SC03 -027

453

<220>

<221> CDS

5 <222> (1)..(348)

<223>

10

<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 Ser Leu Gly
 1 5 10 15

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

20

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

25

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

30

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 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

35

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

40

aaa cgt gcg gcc 348
 Lys Arg Ala Ala
 115

45

<210> 337

<211> 116

<212> PRT

50

<213> Artificial sequence

55

<220>

<223> Variable light chain of SC03 -027

60

<400> 337

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

454

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 5 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 10 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 15 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 20 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
 25 Lys Arg Ala Ala
 115
 30 <210> 338
 <211> 357
 <212> DNA
 35 <213> Artificial sequence
 40 <220>
 <223> Variable heavy chain of SC03-029
 <220>
 45 <221> CDS
 <222> (1)..(357)
 50 <223>
 <400> 338
 55 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
 60 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 coa ggg aag gga ctg gaa 144

455

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

5  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

10 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

15 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

20 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

20 aca atg gtc acc gtc tcg agc      357
   Thr Met Val Thr Val Ser Ser
   115

25 <210> 339
   <211> 119
   <212> PRT
30 <213> Artificial sequence

35 <220>
   <223> Variable heavy chain of SC03 -029
   <400> 339
40 Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
   1          5          10          15

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

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

55 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

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

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456

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

5 Thr Met Val Thr Val Ser Ser
 115

10 <210> 340
 <211> 348
 <212> DNA
 15 <213> Artificial sequence

20 <220>
 <223> Variable light chain of SC03 -029
 <220>
 25 <221> CDS
 <222> (1)..(348)
 30 <223>

<400> 340
 35 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

40 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
 45 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

50 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

55 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

60 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

457

Lys Arg Ala Ala
 115

5 <210> 341
 <211> 116
 <212> PRT
 10 <213> Artificial sequence

15 <220>
 <223> Variable light chain of SC03 -029
 <400> 341

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

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

30 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

35 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

40 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

45 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

50 Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Arg Ala Ala
 115

55 <210> 342
 <211> 357
 <212> DNA
 60 <213> Artificial sequence

458

<220>
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 5 <220>
 <221> CDS
 <222> (1)..(357)
 10 <223>

15 <400> 342
 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
 20 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
 25 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
 30 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
 35 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
 40 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
 45 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
 50 aca atg gtc acc gtc tcg agc 357
 Thr Met Val Thr Val Ser Ser
 115

50 <210> 343
 <211> 119
 <212> PRT
 55 <213> Artificial sequence

60 <220>
 <223> Variable heavy chain of SC03 -030
 <400> 343

459

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

5 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30

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

15 Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
 50 55 60

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

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

30 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110

30 Thr Met Val Thr Val Ser Ser
 115

35 <210> 344
 <211> 348
 <212> DNA

40 <213> Artificial sequence

45 <220>
 <223> Variable light chain of SC03 -030
 <220>

50 <221> CDS
 <222> (1)..(348)
 <223>

55

60 <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

460

	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
				20					25					30			
5	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				
10	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					
15	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		
20	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			
25	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			
30	aaa	cgt	gcg	gcc													348
	Lys	Arg	Ala	Ala													
				115													
35	<210>	345															
40	<211>	116															
	<212>	PRT															
45	<213>	Artificial sequence															
50	<220>																
	<223>	Variable light chain of SC03 -030															
	<400>	345															
55	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	
	1				5				10						15		
60	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				
65	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
			50				55					60					
70	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
	65					70					75				80		

461

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      Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
      85                      90                      95
5      Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
      100                    105                    110

10     Lys Arg Ala Ala
      115

      <210> 346
15     <211> 369
      <212> DNA
20     <213> Artificial sequence

      <220>
25     <223> Variable heavy chain of SC03 -031
      <220>
30     <221> CDS
      <222> (1)..(369)
      <223>
35

      <400> 346
40     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
45     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

50     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

55     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

60     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

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462

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

5 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

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

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

35 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

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

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

50 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

55 <210> 348
 <211> 339
 60 <212> DNA

463

<213> Artificial sequence

5 <220>

<223> Variable light chain of SC03 -031

<220>

10

<221> CDS

<222> (1)..(339)

15 <223>

<400> 348

20	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	

25	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	

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	

35	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	

40	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	

40	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	

45	act ggt gga gtg ttc ggc gga ggg acc 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	

50	gcc	339
	Ala	

<210> 349

55 <211> 113

<212> PRT

60 <213> Artificial sequence

464

<220>

<223> Variable light chain of SC03-031

5 <400> 349

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

10 Arg Val Thr Ile Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ser Asn
 20 25 30

15 Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val
 35 40 45

20 Ile Tyr Ala Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

25 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

30 Thr Gly Gly Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Ser Ala
 100 105 110

35 Ala

40 <210> 350

<211> 381

<212> DNA

45 <213> Artificial sequence

<220>

50 <223> Variable heavy chain of SC03-032

<220>

55 <221> CDS

<222> (1)..(381)

<223>

60

<400> 350

465

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      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

5      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

10     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

15     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

20     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

25     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

30     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

35     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
35     <211> 127
      <212> PRT
40     <213> Artificial sequence

      <220>
45     <223> Variable heavy chain of SC03 -032
      <400> 351

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

      Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
55          20          25          30

      Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
60          35          40          45

      Trp Met Gly Lys Ile Ile Pro Ile Leu Gly Lys Val Thr Tyr Ala Gln
          50          55          60

```

466

5 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
 10 Tyr Cys Ala Arg Asp Gly Trp A sp Leu Thr Gly Ser Phe Leu Gly Tyr
 100 105 110
 15 Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125
 20 <210> 352
 <211> 339
 <212> DNA
 25 <213> Artificial sequence
 <220>
 30 <223> Variable light chain of SC03 -032
 <220>
 35 <221> CDS
 <222> (1)..(339)
 <223>
 40 <400> 352
 45 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
 50 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
 55 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
 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

467

```

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

5  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

10 gcc                                339
Ala

15 <210> 353
    <211> 113
    <212> PRT
20 <213> Artificial sequence

25 <220>
    <221> misc_feature
    <222> (60)..(60)
30 <223> The 'Xaa' at location 60 stands for Pro, or Leu.
    <220>
    <221> misc_feature
35 <222> (74)..(74)
    <223> The 'Xaa' at location 74 stands for Leu.

40 <220>
    <221> misc_feature
    <222> (96)..(96)
45 <223> The 'Xaa' at location 96 stands for Met, or Leu.
    <220>

50 <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
55 1          5          10          15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
60      20          25          30

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

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468

[illegible]

469

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

5 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

10 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

15 caa ggg acc acg gtc acc gtc tcg agc 363
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 355

20 <211> 121

<212> PRT

25 <213> Artificial sequence

<220>

30 <223> Variable heavy chain of SC03 -033

<400> 355

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

40 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

45 Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
 50 55 60

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

55 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
 85 90 95

60 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

470

<210> 356
 5 <211> 351
 <212> DNA
 10 <213> Artificial sequence

 <220>
 15 <223> Variable light chain of SC03 -033
 <220>
 <221> CDS
 20 <222> (1)..(351)
 <223>
 25
 <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
 35 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
 40 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
 45 cct gaa cga ttc agt ggc agc ggc tct 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
 50 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
 55 atc aaa cgt gcg gcc 351
 Ile Lys Arg Ala Ala
 115
 60 <210> 357

471

<211> 117

<212> PRT

5 <213> Artificial sequence

<220>

10 <223> Variable light chain of SC03 -033

<400> 357

15 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 1520 Glu Arg Ala Thr Ile Asn Cys Lys Thr Ser His Asn Ile Phe Ser Arg
20 25 3025 Ser Asn Asn Lys Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45Pro Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val
50 55 6030 Pro Glu Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr
65 70 75 8035 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 9540 Tyr Tyr Ser Ser Pro Met Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu
100 105 110Ile Lys Arg Ala Ala
115

45

<210> 358

<211> 363

50 <212> DNA

<213> Artificial sequence

55

<220>

60 <223> Variable heavy chain of SC0 3-034

<220>

472

<221> CDS

<222> (1)..(363)

5 <223>

<400> 358

10	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	
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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	caa ggg acc acg gtc acc gtc tcg agc	363
	Gln Gly Thr Thr Val Thr Val Ser Ser	
	115 120	

<210> 359

45 <211> 121

<212> PRT

50 <213> Artificial sequence

<220>

55 <223> Variable heavy chain of SC03 -034

<400> 359

60	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

473

	20	25	30	
5	Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu			
	35	40	45	
10	Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro			
	50	55	60	
15	Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr			
	65	70	75	80
20	Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr			
	85	90	95	
25	Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly			
	100	105	110	
30	Gln Gly Thr Thr Val Thr Val Ser Ser			
	115	120		
35	<210> 360			
	<211> 348			
	<212> DNA			
	<213> Artificial sequence			
40	<220>			
	<223> Variable light chain of SC03 -034			
	<220>			
45	<221> CDS			
	<222> (1)..(348)			
	<223>			
50	<400> 360			
55	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			
60	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			

474

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      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

5      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

10     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

15     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
      20                               115

      <210> 361

25     <211> 116

      <212> PRT

30     <213> Artificial sequence

      <220>

35     <223> Variable light chain of SC03 -034

      <400> 361

40     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

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

50     Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
      50                               55                               60

55     Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Asn Leu Thr
      65                               70                               75                               80

60     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

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475

	100	105	110	
5	Lys Arg Ala Ala			
	115			
	<210>	362		
10	<211>	363		
	<212>	DNA		
15	<213>	Artificial sequence		
	<220>			
20	<223>	Variable heavy chain of SC03 -035		
	<220>			
	<221>	CDS		
25	<222>	(1)..(363)		
	<223>			
30	<400>	362		
	atg gcc gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc			48
35	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			
40	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			
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
50	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
55	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			
60	100 105 110			
	caa ggg acc acg gtc acc gtc tog agc			363
	Gln Gly Thr Thr Val Thr Val Ser Ser			
	115 120			

476

<210> 363
 5 <211> 121
 <212> PRT
 10 <213> Artificial sequence

 <220>
 15 <223> Variable heavy chain of SC03 -035
 <400> 363
 20 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
 25
 Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 30
 Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
 50 55 60

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

 40 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
 45
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120
 50
 <210> 364
 <211> 351
 55 <212> DNA
 <213> Artificial sequence

 60
 <220>
 <223> Variable light chain of SC03 -035

477

<220>

<221> CDS

5

<222> (1)..(351)

<223>

10

<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 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 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

45

<210> 365

<211> 117

50

<212> PRT

<213> Artificial sequence

55

<220>

<223> Variable light chain of SC03 -035

60

<400> 365

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

478

```

    Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  

      20                               25                               30
5
    Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  

      35                                40                                45
10
    Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  

      50                              55                              60
15
    Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  

      65                                70                                75                                80
20
    Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  

      85                                90                                95
25
    Tyr Tyr Ser Thr Pro Leu Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu  

      100                             105                             110
30
    Ile Lys Pro Ala Ala  

      115
35
<210>   366
<211>   363
40
<212>   DNA
45
<213>   Artificial sequence
50
<220>
<223>   Variable heavy chain of SC03 -036
55
<220>
<221>   CDS
<222>   (1)..(363)
60
<223>
55
<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
60
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

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479

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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

5  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

10 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

15 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

20 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

20  caa ggg acc acg gtc acc gtc tcg agc      363
   Gln Gly Thr Thr Val Thr Val Ser Ser
      115                      120

25  <210> 367
      <211> 121
30  <212> PRT
      <213> Artificial sequence

35  <220>
      <223> Variable heavy chain of SC03 -036
40  <400> 367
      Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
      1                      5                      10                      15

45  Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
      20                      25                      30

50  Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
      35                      40                      45

55  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

60  Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Ty r
      85                      90                      95

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480

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
 100 105 110
 5
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120
 10
 <210> 368
 <211> 345
 15
 <212> DNA
 <213> Artificial sequence
 20
 <220>
 <223> Variable light chain of SC03 -036
 25
 <220>
 <221> CDS
 <222> (1)..(345)
 30
 <223>
 35
 <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
 40
 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
 45
 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
 50
 cct cct aag ctg ctg 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
 55
 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
 60
 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
 60
 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

481

345

cgt gcg gcc
 Arg Ala Ala
 115

5 <210> 369
 <211> 115
 10 <212> PRT
 <213> Artificial sequence
 15 <220>
 <223> Variable light chain of SC03-036
 20 <400> 369
 Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 25 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Ser
 20 25 30
 30 Pro Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 35 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 40 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 45 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
 50 Arg Ala Ala
 115
 55 <210> 370
 <211> 360
 <212> DNA
 60 <213> Artificial sequence

482

<220>
 <223> Variable heavy chain of SC03 -037
 5 <220>
 <221> CDS
 <222> (1)..(360)
 10 <223>

 15 <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
 20 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
 25 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
 30 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
 35 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
 40 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
 45 ggg acc acg gtc acc gtc tcg agc 360
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

 <210> 371
 50 <211> 120
 <212> PRT
 55 <213> Artificial sequence

 <220>
 60 <223> Variable heavy chain of SC03 -037
 <400> 371

483

Met Ala Lys Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro
 1 5 10 15
 5 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser
 20 25 30
 10 Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 15 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
 20 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 25 Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly Gln
 100 105 110
 30 Gly Thr Thr Val Thr Val Ser Ser
 115 120
 35 <210> 372
 <211> 333
 <212> DNA
 40 <213> Artificial sequence
 45 <220>
 <223> Variable light chain of SC03 -037
 <220>
 50 <221> CDS
 <222> (1)..(333)
 <223>
 55
 <400> 372
 tct tct gag ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag 48
 60 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	Ala		
				20					25						30		
5	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				
10	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					
15	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		
20	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			
25	<210>	373															
	<211>	111															
	<212>	PRT															
30	<213>	Artificial sequence															
35	<220>																
	<223>	Variable light chain of SC03 -037															
	<400>	373															
40	Ser	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	
	1				5					10					15		
45	Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	
				20					25					30			
50	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					
55	Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	
	65					70					75					80	
60	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Gly	Arg	Asp	Ser	Ser	Gly	Asn	His	
				85						90					95		

485

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 100 105 110

5 <210> 374
 <211> 360
 10 <212> DNA
 <213> Artificial sequence

15 <220>
 <223> Variable heavy chain of SC03 -038

20 <220>
 <221> CDS
 <222> (1) .. (360)
 25 <223>

30 <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

35 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

40 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

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

50 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

55 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

55 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

60 ggg acc acg gtc acc gtc tcg agc 360
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

486

<210> 375
 <211> 120
 5 <212> PRT
 <213> Artificial sequence

 10 <220>
 <223> Variable heavy chain of SC03 -038
 15 <400> 375
 Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro
 1 5 10 15
 20 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser
 20 25 30
 25 Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 30 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
 35 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 40 Cys Ala Arg Asp Ala His Arg Gly Phe Gly Met Asp Val Trp Gly Gln
 100 105 110
 45 Gly Thr Thr Val Thr Val Ser Ser
 115 120

 50 <210> 376
 <211> 333
 <212> DNA
 55 <213> Artificial sequence

 60 <220>
 <223> Variable light chain of SC03 -038

487

<220>

<221> CDS

5 <222> (1)..(333)

<223>

10

<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			

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			

20

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				

25

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

30

agc	tca	gga	gac	aca	gct	toc	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		

35

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		

40

<210> 377

<211> 111

45

<212> PRT

<213> Artificial sequence

50

<220>

<223> Variable light chain of SC03 -038

55

<400> 377

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

60

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

488

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 5 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60
 10 Ser Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80
 15 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
 85 90 95
 20 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 100 105 110
 <210> 378
 <211> 369
 25 <212> DNA
 <213> Artificial sequence
 30 <220>
 <223> Variable heavy chain of SC03 -039
 35 <220>
 <221> CDS
 40 <222> (1)..(369)
 <223>
 45 <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
 50 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
 55 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
 60 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

489

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

5  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

10 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

15 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

20 <210> 379
   <211> 123
   <212> PRT
   <213> Artificial sequence

25 <220>
   <223> Variable heavy chain of SC03 -039
30 <400> 379

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

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

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

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

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

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

60 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

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490

<210> 380
 <211> 339
 5 <212> DNA
 <213> Artificial sequence
 10
 <220>
 <223> Variable light chain of SC03 -039
 15 <220>
 <221> CDS
 20 <222> (1)..(339)
 <223>
 25
 <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
 30 acg gta acc atc tcc tgc gcc gcc agc agt gcc 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
 35 tat gtg cag tgg tac cag caa cgc ccg gcc 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
 40 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
 45 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
 50 tat ctt tgg att ttc gcc 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
 55 gcc 339
 Ala
 60 <210> 381
 <211> 113

491

<212> PRT

<213> Artificial sequence

5

<220>

<223> Variable light chain of SC03 -039

10

<400> 381

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15

15

Thr Val Thr Ile Ser Cys Ala Gly Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30

20

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

25

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

30

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80

35

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

40

Ala

45

<210> 382

<211> 357

<212> DNA

50

<213> Artificial sequence

55

<220>

<223> Variable heavy chain of SC03 -040

60

<220>

<221> CDS

492

<222> (1)..(357)

<223>

5

<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	
10	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	
15	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	
20	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	
25	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	
30	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	
35	aca atg gtc acc gtc tcg agc	357
	Thr Met Val Thr Val Ser Ser	
	115	

40

<210> 383

<211> 119

45

<212> PRT

<213> Artificial sequence

50

<220>

<223> Variable heavy chain of SC03 -040

55

<400> 383

	Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
	1 5 10 15
60	Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
	20 25 30

493

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 5 Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
 50 55 60
 10 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 15 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 20 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
 25 <210> 384
 <211> 348
 30 <212> DNA
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 35 <220>
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 40 <220>
 <221> CDS
 <222> (1)..(348)
 45 <223>
 50 <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
 55 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
 60 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

494

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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
5  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
10 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
15 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
20 <210> 385
    <211> 116
25 <212> PRT
    <213> Artificial sequence
30 <220>
    <223> Variable light chain of SC03 -040
35 <400> 385
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1      5      10      15
40 Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
    20      25      30
45 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
    35      40      45
50 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
55 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
    85      90      95
60 Tyr Tyr Ser Ser Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
    100      105      110

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495

Lys Arg Ala Ala
115

5 <210> 386
<211> 357

10 <212> DNA
<213> Artificial sequence

15 <220>
<223> Variable heavy chain of SC03-041

20 <220>
<221> CDS
<222> (1)..(357)
<223>

30 <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

35 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

40 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

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

50 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

55 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

60 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 Gl y Gln Gly
100 105 110

60 aca atg gtc acc gtc tcg agc 357
Thr Met Val Thr Val Ser Ser
115

496

<210> 387
 <211> 119
 5 <212> PRT
 <213> Artificial sequence

 10 <220>
 <223> Variable heavy chain of SC03 -041
 15 <400> 387
 Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 20 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 25 Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 30 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
 35 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 40 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 45 Thr Met Val Thr Val Ser Ser
 115

 50 <210> 388
 <211> 348
 <212> DNA
 55 <213> Artificial sequence

 60 <220>
 <223> Variable light chain of SC03 -041

497

<220>

<221> CDS

5 <222> (1)..(348)

<223>

10

<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	

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	

20

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	

25

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	

30

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	

35

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	

40

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	

45

aaa cgt gcg gcc	348
Lys Arg Ala Ala	
115	

50

<210> 389

<211> 116

<212> PRT

55

<213> Artificial sequence

60

<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

498

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

5 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

10 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

15 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

20 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

25 Lys Arg Ala Ala
 115

30 <210> 390
 <211> 357
 <212> DNA

35 <213> Artificial sequence

40 <220>
 <223> Variable heavy chain of SC03 -042

45 <220>
 <221> misc_feature
 <222> (150)..(151)

50 <223> n can be a, t, c, or g

55 <220>
 <221> CDS
 <222> (1)..(357)

60 <223>

499

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<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

5   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          30

10  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

15  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

20  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

25  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

30  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

35  aca atg gtc acc gtc tcg agc      357
    Thr Met Val Thr Val Ser Ser
          115

35  <210> 391
    <211> 119
    <212> PRT
40  <213> Artificial sequence

45  <220>
    <223> Variable heavy chain of SC03 -042
    <220>
50  <221> misc_feature
    <222> (150)..(151)
55  <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
60  1          5          10          15

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

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500

20 25 30
 5 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
 10 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 15 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 20 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 25 Thr Met Val Thr Val Ser Ser
 115
 <210> 392
 30 <211> 348
 <212> DNA
 <213> Artificial sequence
 35
 <220>
 40 <223> Variable light chain of SC03 -042
 <220>
 <221> CDS
 45 <222> (1)..(348)
 <223>
 50
 <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 Ser Leu Ala Val Ser Leu Gly
 55 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
 60 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

501

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    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

5    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

10   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

15   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
    20      115

    <210> 393

25   <211> 116

    <212> PRT

    <213> Artificial sequence

30

    <220>

35   <223> Variable light chain of SC03 -042

    <400> 393

40   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

45   Ser Asn Asp Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
    35      40      45

50   Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50      55      60

55   Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    65      70      75      80

60   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

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502

	100	105	110	
5	Lys Arg Ala Ala			
	115			
	<210>	394		
10	<211>	357		
	<212>	DNA		
15	<213>	Artificial sequence		
	<220>			
20	<223>	Variable heavy chain of SC03 -043		
	<220>			
	<221>	CDS		
25	<222>	(1)..(357)		
	<223>			
30	<400>	394		
	atg gcc cag gtc cag ctg gtg cag tct ggg gga ggc ttg gtc cag cct		48	
35	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			
40	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			
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	
50	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	
55	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			
60	aca atg gtc acc gtc tcg agc		357	
	Thr Met Val Thr Val Ser Ser			
	115			

503

<210> 395
 5 <211> 119
 <212> PRT
 <213> Artificial sequence
 10
 <220>
 15 <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
 20 1 5 10 15
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 25 20 25 30
 Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Le u Glu
 30 35 40 45
 Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
 50 55 60
 35 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
 40 85 90 95
 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe As p Ile Trp Gly Gln Gly
 45 100 105 110
 Thr Met Val Thr Val Ser Ser
 115
 50 <210> 396
 <211> 348
 55 <212> DNA
 <213> Artificial sequence
 60
 <220>
 <223> Variable light chain of SC 03-043

504

<220>
 <221> CDS
 5 <222> (1)..(348)
 <223>
 10
 <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
 15 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 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
 25 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
 30 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
 35 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
 40 100 105 110
 aaa cgt gcg gcc 348
 Lys Arg Ala Ala
 115
 45 <210> 397
 <211> 116
 50 <212> PRT
 <213> Artificial sequence
 55 <220>
 <223> Variable light chain of SC03 -043
 60 <400> 397
 Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

[illegible]

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30      <210>  398
          <211>  357
35      <212>  DNA
          <213>  Artificial sequence
40
          <220>
          <223>  Variable heavy chain of SC03 -044
45      <220>
          <221>  CDS
          <222>  (1)..(357)
50      <223>

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55 <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

60 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

506

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    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

5   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

10  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

15  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

20  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

25  <210> 399
    <211> 119

30  <212> PRT
    <213> Artificial sequence

35  <220>
    <223> Variable heavy chain of SC03 -044

40  <400> 399
    Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro
    1              5              10              15

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

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

55  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

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

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507

Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 5
 Thr Met Val Thr Val Ser Ser
 115
 10
 <210> 400
 <211> 348
 15
 <212> DNA
 <213> Artificial sequence
 20
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 <223> Variable light chain of SC03 -044
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 <220>
 <221> CDS
 <222> (1)..(348)
 30
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 35
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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
 40
 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
 45
 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
 50
 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
 55
 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
 60
 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
 60
 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

508

348

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aaa cgt gcg gcc
Lys Arg Ala Ala
      115

5
<210> 401
<211> 116
10 <212> PRT
    <213> Artificial sequence

15
<220>
<223> Variable light chain of SC03 -044
20 <400> 401
    Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
    1             5             10             15
25
    Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
    20             25             30
30
    Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
    35             40             45
35
    Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50             55             60
40
    Pro Asp Arg Phe Arg Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    65             70             75             80
45
    Ile Ser Ser Leu Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
    85             90             95
50
    Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
    100            105            110
55
    Lys Arg Ala Ala
    115

<210> 402
<211> 357
<212> DNA
60 <213> Artificial sequence

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509

<220>

<223> Variable heavy chain of SC03 -045

5 <220>

<221> CDS

10 <222> (1)..(357)

<223>

15 <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

20 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

25 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
 30 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

35 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

40 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

45 aca atg gtc acc gtc tcg agc 357
 Thr Met Val Thr Val Ser Ser
 115

<210> 403

50 <211> 119

<212> PRT

55 <213> Artificial sequence

<220>

60 <223> Variable heavy chain of SC03 -045

<400> 403

510

Met Ala Gln Leu Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 5 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 10 Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 15 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
 20 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 25 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 30 Thr Met Val Thr Val Ser Ser
 115
 35 <210> 404
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 <212> DNA
 40 <213> Artificial sequence
 45 <220>
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 <220>
 50 <221> CDS
 <222> (1)..(348)
 <223>
 55
 <400> 404
 60 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

511

	Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
	20 25 30	
5	tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	144
	35 40 45	
10	cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	192
	50 55 60	
15	cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	240
	65 70 75 80	
20	atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	288
	85 90 95	
25	tat tat agt act cca ttc act ttc ggc cct ggg acc aaa gtg gat atc Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile	336
	100 105 110	
30	aaa cgt gcg gcc Lys Arg Ala Ala	348
	115	
35	<210> 405	
	<211> 116	
	<212> PRT	
	<213> Artificial sequence	
40	<220>	
	<223> Variable light chain of SC03 -045	
	<400> 405	
45	Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
	1 5 10 15	
50	Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
	20 25 30	
55	Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
	35 40 45	
60	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	

512

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

5 Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
 100 105 110

10 Lys Arg Ala Ala
 115

<210> 406

15 <211> 357

<212> DNA

20 <213> Artificial sequence

<220>

25 <223> Variable heavy chain of SC03 -046

<220>

30 <221> CDS

<222> (1)..(357)

<223>

35

<400> 406

40 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
 45 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

50 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

55 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

60 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

513

Tyr Cys Ala Arg Thr Thr As n Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 5 aca atg gtc acc gtc tcg agc 357
 Thr Met Val Thr Val Ser Ser
 115
 <210> 407
 10 <211> 119
 <212> PRT
 15 <213> Artificial sequence
 <220>
 20 <223> Variable heavy chain of SC03 -046
 <400> 407
 25 Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 30 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 35 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
 40 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 45 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 50 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
 55 <210> 408
 <211> 348
 60 <212> DNA

514

<213> Artificial sequence

5 <220>

<223> Variable light chain of SC03-046

<220>

10

<221> CDS

<222> (1)..(348)

15 <223>

<400> 408

20 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

25 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

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 ct c 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

35 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 Thr Asp Phe Ser Leu Thr
 65 70 75 80

40 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

45 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

50 aaa cgt gcg gcc 348
 Lys Arg Ala Ala
 115

<210> 409

55 <211> 116

<212> PRT

60 <213> Artificial sequence

515

<220>

<223> Variable light chain of SC03 -046

5 <400> 409

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

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

15 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

20 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

25 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

30 Tyr Tyr Ser Pro Pro Tyr Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
 100 105 110

35 Lys Arg Ala Ala
 115

40 <210> 410

<211> 357

<212> DNA

45 <213> Artificial sequence

<220>

50 <223> Variable heavy chain of SC03 -047

<220>

55 <221> CDS

<222> (1)..(357)

<223>

60

<400> 410

516

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      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

5      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

10     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

15     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

20     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

20     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

25     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

30     aca atg gtc acc gtc tcg agc      357
      Thr Met Val Thr Val Ser Ser
      115

35     <210> 411
      <211> 119
      <212> PRT

40     <213> Artificial sequence

45     <220>
      <223> Variable heavy chain of SC03 -047
      <400> 411

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

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

60     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

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517

5 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
 10 Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 15 Thr Met Val Thr Val Ser Ser
 115
 <210> 412
 20 <211> 348
 <212> DNA
 25 <213> Artificial sequence
 <220>
 30 <223> Variable light chain of SC03 -047
 <220>
 35 <221> CDS
 <222> (1)..(348)
 <223>
 40
 <400> 412
 45 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
 55 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
 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

518

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      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

5    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
10    lys arg ala ala      348
                115

      <210> 413
15    <211> 116
      <212> PRT
20    <213> Artificial sequence

      <220>
25    <223> Variable light chain of SC03 -047
      <400> 413

30    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
35                20          25          30

      ser asn asn lys asn tyr leu ala trp tyr gln gln lys pro gly gln
      35          40          45

40    pro pro lys leu leu ile tyr trp ala ser thr arg glu ser gly val
      50          55          60

45    pro asp arg phe ser gly ser gly ser gly thr asp phe thr leu thr
      65          70          75          80

50    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
55                100          105          110

      lys arg ala ala
60                115

      <210> 414

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519

<211> 357
 <212> DNA
 5 <213> Artificial sequence

 <220>
 10 <223> Variable heavy chain of SC03 -048
 <220>
 15 <221> CDS
 <222> (1)..(357)
 <223>
 20

 <400> 414
 25 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 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
 30 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 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
 40 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
 45 ctg tat ctt caa atg ggc agc ctg aga gct gag gac atg got gtg tat 288
 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 85 90 95
 50 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
 55
 <210> 415
 <211> 119
 60 <212> PRT

520

<213> Artificial sequence

5 <220>

<223> Variable heavy chain of SC03 -048

<400> 415

10

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

15

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

20

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

25

Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
50 55 60Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

30

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

35

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

40

Thr Met Val Thr Val Ser Ser
115

<210> 416

45

<211> 348

<212> DNA

50

<213> Artificial sequence

<220>

55

<223> Variable light chain of SC03 -048

<220>

<221> CDS

60

<222> (1)..(348)

<223>

521

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5      <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

10     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

15     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

20     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

25     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 Thr Asp Phe Thr Leu Thr
      65           70           75           80

30     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

35     tat tac 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

40     <210> 417
      <211> 116
      <212> PRT
      <213> Artificial sequence
45

      <220>
50     <223> Variable light chain 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

60     Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
           35           40           45

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522

	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
	50						55					60					
5																	
	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
	65					70					75					80	
10																	
	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	
					85					90					95		
15																	
	Tyr	Tyr	Ser	Thr	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	
				100					105					110			
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	Lys	Arg	Ala	Ala													
			115														
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40																	
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45																	
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	Met	Ala	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	
50	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			
55																	
	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				
60																	
	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					

523

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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

5  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

10 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
15              115

<210> 419

20 <211> 119

<212> PRT

25 <213> Artificial sequence

<220>

30 <223> Variable heavy chain of SC03 -049

<400> 419

Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
35 1              5              10              15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
40              20              25              30

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

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
55              65              70              75              80

Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
60              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

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524

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    <210> 420
5    <211> 348
    <212> DNA
    <213> Artificial sequence
10
    <220>
15    <223> Variable light chain of SC03 -049
    <220>
    <221> CDS
20    <222> (1)..(348)
    <223>
25
    <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
30    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
35    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
40    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
45    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
50    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
55    aaa cgt gcg gcc
    Lys Arg Ala Ala
    115
60
    <210> 421

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525

<211> 116

<212> PRT

5 <213> Artificial sequence

<220>

10 <223> Variable light chain of SC03 -049

<400> 421

15 Asp Tle Gln Ieu Thr Gln Ser Pro Ser Ser Ieu Ala V al. Ser Ieu Gly
 1 5 10 15

20 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Ieu Tyr Ser
 20 25 30

25 Ser Asn Asn Lys Asn Tyr Ieu Ala Trp Tyr G ln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Ieu Ieu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

30 Pro Asp Arg Phe Ser Gly Ser Gly S er Gly Thr Asp Phe Thr Ieu Thr
 65 70 75 80

35 Ile Ser Ser Ieu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

40 Tyr Tyr Ser Thr Pro Ieu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 100 105 110

Lys Arg Ala Ala
 115

45

<210> 422

<211> 357

50 <212> DNA

<213> Artificial sequence

55

<220>

60 <223> Variable heavy chain of SC03 -050

<220>

526

<221> CDS

<222> (1)..(357)

5 <223>

<400> 422

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10  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

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

20  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

25  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

30  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

35  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
40          115

```

<210> 423

45 <211> 119

<212> PRT

50 <213> Artificial sequence

<220>

55 <223> Variable heavy chain of SC03 -050

<400> 423

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60  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

```

527

	20	25	30	
5	Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu			
	35	40	45	
10	Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn			
	50	55	60	
15	Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr			
	65	70	75	80
20	Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr			
	85	90	95	
25	Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly			
	100	105	110	
30	Thr Met Val Thr Val Ser Ser			
	115			
35	<210> 424			
	<211> 348			
	<212> DNA			
	<213> Artificial sequence			
40	<220>			
	<223> Variable light chain of SC03 -050			
45	<220>			
	<221> CDS			
	<222> (1) .. (348)			
	<223>			
50	<400> 424			
55	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			
60	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			

528

```

    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

5    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

10   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

15   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

25   <211> 116
    <212> PRT
    <213> Artificial sequence

30

    <220>

35   <223> Variable light chain of SC03 -050
    <400> 425

40   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

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

50   Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
      50                      55                      60

55   Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
      65                      70                      75                      80

60   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

```


529

	100	105	110	
5	Lys Arg Ala Ala			
	115			
	<210>	426		
10	<211>	363		
	<212>	DNA		
	<213>	Artificial sequence		
15				
	<220>			
20	<223>	Variable heavy chain of SC03 -051		
	<220>			
	<221>	CDS		
25	<222>	(1)..(363)		
	<223>			
30				
	<400>	426		
	atg gcc cag gtg cag ctg gtg cag tct gga aca gag gtg aaa aag ccg		48	
35	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			
40	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			
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			
50	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	
55	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			
60	caa ggg acc acg gtc acc gtc tcg agc		363	
	Gln Gly Thr Thr Val Thr Val Ser Ser			
	115 120			

530

<210> 427
 5 <211> 121
 <212> PRT
 10 <213> Artificial sequence

 <220>
 15 <223> Variable heavy chain of SC03 -051
 <400> 427
 20 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
 25 20 25 30
 Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 35 40 45
 30 Trp Met Gly Ile Ile Tyr Pro Gly Asp Se r Glu Thr Arg Tyr Ser Pro
 50 55 60
 35 Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 40 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
 45 100 105 110
 Gln Gly Thr Thr Val Th r Val Ser Ser
 115 120
 50 <210> 428
 <211> 348
 55 <212> DNA
 <213> Artificial sequence
 60 <220>
 <223> Variable light chain of SC03 -051

531

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<220>
<221> CDS
5 <222> (1)..(348)
<223>

10
<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
15 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 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
35 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
40 100 105 110

aaa cgt gcg gcc 348
Lys Arg Ala Ala
115

45
<210> 429
<211> 116
50 <212> PRT
<213> Artificial sequence

55
<220>
<223> Variable light chain of SC03 -051
60
<400> 429
Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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533

```

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

5  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

10 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

15 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

20 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

25 <210> 431
   <211> 121

30 <212> PRT
   <213> Artificial sequence

35 <220>
   <223> Variable heavy chain of SC03 -052

40 <400> 431
   Met Ala Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro
      1      5      10      15

45 Gly Glu Ser Leu Lys Val Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile
      20      25      30

50 Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
      35      40      45

55 Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
      50      55      60

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

```

534

Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
 100 105 110
 5
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120
 10
 <210> 432
 <211> 348
 15 <212> DNA
 <213> Artificial sequence
 20
 <220>
 <223> Variable light chain of SC03 -052
 25 <220>
 <221> CDS
 <222> (1)..(348)
 30 <223>
 35 <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
 40 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
 45 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
 50 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
 55 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
 60 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

535

348

aaa cgt gcg gcc
 Lys Arg Ala Ala
 115

5 <210> 433
 <211> 116
 10 <212> PRT
 <213> Artificial sequence
 15 <220>
 <223> Variable light chain of SC03 -052
 20 <400> 433
 Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 25 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 30 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 35 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 40 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 45 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 50 Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 50 Lys Arg Ala Ala
 115
 55 <210> 434
 <211> 372
 <212> DNA
 60 <213> Artificial sequence

536

<220>
 <223> Variable heavy chain of SC03 -053
 5 <220>
 <221> CDS
 <222> (1)..(372)
 10 <223>

 15 <400> 434
 atg gcc cag gtg cag ctg gtg cag tot 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
 20 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
 25 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
 30 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
 35 gcc tac atg gac ctg agc agc ctg aga tot 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
 40 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
 45 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
 50 <211> 124
 <212> PRT
 55 <213> Artificial sequence

 <220>
 60 <223> Variable heavy chain of SC03 -053
 <400> 435

537

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

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

10 Asn Tyr Ala Met His Trp Val Arg Gln Gl y Pro Gly Gln Arg Leu Glu
      35      40      45

15 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

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

25 Tyr Cys Ala Arg Gly Thr Gly Tyr Leu Arg Ser Tyr His Gly Met Asp
      100      105      110

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

35 <210> 436
    <211> 345
    <212> DNA
40 <213> Artificial sequence

    <220>
45 <223> Variable light chain of SC03 -053
    <220>

50 <221> CDS
    <222> (1)..(345)
    <223>

55

    <400> 436
60 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

```

538

	Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
	20 25 30	
5	aat gga tac aac tat ttg gat tgg tac ctg cag aag cca ggt cag tct Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser	144
	35 40 45	
10	cca cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro	192
	50 55 60	
15	gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	240
	65 70 75 80	
20	agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala	288
	85 90 95	
25	cta caa act cct ctc acc ttc ggc caa ggg aca cga ctg gag att aaa Leu Gln Thr Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys	336
	100 105 110	
30	cgt gcg gcc Arg Ala Ala	345
	115	
35	<210> 437	
	<211> 115	
	<212> PRT	
	<213> Artificial sequence	
40	<220>	
	<223> Variable light chain of SC03 -053	
	<400> 437	
45	Asp Val Val Met Thr Gln Ser Pro Pro Ser Leu Pro Val Thr Pro Gly	
	1 5 10 15	
50	Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
	20 25 30	
55	Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
	35 40 45	
60	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	

539

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

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

10 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

540

```

Tyr Cys Ala Arg Thr Thr Asn Arg Ala Phe Asp Ile Trp Gly Gln Gly
      100                      105                      110
5  aca atg gtc acc gtc tcg agc
   Thr Met Val Thr Val Ser Ser
      115
357

<210> 439
10 <211> 119
   <212> PRT
15 <213> Artificial sequence

<220>
20 <223> Variable heavy chain of SC03 -054
   <400> 439
25 Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro
   1          5          10          15
30 Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
   20          25          30
35 Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
   35          40          45
40 Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
   50          55          60
45 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
   65          70          75          80
45 Leu Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
   85          90          95
50 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
55
60 <210> 440
   <211> 348
   <212> DNA

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541

<213> Artificial sequence

5 <220>

<223> Variable light chain of SC03 -054

<220>

10 <221> CDS

<222> (1) .. (348)

15 <223>

<400> 440

20 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

25 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

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

35 oct 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

40 cct gac cga ttc agt ggc ggc ggg tct ggg aca gat ttc act ctc acc 240
 Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

40 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

45 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

50 aaa cgt gcg gcc 348
 Lys Arg Ala Ala
 115

<210> 441

55 <211> 116

<212> PRT

60 <213> Artificial sequence

542

<220>

<223> Variable light chain of SC03 -054

5 <400> 441

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

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

15 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

20 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

25 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

30 Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

35 Lys Arg Ala Ala
 115

40 <210> 442

<211> 390

<212> DNA

45 <213> Artificial sequence

<220>

50 <223> Variable heavy chain of SC03 -055

<220>

55 <221> CDS

<222> (1)..(390)

60 <223>

<400> 442

543

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      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

5      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

10     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

15     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

20     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

20     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

25     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

30     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

35     tcg agc
      Ser Ser
          130      390

<210> 443
40 <211> 130
      <212> PRT
45 <213> Artificial sequence

      <220>
50 <223> Variable heavy chain of SC03 -055
      <400> 443

55 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

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

```

544

5 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
 10 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Ty r Tyr
 85 90 95
 15 Cys Ala Arg Arg Val Glu Val Val Glu Tyr Gln Leu Leu Arg Pro Arg
 100 105 110
 20 Tyr Lys Ser Trp Phe Asp Pro Trp Gly Gln Gly Thr Le u Val Thr Val
 115 120 125
 Ser Ser
 25 130
 <210> 444
 <211> 339
 30 <212> DNA
 <213> Artificial sequence
 35 <220>
 <223> Variable light chain of SC03 -055
 40 <220>
 <221> CDS
 45 <222> (1)..(339)
 <223>
 50 <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
 55 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
 60 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

545

```

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

5  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

10 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

15 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
   Ala
20
   <210> 445
   <211> 113
25   <212> PRT
   <213> Artificial sequence
30
   <220>
   <223> Variable light chain of SC03 -055
35   <400> 445

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

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

45   Pro Val Ser Trp Tyr Gln Lys Phe Pro Gly Thr Ala Pro His Leu Leu
                        35                      40                      45

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

55   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

60   Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser Ala
                        100                      105                      110

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546

Ala

5

<210> 446

<211> 363

10

<212> DNA

<213> Artificial sequence

15

<220>

<223> Variable heavy chain of SC03 -056

20

<220>

<221> CDS

25

<222> (1) .. (363)

<223>

30

<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	

35

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	

40

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	

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	

50

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	

55

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	

60

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	

60

caa ggg acc acg gtc acc gtc tcg agc	363
Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120	

547

<210> 447
 <211> 121
 5 <212> PRT
 <213> Artificial sequence
 10
 <220>
 <223> Variable heavy chain of SC03-056
 15 <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 20 25 30
 Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 25 35 40 45
 Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro
 30 50 55 60
 Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 35 65 70 75 80
 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr
 40 85 90 95
 Tyr Cys Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly
 100 105 110
 45 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120
 50 <210> 448
 <211> 348
 <212> DNA
 55 <213> Artificial sequence
 60 <220>
 <223> Variable light chain of SC03-056

548

<220>

<221> CDS

5 <222> (1)..(348)

<223>

10

<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

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

20

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

25

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

30

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 Thr Asp Phe Thr Leu Thr
 65 70 75 80

35

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

40

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

45

aaa cgt gcg gcc 348
 Lys Arg Ala Ala
 115

45

<210> 449

<211> 116

<212> PRT

50

<213> Artificial sequence

55

<220>

<223> Variable light chain of SC03-056

60

<400> 449

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

549

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 5 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 10 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 15 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 20 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
 25 Lys Arg Ala Ala
 115
 30 <210> 450
 <211> 387
 <212> DNA
 35 <213> Artificial sequence
 40 <220>
 <223> Variable heavy chain of SC03 -057
 <220>
 45 <221> CDS
 <222> (1)..(387)
 50 <223>
 <400> 450
 55 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
 60 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

550

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      Arg Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
      35          40          45
5    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
10   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
15   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
20   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
25   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
25   agc
    Ser
      387

30   <210> 451
      <211> 129
      <212> PRT
35   <213> Artificial sequence

40   <220>
      <223> Variable heavy chain of SC03 -057
      <400> 451
45   Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ly s Pro
      1          5          10          15
50   Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
      20          25          30
55   Arg Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gl n Gly Leu Glu
      35          40          45
60   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

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551

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

5 Tyr Cys Ala Ser Pro Asp Ile Val Val Ala Gly His Ala Ser Pro Pro
100 105 110

10 His Tyr Thr Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

15

<210> 452

20 <211> 330

<212> DNA

<213> Artificial sequence

25

<220>

30 <223> Variable light chain of SC03 -057

<220>

<221> CDS

35 <222> (1)..(330)

<223>

40

<400> 452

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

45 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

50 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

55 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

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

552

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
 5 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
 100 105 110

<210> 453
 10 <211> 110
 <212> PRT
 15 <213> Artificial sequence

<220>
 20 <223> Variable light chain of SC03-057
 <400> 453

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

30 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 35 40 45

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

40 Ser Glu Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu His Pro
 65 70 75 80

45 Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asp Phe Pro Ile
 85 90 95

50 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala
 100 105 110

<210> 454
 55 <211> 357
 <212> DNA
 60 <213> Artificial sequence

553

<220>
 <223> Variable heavy chain of SC03 -058
 5 <220>
 <221> CDS
 <222> (1)..(357)
 10 <223>

 15 <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 Leu Val Gln Pro
 1 5 10 15
 20 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
 25 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
 30 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
 35 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
 40 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
 45 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
 50 aca atg gtc acc gtc tcg agc 357
 Thr Met Val Thr Val Ser Ser
 115
 <210> 455
 50 <211> 119
 <212> PRT
 55 <213> Artificial sequence

 60 <220>
 <223> Variable heavy chain of SC03 -058
 <400> 455

554

Met Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 5 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 10 Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 15 Tyr Val Ser Gly Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn
 50 55 60
 20 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 25 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
 30 Thr Met Val Thr Val Ser Ser
 115
 35 <210> 456
 <211> 348
 <212> DNA
 40 <213> Artificial sequence
 45 <220>
 <223> Variable heavy chain of SC03 -058
 <220>
 50 <221> CDS
 <222> (1)..(348)
 <223>
 55
 <400> 456
 gac atc cag atg acc cag tct oca gac tcc ctg gct gtg tct ctg ggc 48
 60 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

555

	Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
	20 25 30	
5	tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	144
	35 40 45	
10	cct cct aag ctg ctc att tac tgg gca tct ac c cgg gaa tcc ggg gtc Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	192
	50 55 60	
15	cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttt act ctc acc Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	240
	65 70 75 80	
20	atc agc agt ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	288
	85 90 95	
25	tat tat agt act cct ctg acg ttc ggc caa ggg acc aag gtg gaa atc Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	336
	100 105 110	
30	aaa cgt gcg gcc Lys Arg Ala Ala	348
	115	
35	<210> 457	
	<211> 116	
	<212> PRT	
40	<213> Artificial sequence	
	<220>	
	<223> Variable heavy chain of SC03 -058	
	<400> 457	
45	Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
	1 5 10 15	
50	Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
	20 25 30	
55	Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
	35 40 45	
60	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	

. 556

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

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

10 Lys Arg Ala Ala
 115

<210> 458

15 <211> 375

<212> DNA

20 <213> Artificial sequence

<220>

25 <223> Variable heavy chain of SC03 -059

<220>

30 <221> CDS

<222> (1)..(375)

<223>

35

<400> 458

40 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 tgc 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
 45 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

50 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

55 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

60 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 ggc aga ttc cct ggt ggt acc aga agc cgc ggc tac atg 336

557

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

5 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

10 <210> 459
 <211> 125
 <212> PRT

15 <213> Artificial sequence

20 <220>
 <223> Variable heavy chain of SC03 -059
 <400> 459

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

30 Gly Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Gly Val Phe
 20 25 30

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

40 Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
 50 55 60

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

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

55 Tyr Tyr Cys Ala Arg Phe Pro Gly Gly Thr Arg Ser Arg Gly Tyr Met
 100 105 110

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

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

35 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

40 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

45 gct ttc ggc gga ggg acc aag gtg gag atc aaa cgt gcg gcc 330
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 10 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 15 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
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 in Frankfurt 1
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 60 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
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560

	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	
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	Phe Arg Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe	
	50 55 60	
10	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	
15	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	
20	agc aat gtg gtg cgg ggc tgg gtg ttc gcc 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	
25	gcc tgc aac ttc gag ctg tgc gac aac cct ttc ttc gcc gtg tcc aaa	435
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	130 135 140	
30	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	
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35	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	
40	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	
45	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	
50	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	
55	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	
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60	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	

561

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10	agc aac ttc aga gtg gtg ccc agc ggc gat gtg gtg agg ttc ccc aac Ser Asn Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn 305 310 315	963		
15	atc acc aac ctg tgc cct ttc ggc gag gtg ttc aac gcc acc aag ttc Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe 320 325 330	1011		
20	cct agc gtg tac gcc tgg gag cgg aag aag atc agc aac tgc gtg gcc Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala 335 340 345 350	1059		
25	gat tac agc gtg ctg tac aac agc acc ttc ttc agc acc ttc aag tgc Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys 355 360 365	1107		
30	tac ggc gtg agc gcc acc aag ctg aac gac ctg tgc ttc agc aac gtg Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val 370 375 380	1155		
35	tac gcc gac agc ttc gtg gtg aag ggc gac gac gtg aga cag atc gcc Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala 385 390 395	1203		
40	cct ggc cag acc ggc gtg atc gcc gac tac aat tac aag ctg ccc gac Pro Gly Gln Thr Gly Val Ile Ala Asp Tyr As n Tyr Lys Leu Pro Asp 400 405 410	1251		
45	gac ttc atg ggc tgc gtg ctg gcc tgg aac acc aga aac atc gac gcc Asp Phe Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala 415 420 425 430	1299		
50	acc tcc acc ggc aac tac aac tac aag tac cgc tac ctg agg cac ggc Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly 435 440 445	1347		
55	aag ctg aga ccc ttc gag cgg gac atc agc aac gtg ccc ttc agc cct Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro 450 455 460	1395		
60	gac ggc aag ccc tgc acc ccc cct gcc ctg aac tgc tac tgg ccc ctg Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu 465 470 475	1443		
65	aac gac tac ggc ttc tac acc acc acc ggc atc ggc tac cag cct tac Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr 480 485 490	1491		
70	aga gtg gtg gtg ctg agc ttc gag ctg ctg aac gcc cct gcc acc gtg Arg Val Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val 495 500 505 510	1539		
75	tgc ggc ccc aag ctg agc acc gac ctg atc aag aac cag tgc gtg aac Cys Gly Pro Lys Leu Ser Thr Asp Leu Il e Lys Asn Gln Cys Val Asn 515 520 525	1587		
80	ttc aac ttc aac ggc ctg acc ggc acc ggc gtg ctg acc cct agc agc	1635		

562

	Phe	Asn	Phe	Asn	Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Pro	Ser	Ser	
				530					535					540			
5	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				
10	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					
15	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	
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	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		
20	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			
25	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	Thr	Gln	Ala	Gly	Cys	Leu	Ile	Gly	
			625					630					635				
30	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					
35	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		
40	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			
45	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				
50	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					
55	ctg	ctg	cag	tac	ggc	agc	ttc	tgc	acc	cag	ctg	aac	aga	gcc	ctg	agc	2259
	Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	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		
60	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	
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563

	aac ttc agc cag atc ctg ccc gat cct ctg aag ccc acc aag cgg agc	2403
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5	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	
10	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	
15	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	
20	ctg acc gac gac atg atc gcc gcc tac aca gcc gcc ctg gtg agc ggc	2595
	Leu Thr Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly	
	850 855 860	
25	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 Ile	
	865 870 875	
30	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	
	880 885 890	
35	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	
	895 900 905 910	
40	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	
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	Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn	
	930 935 940	
50	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	
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	Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln	
	960 965 970	
60	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 Tyr Val	
	975 980 985 990	
65	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	
70	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 1020	
75	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	

564

	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	
5	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	
10	ggc aag gcc tac	ttc ccc aga gag gcc	gtg ttc gtg ttc aat gcc	3252
	Gly Lys Ala Tyr	Phe Pro Arg Glu Gly	Val Phe Val Phe Asn Gly	
	1070	1075	1080	
15	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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	gcc aag aac ctg	aac gag agc ctg atc	gac ctg cag gag ctg gcc	3567
	Ala Lys Asn Leu	Asn Glu Ser Leu Ile	Asp Leu Gln Glu Leu Gly	
	1175	1180	1185	
50	aag tac gag cag	tac atc aag tgg ccc	tgg tac gtg tgg ctg gcc	3612
	Lys Tyr Glu Gln	Tyr Ile Lys Trp Pro	Trp Tyr Val Trp Leu Gly	
	1190	1195	1200	
55	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	
60	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	
65	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	
70	ctg aag ggc gtg	aag ctg cac tac acc	tga tgaattctcg ag	3789
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565

<210> 463
 <211> 1255
 5 <212> PRT
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 25 His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
 35 40 45
 30 Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
 50 55 60
 35 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
 40 Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
 100 105 110
 45 Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
 115 120 125
 50 Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
 130 135 140
 55 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
 60 Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
 180 185 190

566

5 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
 10 Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
 225 230 235 240
 15 Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
 245 250 255
 20 Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
 260 265 270
 25 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
 30 Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
 305 310 315 320
 35 Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
 325 330 335
 40 Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
 340 345 350
 45 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
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 50 Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
 385 390 395 400
 55 Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
 405 410 415
 60 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

567

	435	440	445
5	Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly 450 455 460		
10	Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp 465 470 475 480		
15	Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val 485 490 495		
20	Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly 500 505 510		
25	Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn 515 520 525		
30	Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg 530 535 540		
35	Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp 545 550 555 560		
40	Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys 565 570 575		
45	Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser 580 585 590		
50	Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr 595 600 605		
55	Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr 610 615 620		
60	Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu 625 630 635 640		
65	His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile 645 650 655		
70	Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys 660 665 670		
75	Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala 675 680 685		

568

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
 690 695 700

5 Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
 705 710 715 720

10 Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
 725 730 735

15 Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
 740 745 750

20 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

25 Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
 785 790 795 800

30 Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
 805 810 815

35 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

40 Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
 850 855 860

45 Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
 865 870 875 880

50 Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
 885 890 895

55 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

60 Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
 930 935 940

569

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
 945 950 955 960
 5 Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
 965 970 975
 10 Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
 980 985 990
 15 Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
 995 1000 1005
 20 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
 25 Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
 1040 1045 1050
 30 Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
 1055 1060 1065
 35 Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
 1070 1075 1080
 40 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
 45 Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
 1115 1120 1125
 50 Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
 1130 1135 1140
 55 Pro Asp Val Asp Phe Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
 1145 1150 1155
 60 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

570

5 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
 10
 Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
 1220 1225 1230

 15 Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
 1235 1240 1245

 20 Gly Val Lys Leu His Tyr Thr
 1250 1255

 <210> 464
 25 <211> 29
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 35 <223> Primer XhoISpikeRevCOG
 <400> 464
 gttcctcgag gggccacttg atgtactgc 29
 40
 <210> 465
 <211> 18
 45 <212> DNA
 <213> Artificial sequence

 50 <220>
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 55 <400> 465
 ccaggtgaag cagatgta 18

 60 <210> 466
 <211> 32

571

<212> DNA
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10 <400> 466
cttgggtaccg ccaccatgtc tgataatgga cc 32
15 <210> 467
<211> 28
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20 <213> Artificial sequence
25 <220>
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<400> 467
30 gttctctaga tgcctgagtt gaatcagc 28
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35 <211> 9
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<213> Artificial sequence
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<220>
45 <223> Peptide
<400> 468
Arg Ser Ala Pro Arg Ile Thr Phe Gly
50 1 5
<210> 469
55 <211> 32
<212> DNA
<213> Artificial sequence
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572

<220>
 <223> oligonucleotide primer EcoRIspikeFor318
 5 <400> 469
 cctggaattc tccatggcca acatcaccaa cc 32

 <210> 470
 10 <211> 27
 <212> DNA
 15 <213> Artificial sequence

 <220>
 20 <223> Oligonucleotide primer XbaIspikeRev510
 <400> 470
 gaagggccct ctagacacgg tggcagg 27
 25
 <210> 471
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 30 <212> DNA
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 40 <220>
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 45 <222> (1)..(1350)
 <223>
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 <400> 471
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 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 55 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
 60 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

573

	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	
5	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	
10	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	
15	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	
20	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	
25	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	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	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	
65	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	
70	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	
75	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	

574

5 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
 10 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
 15 acc ctg ccc ccc agc cgg gag gag atg acc aag aac cag gtg tcc ctc 1104
 Thr Ieu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Ieu
 355 360 365
 20 acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag tgg 1152
 Thr Cys Ieu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 25 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
 30 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
 35 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
 40 ggc aag 1350
 Gly Lys
 450
 45 <210> 472
 <211> 450
 <212> PRT
 50 <213> Artificial sequence
 <220>
 55 <223> IgG heavy chain of 03-006
 <400> 472
 60 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

575

	20	25	30
5	Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45		
10	Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 50 55 60		
15	Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80		
20	Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95		
25	Ala Lys Asp Gly Ser Pro Arg Thr Pro Ser Phe Asp Tyr Trp Gly Gln 100 105 110		
30	Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val 115 120 125		
35	Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 130 135 140		
40	Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 145 150 155 160		
45	Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 165 170 175		
50	Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 180 185 190		
55	Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 195 200 205		
60	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		
	Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu 260 265 270		

576

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

5 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

10 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

15 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

20 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365

25 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

30 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

35 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

40 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

45 Gly Lys
 450

50 <210> 473
 <211> 1335
 <212> DNA

55 <213> Artificial sequence

60 <220>
 <223> IgG heavy chain of 03 -015

577

<220>

<221> CDS

5 <222> (1)..(1335)

<223>

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<400> 473

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

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

20

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 Gl u Trp Val
 35 40 45

25

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

30

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

35

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

40

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

45

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

50

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 As n 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

55

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

60

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

578

	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	
5	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	
10	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	
15	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	
20	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	
25	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	
	290 295 300	
30	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	
35	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	
40	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	
45	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	
50	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	
55	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	
60	agc ttc ttc ctg tac agc aag ctc acc gtg gac aag agc cgg tgg cag	1248
	Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln	
	405 410 415	
65	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	
70	cac tac acc cag aag agc ctg agc ctg agc ccc ggc aag	1335
	His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
	435 440 445	
	<210> 474	

579

<211> 445
 <212> PRT
 5 <213> Artificial sequence

<220>
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 <400> 474

15 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 20 25 30
 Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 25 35 40 45
 Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
 50 55 60
 30 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 35 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 40 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
 45 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 130 135 140
 50 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 145 150 155 160
 55 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 165 170 175
 60 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

580

	195	200	205
5	Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys 210 215 220		
10	Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu 225 230 235 240		
15	Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu 245 250 255		
20	Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys 260 265 270		
25	Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys 275 280 285		
30	Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu 290 295 300		
35	Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys 305 310 315 320		
40	Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys 325 330 335		
45	Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser 340 345 350		
50	Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 355 360 365		
55	Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln 370 375 380		
60	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 405 410 415		
	Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn 420 425 430		
	His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 435 440 445		

581

<210> 475
 <211> 642
 5 <212> DNA
 <213> Artificial sequence

 10 <220>
 <223> IgG light chain of 03-006
 15 <220>
 <221> CDS
 <222> (1)..(642)
 20 <223>

 25 <400> 475
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 Asp Ile Gln Met Thr Gln Ser Pro His Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 30 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
 35 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
 40 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
 45 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
 50 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
 55 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
 60 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
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

582

	145		150		155		160	
	gag agc gtg acc gag cag gac agc aag gac tcc acc tac agc ctg agc							528
5	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		
10	gcc tgc gag gtg acc cac cag gcc 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		
15	ttc aac cgg gcc gag tgt							642
	Phe Asn Arg Gly Glu Cys							
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583

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10 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
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 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
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584

	35	40	45	
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10	agc tca gga aac aca gct tcc ttg acc atc act ggg g ct cag gcg gaa Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu 65 70 75 80			240
15	gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac cat Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His 85 90 95			288
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 Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
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 50 Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
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 55 Ala Pro Thr Glu Cys Ser
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CLAIMS

1. A binding molecule capable of specifically binding to amino acid residues 11-19 of the N protein of SARS-CoV.
2. A binding molecule according to claim 1, wherein the binding molecule comprises at least a CDR3 region comprising the amino acid sequence of SEQ ID NO:78.
3. A binding molecule according to claim 1 or 2, wherein the binding molecule comprises a heavy chain comprising the amino acid sequence of SEQ ID NO:86.
4. An immunoconjugate comprising a binding molecule according to any one of the claims 1-3, the immunoconjugate further comprising at least one tag.
5. An immunoconjugate according to claim 4, wherein the tag is selected from the group consisting of a radioactive substance, an enzyme and combinations thereof.
6. A nucleic acid molecule encoding a binding molecule according to any one of the claims 1-3.
7. A vector comprising at least one nucleic acid molecule according to claim 6.
8. A host comprising at least one vector according to claim 7.
9. A host according to claim 8, wherein the host is a cell derived from a human cell.

10. A method of producing a binding molecule according to any one of the claims 1-3, wherein the method comprises the steps of:

- a) culturing a host according to claim 8 or 9 under conditions conducive to the expression of the binding molecule, and optionally,
- b) recovering the expressed binding molecule.

11. A binding molecule as obtainable by the method according to claim 10.

12. A composition comprising a binding molecule according to any one of the claims 1-3 or 11 or an immunoconjugate according to claim 4 or 5.

13. A composition comprising a nucleic acid molecule according to claim 6.

14. A pharmaceutical composition comprising a binding molecule according to any one of the claims 1-3 or 11, an immunoconjugate according to claim 4 or 5, or a composition according to claim 12 or 13, the pharmaceutical composition further comprising at least one pharmaceutically acceptable excipient.

15. A pharmaceutical composition according to claim 14 further comprising at least one other therapeutic agent.

16. A binding molecule according to any one of the claims 1-3 or 11, an immunoconjugate according to claim 4 or 5, a composition according to claim 12 or 13, or a

pharmaceutical composition according to claim 14 or 15 for use as a medicament.

17. A binding molecule according to any one of the claims 1-3 or 11, an immunoconjugate according to claim 4 or 5, a composition according to claim 12 or 13, or a pharmaceutical composition according to claim 14 or 15 for use in the diagnosis, prophylaxis, treatment, or combination thereof, of a condition resulting from a SARS-CoV.

18. Use of a binding molecule according to any one of the claims 1-3 or 11, an immunoconjugate according to claim 4 or 5, a composition according to claim 12 or 13, or a pharmaceutical composition according to claim 14 or 15 in the preparation of a medicament for the diagnosis, prophylaxis, treatment, or combination thereof, of a condition resulting from a SARS-CoV.

19. A kit comprising a binding molecule according to any one of the claims 1-3 or 11, an immunoconjugate according to claim 4 or 5, a nucleic acid molecule according to claim 6, a vector according to claim 7, a host according to claim 8 or 9, a composition according to claim 12 or 13, a pharmaceutical composition according to claim 14 or 15, or a combination thereof.

20. 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 1-3 or 11 or an immunoconjugate according to claim 4 or 5, and

b) determining whether the binding molecule or immunoconjugate specifically binds to a molecule of the sample.

21. A method according to claim 20, wherein the sample is a sample from a human subject potentially infected with a SARS-CoV.

22. A method of screening 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 1-3 or 11, wherein the method comprises the steps of:

a) contacting a binding molecule to be screened, a binding molecule according to any one of the claims 1-3 or 11 and a SARS-CoV or fragments thereof, and

b) measure if the binding molecule 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 1-3 or 11.

23. 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.

24. A method according to claim 23, characterized in that
the inactivation is performed by gamma- or UV-irradiation.

25. A method according to claim 23 or 24, 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.

26. A method according to any of the claims 23-25,
characterized in that the binding molecule is a human
binding molecule.

27. A method according to any of the claims 23-26,
characterized in that the binding molecule is a single
chain Fv.

28. A method according to any of the claims 23-27,
characterized in that the inactivated SARS-CoV is purified
before being inactivated.

29. A method according to any of the claims 23-28,
characterized in that the inactivated SARS-CoV in step a is
immobilized.

30. A binding molecule obtainable by the method according to any of the claims 23-29, the binding molecule having neutralizing activity against the SARS-CoV.

31. A pharmaceutical composition comprising a binding molecule according to claim 30, the pharmaceutical composition further comprising at least one pharmaceutically acceptable excipient.

32. A pharmaceutical composition according to claim 31 further comprising at least one other therapeutic agent.

33. A binding molecule according to claim 30 or a pharmaceutical composition according to claim 31 or 32 for use as a medicament.

34. A binding molecule according to claim 30 or a pharmaceutical composition according to claim 31 or 32 for use in the diagnosis, prophylaxis, treatment, or combination thereof of a condition resulting from SARS-CoV.