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(54) PROTEIN ANALYSIS

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(57) **ABSTRACT**

Disclosed, inter alia, is a method of evaluating a sample that includes a serum protein and one or more one or more compounds physically associated with the serum protein. The method can include using a peptide ligand that specifically interacts with the serum protein to analyze a complex formed by the serum protein and its associated compounds.

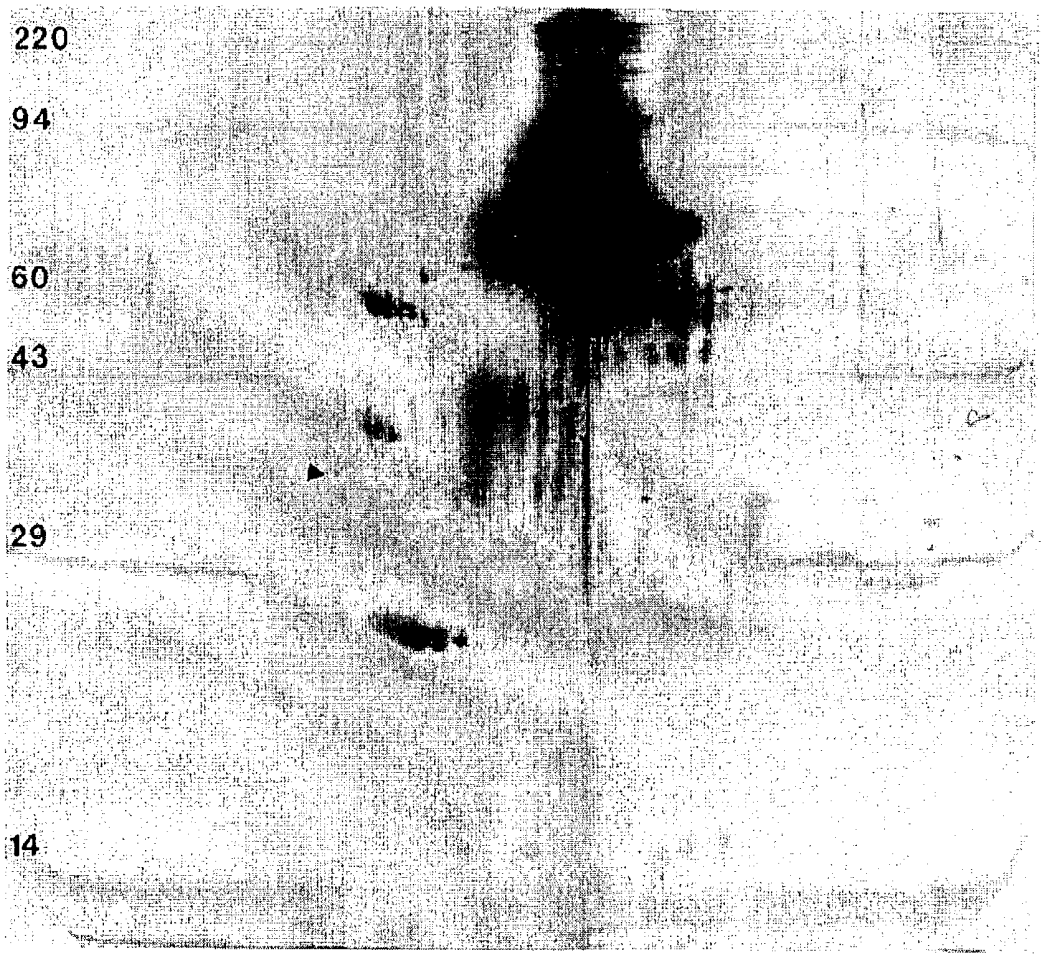

FIG. 1

PROTEIN ANALYSIS

RELATED APPLICATIONS

[0001] This application claims benefit of priority to U.S. Provisional Patent Application Serial No. 60/388,642, filed Jun. 14, 2002, the contents of which are incorporated herein by reference.

BACKGROUND

[0002] This application relates to the analysis of proteins, including serum proteins.

[0003] Serum is the blood-derived fluid that remains after blood has clotted. The more abundant serum proteins include serum albumin and antibodies (e.g., IgG, IgM, and the like). Other proteins that can be present in serum include: transferrin, α-macroglobulins, ferritin, apolipoproteins, transthyretin, protease inhibitors, retinol binding protein, thiostatin, α-fetoprotein, vitamin-D binding protein, and afamin (see, e.g., U.S. Pat. No. 5,767,243).

[0004] The most abundant protein component in circulating blood of mammalian species is serum albumin, which is normally present at a concentration of approximately 3 to 4.5 grams per 100 ml of whole blood. Serum albumin is a blood protein of approximately 70 kilo-Daltons which provides several important functions in the circulatory system. For instance, it functions as a transporter of a variety of organic molecules found in the blood, as the main transporter of various metabolites such as fatty acids, hematin, and bilirubin, and, owing to its abundance, as an osmotic regulator of the circulating blood. It also has a broad affinity for small, negatively charged aromatic compounds. These binding functions enable serum albumin to serve as the principal carrier of fatty acids that are otherwise insoluble in circulating plasma. Likewise, it can sequester oxygen free radicals and to inactivate toxic lipophilic metabolites such as bilirubin. It can also form covalent adducts with pyridoxal phosphate cysteine, glutathione, and various metals, such as Cu(II), Ni(II) Hg(II), Ag(II), and Au(I).

[0005] Serum albumin can also bind to drugs that are present in the body. Indeed, one indicator of the efficacy of a drug is its affinity for serum albumin or other serum proteins. Binding to serum albumin can affect the overall distribution, metabolism, and bioavailability of many drugs. At least in some cases, unusually high affinity to serum albumin has been associated with the failure of candidate drugs.

[0006] It is also known to conjugate drugs to serum albumin to extend their half-life and distribution. Recently, chimeric albumin molecules such as HSA-CD4 and HSA-Cu,Zn-superoxide dismutase have been utilized to increase the half-life and distribution and to reduce the immunogenicity of these potential protein therapeutics.

SUMMARY

[0007] In one aspect, the invention features a method that includes: providing a sample that includes (i) a serum albumin, (ii) one or more compounds physically associated with the serum albumin and (iii) a serum albumin-binding agent; allowing the serum albumin-binding agent to bind to the serum albumin to form a complex; separating the complex from one or more components of the sample; and evaluating one or more of the physically associated compounds. The method can be used to evaluating a sample. The method can further include separating one or more of the physically associated compounds from the serum albumin, e.g., prior to the evaluating. In one embodiment, the serum albumin is a human serum albumin.

[0008] In an embodiment, the serum albumin-binding agent has one or more of the following properties: is synthetic; includes a protein other than an antibody or antibody derivative; is non-naturally occurring; is free of an immunoglobulin variable domain; includes a peptide that independently binds to serum albumin.

[0009] In the latter case, the peptide can include at least one intra-molecular disulfide bonds, e.g., one or two intra-molecular disulfide bonds. The peptide can include a peptide described herein, e.g., DX-321, DX-321-A, DX-321-B, DX-236, DX-236-A, or DX-236B, or a variant thereof, or a peptide described in U.S. Published application 2003/0069395; Ser. No. 10/094,401; Ser. No. 60/331,352; or Ser. No. 60/292,975, or a variant thereof. Particular variants include: functional variants having between one and six substitutions (e.g., between one and four, e.g., one, two, three, or four), e.g., conservative substitutions, truncations, chemically modified forms, peptido-mimetics, and substitutions with non-naturally occurring residues. The peptide may also include be a functional variant with between one and four insertions or deletions, e.g., one , two, three or four. The peptide can be a peptide ligand that competes for binding to serum albumin with a ligand described herein, or a ligand binding an epitope that overlaps with an epitope bound by a ligand described herein. The peptide ligand can be a ligand isolated by screening a display library. The peptide that independently binds to serum albumin can be less than 32, 28, 24, 20, or 16 amino acids in length, or between 12 and 32, 8 and 16, or 12 and 24 amino acids in length.

[0010] In one embodiment, the serum albumin-binding agent is coupled to an insoluble support, e.g., a bead (such as a magnetic bead), a matrix (such as a chromatography matrix, agarose, or a porous material), or a planar surface. For example, the support may include a planar surface, and the serum albumin-binding agent is immobilized to a discrete address on the planar surface. The planar surface can also include a second binding agent at a second discrete address, e.g., another serum albumin-binding agent or an agent that binds to a different serum protein.

[0011] The serum albumin-binding agent can have a binding affinity (K_D) of less than 5, 4, 2, 1, 0.5, 0.1 μM, or less than 50, 10, 5, or 0.5 nM and/or of greater than 0.05, 0.5, 5, or 50 nM, 0.001, 0.1, or 0.1 μM, and ranges therebetween. In one embodiment, the serum albumin-binding agent binds to serum albumin under physiological conditions. In one embodiment, the serum albumin-binding agent and the serum albumin preferentially dissociate at least in solutions above pH 8, 8.5, or 9, e.g., between pH 8 and 11; pH 8 and 10.5; pH 8 and 10; pH 8.5 and 10; or pH 8.7 and 9.5. In another embodiment, the serum albumin-binding agent and the serum albumin preferentially dissociate at least in solutions below pH 6, 5.5, or 6, e.g., between pH 4 and 6; pH 4.6 and 6.5; pH 5 and 6.5; or pH 4.7 and 6.0.

[0012] In one embodiment, the serum albumin-binding agent is less than 7, 5, 3, or 2 kDa molecular weight or between 1.5 and 7 or 2 and 6 kDa molecular weight.

[0013] The serum albumin-binding agent may bind to serum albumin from a plurality of species, e.g., a plurality of mammalian species, e.g., human and mouse. In another embodiment, the serum albumin-binding agent binds to human serum albumin but not murine serum albumin nor bovine serum albumin.

[0014] In one embodiment, at least one of the evaluated physically associated compounds is non-covalently associated with the serum albumin. Such compounds may be directly or indirectly physically associated with the serum albumin. An indirect interaction may be bridged by one or more compounds, at least one of which is directly associated with the serum albumin. In another embodiment, at least one of the evaluated physically associated compounds is covalently associated with the serum albumin. In some embodiments, at least one of the evaluated physically associated compounds is covalently associated and at least another is non-covalently associated.

[0015] The method can include further including separating the at least one non-covalently associated compounds from the serum albumin, e.g., prior to the evaluating. The separating from the serum albumin can include covalently attaching the serum albumin to an insoluble support, e.g., a matrix, a particle, or a surface. For example, the covalent attachment can be to a free cysteine of the serum albumin. The covalent attachment can be formed using a thiol reactive group, e.g., a halogen derivative (such as iodoacetamide), a maleimide, or a thiol exchange reagent (e.g., a pyridyl disulfide).

[0016] The separating can include denaturing the serum albumin, e.g., using a chaotrope, an organic solvent, high or low pH, or heat. In another embodiment, where at least one of the evaluated covalently associated compounds is protease resistant (e.g., includes a non-proteinaceous component), the separating can include degrading the serum albumin, e.g., using a protease.

[0017] The evaluating can include one or more of: gel electrophoresis, mass spectroscopy, chromatography, protein sequencing, detecting a label (e.g., a radioactive, fluorescent, enzymatic, or chemical label), detecting a given compound using an affinity reagent specific for the given compound, or another method described herein. The affinity reagent may be an antibody. For example, the detecting can include performing an immuno-blot or an immuno-precipitation. Information from the evaluating can be recorded on a machine-readable medium, transmitted across a computer network, or stored in a database.

[0018] The subject of the evaluating can include a proteinaceous or a non-proteinaceous chemical compound. For example, the subject can include a peptide, a polypeptide, a protein complex, or a drug. In one embodiment, the compound is other than one or more of the compounds in Table 1 or Table 2, e.g., a compound other than a fatty acid, hematin, bilirubin, or an exogenous compound.

[0019] In one embodiment, the evaluating includes eluting an associated compound from the serum albumin by competition using a synthetic affinity ligand specific for an epitope of the serum albumin or a natural compound (e.g., a fatty acid, hematin, and bilirubin) that binds to the serum albumin. The natural compound can include a negatively charged aromatic group having a molecular weight of less than 500 Daltons.

[0020] In one embodiment, the serum albumin is an artificial mutant of a naturally-occurring serum albumin. For example, the serum albumin can be fused to a heterologous polypeptide or covalently coupled to a therapeutic agent (e.g., a cytotoxic drug).

[0021] The method can further include digitally recording information that (i) indicates the presences or absence of a given compound among the evaluated one or more physically associated compounds, or (ii) describes the one or more physically associated compounds.

[0022] In one embodiment, the sample is obtained from a subject, e.g., a human, e.g., a patient. The sample may include blood or serum. In another example, the sample is obtained from a biopsy, e.g., obtained from a tumor, a region adjacent to a tumor, or a lymph node. The subject may be treated with a therapeutic composition prior to obtaining the sample.

[0023] In one embodiment, one or more of the evaluated physically associated compounds is an endogenous compound. In another embodiment, one or more of the evaluated physically associated compounds is a component of the therapeutic composition.

[0024] In one embodiment, the method further includes providing a second sample, and evaluating one or more of the physically associated compounds in the second sample. The method can further include comparing results of evaluating the one or more of the physically associated compounds for the first sample to the second sample.

[0025] In one embodiment, the first and second samples are obtained from a first and a second subject, respectively. In one example, the first subject and second subject are respectively treated with an agent and untreated with the agent, e.g., a small molecule. The agent may be administered parenterally. In another example, the first subject and second subject are subjected to different environmental conditions. In still another example, the first subject is a reference subject and the second subject is an experimental subject. In another example, the first subject is a reference subject and the second subject is an affected and/or diseased subject. In still another example, the first and second samples are obtained from the same subject, e.g., at different times, e.g., at different times during a treatment.

[0026] The results can be recorded in a machine or on machine-readable media. For example, the results are stored in a computer database.

[0027] In one embodiment, the results for the first and second samples are compared to a reference sample. In one embodiment, results for the first and second samples are compared to a database that includes records for samples, each sample record being associated with information about the sample (e.g., origin, disease, environmental condition, physiological condition, and so forth).

[0028] In another aspect, the invention features a method that includes providing a sample that includes a serum albumin, one or more compounds associated with the serum albumin, and a component that does not associate with the serum albumin; contacting the sample to an affinity ligand specific for the serum albumin; and separating the unassociated component from a composition that includes the serum albumin and one or more of the associated com-

pounds, thereby providing a serum albumin-associated compound. The method can be used to provide a serum albumin-associated compound. The method can include other features described herein. The invention also provides a composition prepared by the above method or a method described herein.

[0029] The method can further include separating the associated compound from the serum albumin to provide a serum-albumin free preparation. The invention also features a serum-albumin free preparation prepared according to the above method or another method described herein.

[0030] In another aspect, the invention features a method that includes providing (e.g., receiving or obtaining) a first and second sample that each includes a serum protein (e.g., a serum albumin, a soluble immunoglobulin, or other serum protein); evaluating each sample for associated compound(s), if present, e.g., according to a method described herein; and comparing results of the evaluating for the first and second samples. The method can further include, prior to the evaluating, isolating the serum protein and compounds associated with the serum protein from each sample. The separating can include covalently attaching the serum protein to an insoluble matrix. The serum protein can be an abundant serum protein, e.g., a serum protein that is forms at least 0.01, 0.05, or 0.1% of the blood serum.

[0031] In one embodiment, the first and second samples are obtained from a first and a second subject, respectively. In one example, the first subject and second subject are respectively treated with an agent and untreated with the agent, e.g., a small molecule. The agent may be administered parenterally. In another example, the first subject and second subject are subjected to different environmental conditions. In still another example, the first subject is a reference subject and the second subject is an experimental subject. In another example, the first subject is a reference subject and the second subject is an affected and/or diseased subject.

[0032] The results can be recorded in a machine or on machine-readable media. For example, the results are stored in a computer database.

[0033] In one embodiment, the results for the first and second samples are compared to a reference sample. In one embodiment, results for the first and second samples are compared to a database that includes records for samples, each sample record being associated with information about the sample (e.g., origin, disease, environmental condition, physiological condition, and so forth).

[0034] The method can also include other features described herein.

[0035] In another aspect, the invention features a method that includes: providing a sample that includes (i) a soluble immunoglobulin protein that includes at least one immunoglobulin domain (ii) one or more compounds physically associated with the soluble immunoglobulin protein and (iii) a peptide immunoglobulin-binding agent; allowing the immunoglobulin-binding agent to bind to the soluble immunoglobulin protein to form a complex that includes one or more compounds physically associated with the soluble immunoglobulin protein; separating the complex from one or more components of the sample; and evaluating one or more of the physically associated compounds. The method can be used to evaluate a sample.

[0036] In one embodiment, the soluble immunoglobulin protein is a naturally-occurring protein, e.g., IgG, IgM, IgA, IgE, or IgD. In another embodiment, the soluble immunoglobulin protein is a Fab or single-chain antibody. Such protein may include at least one synthetic complementarity determining region (CDR).

[0037] In one embodiment, the one or more physically associated compounds includes an antigen of a pathogen.

[0038] The sample can be obtained from a subject having an infection, immunological disorder (e.g., an auto-immune disorder), or a genetic disorder. The subject may also be a normal subject.

[0039] In an embodiment, the immunoglobulin-binding agent has one or more of the following properties: is synthetic; includes a protein other than an antibody or antibody derivative; is non-naturally occurring; is free of an immunoglobulin variable domain; includes a peptide that independently binds to immunoglobulin. The immunoglobulin-binding agent can bind to the Fc region, to a constant domain (e.g., CH1, CH2, CH3, CH4, or CL), or to a framework region of a variable domain. In a principal embodiment, the immunoglobulin binding agent does not bind to the antigen-binding site of an immunoglobulin.

[0040] The peptide can include one or more intra-molecular disulfide bonds, e.g., one or two intra-molecular disulfide bonds. In the case of an immunoglobulin binding agent that binds to an Fc region, the peptide can include a peptide described herein, e.g., DX249, DX249-A, DX249-B, DX253, DX253-A, DX253-B, DX398, DX398-A, DX398-B or a variant thereof, or a compound described in Ser. No. 10/125,869, filed Apr. 18, 2002, or a variant thereof. Exemplary variants include: functional variants having between one and six substitutions, e.g., conservative substitutions, truncations, chemically modified forms, peptidomimetics, and substitutions with non-naturally occurring residues. The peptide can be a peptide ligand that competes for binding to an immunoglobulin with a ligand described herein, or a ligand binding an epitope that overlaps with an epitope bound by a ligand described herein. The peptide ligand can be a ligand isolated by screening a display library. The peptide that independently binds to an immunoglobulin can be less than 32, 28, 24, 20, or 16 amino acids in length, or between 12 and 32, 8 and 16, or 12 and 24 amino acids in length.

[0041] In one embodiment, the immunoglobulin-binding agent is coupled to an insoluble support, e.g., a bead (such as a magnetic bead), a matrix (such as a chromatography matrix), or a planar surface. For example, the support may include a planar surface, and the immunoglobulin-binding agent is immobilized to a discrete address on the planar surface. The planar surface can also include a second binding agent at a second discrete address, e.g., another immunoglobulin-binding agent or an agent that binds to a different serum protein.

[0042] The immunoglobulin-binding agent can have a binding affinity (K_D) of less than 5, 4, 2, 1, 0.5, or 0.1 μM and/or of greater than 0.001, 0.1, or 0.1 μM, and ranges therebetween. In one embodiment, the immunoglobulin-binding agent binds to immunoglobulin under physiological conditions.

[0043] In one embodiment, the immunoglobulin-binding agent is less than 7, 5, 3, or 2 kDa molecular weight or between 1.5 and 7 or 2 and 6 kDa molecular weight.

[0044] The immunoglobulin-binding agent may bind to immunoglobulins from a plurality of species, e.g., a plurality of mammalian species, e.g., human and mouse. In another embodiment, the immunoglobulin-binding agent binds to a human immunoglobulin but not a murine immunoglobulin.

[0045] In one embodiment, at least one of the evaluated physically associated compounds is non-covalently associated with the immunoglobulin. Such compounds may be directly or indirectly physically associated with the immunoglobulin. An indirect interaction may be bridged by one or more compounds, at least one of which is directly associated with the immunoglobulin. In one embodiment, an associated compound is an antigen recognized by the immunoglobulin. For example, an antigen that is a component of a pathogen, e.g., a virus or bacterium, e.g., a replicable virus or live bacterium.

[0046] The method can include further including separating the at least one non-covalently associated compounds from the immunoglobulin, e.g., prior to the evaluating. The separating from the immunoglobulin can include covalently attaching the immunoglobulin to an insoluble support, e.g., a matrix, a particle, or a surface.

[0047] The separating can include denaturing the immunoglobulin, e.g., using a chaotrope, an organic solvent, high or low pH, or heat. In another embodiment, wherein at least one of the evaluated associated compounds is protease resistant (e.g., includes a non-proteinaceous component), the separating can include degrading the immuno-globulin.

[0048] The evaluating can include one or more of: gel electrophoresis, mass spectroscopy, chromatography, protein sequencing, detecting a label (e.g., a radioactive, fluorescent, enzymatic, or chemical label), detecting a given compound using an affinity reagent specific for the given compound, or another method described herein. The affinity reagent may be an antibody. For example, the detecting can include performing an immuno-blot or an immuno-precipitation.

[0049] The evaluating can include culturing a pathogen (e.g., virus or bacterium) that is associated with the immunoglobulin.

[0050] The subject of the evaluating can include a proteinaceous or a non-proteinaceous chemical compound. For example, the subject can include a peptide, a polypeptide, a protein complex, or a drug. In one embodiment, the compound is other than an antigen, e.g., the compound is associated with the immunoglobulin by interactions outside the CDR region.

[0051] In one embodiment, the evaluating includes eluting an associated compound from the immunoglobulin by competition using a synthetic affinity ligand specific for an epitope of the immunoglobulin or an antigen. The natural compound can include a negatively charged aromatic group having a molecular weight of less than 500 Daltons.

[0052] In one embodiment, the immunoglobulin is an artificial variant of a naturally-occurring immunoglobulin. For example, the immunoglobulin can be fused to a heterologous polypeptide or covalently coupled to a therapeutic agent (e.g., a cytotoxic drug).

[0053] The method can further include digitally recording information that (i) indicates the presences or absence of a given compound among the evaluated one or more physically associated compounds, or (ii) describes the one or more physically associated compounds.

[0054] In one embodiment, the method further includes providing a second sample, and evaluating one or more of the physically associated compounds in the second sample. The method can further include comparing results of evaluating the one or more of the physically associated compounds for the first sample to the second sample.

[0055] In one embodiment, the sample is obtained from a subject, e.g., a human, e.g., a patient. The sample may include blood or serum. In another example, the sample is obtained from a biopsy, e.g., obtained from a tumor, a region adjacent to a tumor, or a lymph node. The subject may be treated with a therapeutic composition prior to obtaining the sample.

[0056] In one embodiment, one or more of the evaluated physically associated compounds is an endogenous compound. In another embodiment, one or more of the evaluated physically associated compounds is a component of the therapeutic composition.

[0057] In still another aspect, the invention features a method that includes: providing a complex including a serum albumin and an associated compound; evaluating binding of a non-antibody ligand (e.g., a peptide ligand described herein) to the complex, wherein the non-antibody ligand binds to serum albumin, e.g., with an affinity of less than 5, 3, 2, 1, 0.5, or 0.1 μM and binding of the non-antibody ligand to the complex indicates that the associated compound does not bind an epitope that overlaps the epitope bound by the non-antibody ligand. The method can be used to map a physical interaction between serum albumin and an associated compound. The method can also be varied, e.g., by first binding the ligand and then binding the associated compound.

[0058] The method can further include: evaluating binding of a ligand to the complex, wherein the second ligand binds to serum albumin, e.g., with an affinity of less than 5, 3, 2, 1, 0.5, or 0.1 μM. For example, the second ligand is other than an antibody, e.g., a peptide ligand. In one embodiment, one of the first and second non-antibody ligand binds is prevented from binding to the complex. For example, the associated compound sterically hinders binding of the non-antibody ligand to serum albumin or occludes the binding site of the non-antibody ligand for serum albumin. The ligand can be a ligand described herein. The method can also be varied, e.g., by first binding the ligands and then binding the associated compound.

[0059] In a related aspect, the invention features a method that includes: providing a complex including a serum albumin and a non-antibody ligand, and evaluating binding of a given compound to the complex. The given compound can be a compound known to bind to serum albumin or a compound isolated from a sample in association with serum albumin, e.g., by a method described herein. The method can be used to map a physical interaction between serum albumin and a given compound.

[0060] The method can be repeated for a second ligand. In one embodiment, the second ligand does not include an antigen binding immunoglobulin domain.

[0061] The method can be repeated for a second given compound.

[0062] The method can include other features described herein.

[0063] In another aspect, the invention features a database, including (i) data describing compounds associated with a serum protein in a sample; and (ii) data indicating information about the sample, wherein instances of (i) are linked to instances of (ii). The data can be obtained from results of a method described herein.

[0064] In another aspect, the invention features a method (e.g., a machine-based method) that includes: receiving information about compounds associated with a serum protein in a given sample; comparing the information to a database that includes information about compounds associated with the serum protein in a plurality of reference samples to locate information about a compound or a sample indicated by the received information; and providing the located information or a reference to the located information to a user. The method can include other features described herein.

[0065] In still another aspect, the invention features a machine-readable medium having encoded thereon information representing a separation process that separates compounds in a composition described herein and/or information representing a characteristic (e.g., physical characteristic, chemical structure, and so forth) of a compound associated with a serum protein (e.g., a serum albumin or an immunoglobulin).

[0066] The invention also features an image of a two-dimensional gel that separates a composition described herein. Also featured is a database including a plurality of images, each image corresponding to a two-dimensional gel separation of a composition described herein.

[0067] Also featured is a machine-readable medium having encoded thereon information representing characteristics of a plurality of compounds detectable in a composition described herein. Exemplary characteristics include molecular weight, isoelectric point, sequence, chemical composition, abundance, proteolytic fragment profile, and so forth.

[0068] In another aspect, the invention features a method that includes a sample that includes (i) a serum protein, (ii) one or more compound physically associated with the serum protein and (iii) a serum protein-binding agent; allowing the serum protein-binding agent to bind to the serum protein to form a complex; separating said complex from one or more components of the sample; and evaluating one or more of the physically associated compounds. Examples of serum proteins include serum albumin, antibodies (e.g., IgG, IgM, and so forth), transferrin, α-macroglobulins, ferritin, apolipoproteins, transthyretin, protease inhibitors, retinol binding protein, thiostatin, α-fetoprotein, vitamin-D binding protein, and afamin. The method can include other features, e.g., as described above and elsewhere herein.

[0069] In one embodiment, the method includes obtaining the sample from a subject. For example, the subject may have a metabolic disorder, and the serum protein is a non-albumin carrier protein for one or more metabolites.

[0070] In another related aspect, the invention features a method that includes: providing a sample that comprises a serum albumin having one or more compounds physically associated with the serum albumin; isolating the serum albumin and one or more compounds physically associated with the serum albumin from the sample using an affinity reagent that binds the serum albumin; and detecting the one or more physically associated compounds. The method can be used for detecting a serum albumin-associated compound.

[0071] In one embodiment, the affinity reagent includes a proteinaceous ligand that is does not have an antigen-binding immunoglobulin domain. For example, the proteinaceous ligand is a peptide ligand that binds serum albumin, e.g., with an affinity of less than 5, 4, 2, 1, 0.5, or 0.1 μM. The affinity reagent can include one or more peptide ligands described herein, e.g., DX-236 and DX-321. In one embodiment, the affinity reagent includes two ligands that bind different epitopes. The method can include other features, e.g., as described above and elsewhere herein.

[0072] In still other aspects, the invention features a method that includes administering a composition that comprises a compound to a subject and determining association of the compound with a serum protein from the subject. The determining can include covalently or non-covalently binding the serum protein (e.g., a serum albumin) from the subject to an affinity reagent, e.g., a ligand described herein. The method can include one or more other features described herein.

[0073] In another aspect, the invention features a method that includes contacting a serum albumin to a given compound; binding the serum albumin to an affinity reagent described herein; and determining association of the given compound to the serum albumin. The method can include one or more other features described herein.

[0074] The method can be used for discovering associations between serum proteins and natural compounds, and, similarly, associations between serum proteins and non-natural compounds, such as pharmaceuticals. The method can also be used to characterize a subject (e.g., a human patient or an animal) by the profile of compounds associated with a given serum protein (e.g., serum albumin).

[0075] In some embodiments, peptide ligands are used as affinity reagents to bind a serum protein. Peptide ligands offer several advantages. For example, the mass per binding site is low, e.g., such low molecular weight peptide domains can show higher bind activity per gram than larger proteins such as antibodies. The possibility of non-specific binding is reduced because there is only a small surface available. Peptides can be engineered to have unique tethering sites such as N-terminal Ser or Thr residues or terminal single or multiple lysine segments, e.g., by chemical synthetic methods. (N-terminal Ser or Thr can be specifically oxidized to aldehydes that can be joined to other molecules with high specificity.) Further, as used in some embodiments, a constrained peptide structure is likely to retain its functionality in a variety of contexts.

[0076] The invention also features isolated preparations of an endogenous compound associated with a serum albumin.

The preparations can be isolated by a method described herein. The preparation can include a single species that also be at least 50, 60, 70, 80, 90, or 95% pure (weight/volume). The species can have an isoelectric point and molecular weight according to a species isolated in **FIG. 1**.

[0077] An example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0078] Cys-Xaa_1-Xaa_2-Xaa_3-Xaa_4-Cys (SEQ ID NO: 1),

[0079] wherein Xaa_1 is Asp, Asn, Ser, Thr, or Trp; Xaa_2 is Asn, Gln, His, lie, Leu, or Lys; Xaa_3 is Ala, Asp, Phe, Trp, or Tyr; and Xaa_4 is Asp, Gly, Leu, Phe, Ser, or Thr.

[0080] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0081] Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Cys-Xaa_8-Xaa_9-Xaa_{10} (SEQ ID NO: 2),

[0082] wherein Xaa_1 is Asn, His, Leu, Phe, Trp, or Val; Xaa_2 is Ala, Glu, His, Lys, Trp, or Val; Xaa_3 is Asp, Gly, Ile, His, Ser, Trp, or Val; Xaa_4 is Asp, Asn, Ser, Thr, or Trp; Xaa_5 is Asn, Gln, His, Ile, Leu, or Lys; Xaa_6 is Ala, Asp, Phe, Trp, or Tyr; Xaa_7 is Asp, Gly, Leu, Phe, Ser, or Thr; Xaa_8 is Glu, Ile, Leu, Met, Ser, or Val; Xaa_9 is Asn, Asp, Gln, Gly, Met, Ser, or Trp; and Xaa_{10} is Ala, Asn, Asp, Pro, Tyr, or Val.

[0083] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0084] Ala-Glu-Gly-Thr-Gly-Ser-Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Cys-Xaa_8-Xaa_9-Xaa_{10}-Ala-Pro-Glu (SEQ ID NO: 3),

[0085] wherein Xaa_1 is Asn, His, Leu, Phe, Trp, or Val; Xaa_2 is Ala, Glu, His, Lys, Trp, or Val; Xaa_3 is Asp, Gly, Ile, His, Ser, Trp, or Val; Xaa_4 is Asp, Asn, Ser, Thr, or Trp; Xaa_5 is Asn, Gln, His, Ile, Leu, or Lys; Xaa_6 is Ala, Asp, Phe, Trp, or Tyr; Xaa_7 is Asp, Gly, Leu, Phe, Ser, or Thr; Xaa_8 is Glu, Ile, Leu, Met, Ser, or Val; Xaa_9 is Asn, Asp, Gln, Gly, Met, Ser, or Trp; and Xaa_{10} is Ala, Asn, Asp, Pro, Tyr, or Val.

[0086] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0087] Cys-Xaa_1-Xaa_2-Xaa_3-Xaa_4-Xaa_5-Xaa_6-Cys (SEQ ID NO: 431)

[0088] wherein Xaa_1 is Ala, Leu, His, Met, Phe, Ser, or Thr; Xaa_2 is Ile, Phe, Pro, Ser, Trp, or Tyr; Xaa_3 is Asp, Gln, Glu, Lys, Pro, Trp, or Tyr; Xaa_4 is Asp, Gln, Gly, Leu, Pro, or Trp; Xaa_5 is Asp, Ile, Leu, Lys, Met, Pro, Trp, or Tyr; and Xaa_6 is Gln, Gly, Ile, Phe, Thr, Trp, or Val.

[0089] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0090] Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaas-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Cys-Xaa_{10}-Xaa_{11}-Xaa_{12} (SEQ ID NO: 99), wherein Xaa_1 is Ala, Gln, Leu, Lys, Phe, Trp, or Tyr;Xaa_2 is Asn, Gln, Glu, Ile, Thr, or Trp; Xaa_3 is Asn, Gly, Phe, Thr, Trp, or Tyr; Xaa_4 is Ala, Leu, His, Met, Phe, Ser, or Thr; Xaa_5 is Ile, Phe, Pro, Ser, Trp, or Tyr; Xaa_6 is Asp, Gln, Glu, Lys, Pro, Trp, or Tyr; Xaa_7 is Asp, Gln, Gly, Leu, Pro, or Trp; Xaa_8 is Asp, Ile, Leu, Lys, Met, Pro, Trp, or Tyr; Xaa_9 is Gln, Gly, Ile, Phe, Thr, Trp, or Val; Xaa_{10} is Asp, Glu, Gly, Leu, Lys, Pro, or Ser; Xaa_{11} is Glu, His, Ile, Leu, Lys, Ser, Trp, or Val; and Xaa_{12} is Ala, Asn, His, Ile, Met, Phe, Pro, or Ser.

[0091] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0092] Ala-Gly-Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Cys-Xaa_{10}-Xaa_{11}-Xaa_{12}-Gly-Thr (SEQ ID NO: 100),

[0093] wherein Xaa_1 is Ala, Gln, Leu, Lys, Phe, Trp, or Tyr; Xaa_2 is Asn, Gln, Glu, Ile, Thr, or Trp; Xaa_3 is Asn, Gly, Phe, Thr, Trp, or Tyr; Xaa_4 is Ala, Leu, His, Met, Phe, Ser, or Thr; Xaa_5 is Ile, Phe, Pro, Ser, Trp, or Tyr; Xaa_6 is Asp, Gln, Glu, Lys, Pro, Trp, or Tyr; Xaa_7 is Asp, Gln, Gly, Leu, Pro, or Trp; Xaa_8 is Asp, Ile, Leu, Lys, Met, Pro, Trp, or Tyr; Xaa_9 is Gln, Gly, Ile, Phe, Thr, Trp, or Val; Xaa_{10} is Asp, Glu, Gly, Leu, Lys, Pro, or Ser; Xaa_{11} is Glu, His, Ile, Leu, Lys, Ser, Trp, or Val; and Xaa_{12} is Ala, Asn, His, Ile, Met, Phe, Pro, or Ser.

[0094] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0095] Cys-Xaa_1-Xaa_2-Xaa_3-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Cys (SEQ ID NO: 101),

[0096] wherein Xaa_1 is Gln, Glu, Phe, or Met; Xaa_2 is Asp, Pro, or Thr; Xaa_3 is Ile, Ser, or Trp; Xaa_4 is His, Met, Phe or Pro; Xaa_5 is Asn, Leu, or Thr; Xaa_6 is Arg, Asn, His, or Thr; Xaa_7 is Arg, Met, Phe, or Tyr; and Xaa_8 is Asp, Gly, Phe, or Trp.

[0097] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0098] Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Cys-Xaa_{12}-Xaa_{13}-Xaa_{14} (SEQ ID NO: 102),

[0099] wherein Xaa_1 is Arg, Phe, or Tyr; Xaa_2 is Arg, Leu, Ser, or Trp; Xaa_3 is Asn, Asp, Phe, or Tyr; Xaa_4 is Gln, Glu, Phe, or Met; Xaa_5 is Asp, Pro, or Thr; Xaa_6 is Ile, Ser, or Trp; Xaa_7 is His, Met, Phe or Pro; Xaa_8 is Asn, Leu, or Thr; Xaa_9 is Arg, Asn, His, or Thr; Xaa_{10} is Arg, Met, Phe, or Tyr; Xaa_{11} is Asp, Gly, Phe, or Trp; Xaa_{12} is Ala, Asn, or Asp; Xaa_{13} is Arg, Phe, Pro, or Tyr; and Xaa_{14} is Arg, His, Phe, or Ser.

[0100] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0101] Gly-Ser-Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Cys-Xaa_{12}-Xaa_{13}-Xaa_{14}-Ala-Pro (SEQ ID NO: 103),

[0102] wherein Xaa_1 is Arg, Phe, or Tyr; Xaa_2 is Arg, Leu, Ser, or Trp; Xaa_3 is Asn, Asp, Phe, or Tyr; Xaa_4 is Gln, Glu, Phe, or Met; Xaa_5 is Asp, Pro, or Thr; Xaa_6 is Ile, Ser, or Trp; Xaa_7 is His, Met, Phe or Pro; Xaa_8 is Asn, Leu, or Thr; Xaa_9 is Arg, Asn, His, or Thr; Xaa_{10} is Arg, Met, Phe, or Tyr; Xaa_{11} is Asp, Gly, Phe, or Trp; Xaa_{12} is Ala, Asn, or Asp; Xaa_{13} is Arg, Phe, Pro, or Tyr; and Xaa_{14} is Arg, His, Phe, or Ser.

[0103] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0104] Cys-Xaa_1-Xaa_2-Xaa_3-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Cys (SEQ ID NO: 4),

[0105] wherein Xaa_1 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_2 is Ala, Arg, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr, or Val; Xaa_3 is Ala, Arg, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_4 is Ala, Arg, Asn, Asp, Ile, Leu, Phe, Pro, Ser, Trp, or Tyr; Xaa_5 is Ala, Asp, Glu, Gly, Ile, Met, Phe, Pro, Thr, Trp, or Tyr; Xaa_6 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Lys, Phe, Ser, Thr, Trp, or Tyr; Xaa_7 is Ala, Arg, Asp, Glu, Gly, His, Met, Phe, Pro, Ser, Thr, or Trp; Xaa_8 is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, or Val; Xaa_9 is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{10} is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

[0106] Another example of a non-naturally occurring, serum albumin-binding agent is a polypeptide comprising the amino acid sequence of:

[0107] Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-Xaa_{13}-Cys-Xaa_{14}-Xaa_{15}-Xaa_{16} (SEQ ID NO: 5),

[0108] wherein Xaa_1 is Ala, Arg, Asp, Asn, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr; Xaa_2 is Ala, Arg, Asp, Asn, Gly, His, Phe, Pro, Ser, or Trp; Xaa_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Met, Phe, Ser, Thr, Trp, Tyr, or Val; Xaa_4 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_5 is Ala, Arg, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr, or Val; Xaa_6 is Ala, Arg, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_7 is Ala, Arg, Asn, Asp, Ile, Leu, Phe, Pro, Ser, Trp, or Tyr; Xaa_8 is Ala, Asp, Glu, Gly, Ile, Met, Phe, Pro, Thr, Trp, or Tyr; Xaa_9 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Lys, Phe, Ser, Thr, Trp, or Tyr; Xaa_{10} is Ala, Arg, Asp, Glu, Gly, His, Met, Phe, Pro, Ser, Thr, or Trp; Xaa_{11} is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, or Val; Xaa_{12} is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{13} is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{14} is Ala, Arg, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, or Tyr; Xaa_{15} is Ala, Arg, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, or Tyr; and Xaa_{16} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, or Tyr.

[0109] Further examples of serum albumin-binding ligands that have the structure of SEQ ID NO: 5, above, include polypeptides comprising the amino acid sequence (A) or (B):

[0110] (A) Xaa_1-Arg-Xaa_2-Cys-Xaa_3-Thr-Xaa_4-Xaa_5-Pro-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Cys-Xaa_{11}-Xaa_{12}-Xaa_{13} (SEQ ID NO: 425),

[0111] wherein Xaa_1 is Asn, Leu, or Phe, preferably Leu; Xaa_2 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Met, Phe, Ser, Thr, Trp, Tyr, or Val; Xaa_3 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_4 is Ala, Arg, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_5 is Phe, Trp, or Tyr, preferably Trp; Xaa_6 is His or Phe, preferably Phe; Xaa_7 is Asp, Glu, or Thr; Xaa_8 is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, or Val; Xaa_9 is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{10} is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{11} is Pro or Ser; Xaa_{12} is Asn or Pro; and Xaa_{13} is Asn or Pro; or

[0112] (B) Xaa_1-Xaa_2-Xaa_3-Cys-Ile-Thr-Xaa_4-Pro-Phe-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Cys-Xaa_{10}-Asn-Xaa_{11} (SEQ ID NO: 426),

[0113] wherein Xaa_1 is Ala, Arg, Asp, Asn, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr; Xaa_2 is Ala, Arg, Asp, Asn, Gly, His, Phe, Pro, Ser, or Trp; Xaa_3 is Glu, Leu, or Met, preferably Met; Xaa_4 is Trp or Tyr, preferably Trp; Xaa_5 is Gln, Glu, or Lys; Xaa_6 is Ala, Arg, Asp, Glu, Gly, His, Met, Phe, Pro, Ser, Thr, or Trp; Xaa_7 is Met, Pro, or Ser, preferably Pro; Xaa_8 is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_9 is His or Pro, preferably Pro; Xaa_{10} is Ala, Arg, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, or Tyr; and Xaa_{11} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, or Tyr.

[0114] Still other non-naturally occurring, serum albumin-binding ligands include a polypeptide comprising the amino acid sequence of:

[0115] Ala-Glu-Gly-Thr-Gly-Xaa_0-Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-Xaa_{13}-Cys-Xaa_{14}-Xaa_{15}-Xaa_{16}-Xaa_{17}-Pro-Glu (SEQ ID NO: 6),

[0116] wherein Xaa_0 is Ala or Asp; Xaa_1 is Ala, Arg, Asp, Asn, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr; Xaa_2 is Ala, Arg, Asp, Asn, Gly, His, Phe, Pro, Ser, or Trp; Xaa_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Met, Phe, Ser, Thr, Trp, Tyr, or Val; Xaa_4 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_5 is Ala, Arg, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr, or Val; Xaa_6 is Ala, Arg, Asp, Gln,

Glu, Gly, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_7 is Ala, Arg, Asn, Asp, Ile, Leu, Phe, Pro, Ser, Trp, or Tyr; Xaa_8 is Ala, Asp, Glu, Gly, Ile, Met, Phe, Pro, Thr, Trp, or Tyr; Xaa_9 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Lys, Phe, Ser, Thr, Trp, or Tyr; Xaa_{10} is Ala, Arg, Asp, Glu, Gly, His, Met, Phe, Pro, Ser, Thr, or Trp; Xaa_{11} is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, or Val; Xaa_{12} is Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{13} is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa_{14} is Ala, Arg, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, or Tyr; Xaa_{15} is Ala, Arg, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, or Tyr; Xaa_{16} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, or Tyr; and Xaa_{17} is Ala or Asp.

[0117] In a further embodiment, the invention provides a non-naturally occurring, serum albumin-binding agent comprising a linear polypeptide comprising an amino acid sequence selected from the group consisting of:

(SEQ ID NO:104)
P T V V Q P K F H A F T H E D L L W I F,

(SEQ ID NO:105)
L K S Q M V H A L P A A S L H D Q H E L, and

(SEQ ID NO:106)
S Q V Q G T P D L Q F T V R D F I Y M F.

[0118] Examples of serum albumin-binding agents include polypeptides that include an amino acid sequence selected from the group consisting of (depicted using the standard single letter abbreviations for the twenty common L-amino acids):

C T I F L C, (SEQ ID NO:7)

C E G K D M I D W V Y C, (SEQ ID NO:8)

C D R I A W Y P Q H L C, (SEQ ID NO:9)

C D R I A W Y P Q H A C, (SEQ ID NO:41)

C D R I A W Y P Q A L C, (SEQ ID NO:42)

C D R I A W Y P A H L C, (SEQ ID NO:43)

C D R I A W Y A Q H L C, (SEQ ID NO:44)

C D R I A W A P Q H L C, (SEQ ID NO:45)

C D R I A A Y P Q H L C, (SEQ ID NO:46)

C D R A A W Y P Q H L C, (SEQ ID NO:47)

C D A I A W Y P Q H L C, (SEQ ID NO:48)

C A R I A W Y P Q H L C, (SEQ ID NO:49)

C E P W M L R F G C, (SEQ ID NO:10)

C D Q W F C, (SEQ ID NO:11)

C N N A L C, (SEQ ID NO:12)

-continued

C D H F F C, (SEQ ID NO:13)

C W H F S C, (SEQ ID NO:14)

C V T R W A N R D Q Q C, (SEQ ID NO:15)

C V T D W A N R H Q H C, (SEQ ID NO:16)

C V K D W A N R R R G C, (SEQ ID NO:17)

C K F S W I R S P A F C, (SEQ ID NO:18)

C Q T T W P F T M M Q C, (SEQ ID NO:107)

C V T M W P F E Q I F C, (SEQ ID NO:108)

C F T Y Y P F T T F S C, (SEQ ID NO:109)

C W T K F P F D L V W C, (SEQ ID NO:110)

C V S Y W P H F V P V C, (SEQ ID NO:111)

C Y I S F P F D Q M Y C, (SEQ ID NO:112)

C S V Q Y P F E V V V C, (SEQ ID NO:113)

C W T Q Y P F D H S T C, (SEQ IID NO:114)

C I T W P F K R P W P C, (SEQ ID NO:115)

C I S W P F E M P F H C, (SEQ ID NO:116)

C I T W P F K R P W P C, (SEQ ID NO:117)

C I T Y P F H E M F P C, (SEQ ID NO: 118)

C I T W P F Q T S Y P C, (SEQ ID NO:119)

C K F S W I R S P A F C, (SEQ ID NO:120)

C W I V D E D G T K W C, (SEQ ID NO:121)

C D S A Y W Q E I P A C, (SEQ ID NO:122)

C L W D P M L C, (SEQ ID NO:123)

C E H P Y W T E V D K C, (SEQ ID NO:124)

C D T P Y W R D L W Q C, (SEQ ID NO:125)

C Q L P Y M S T P E F C, (SEQ ID NO:126)

C G R G F D K E S I Y C, (SEQ ID NO:127)

C V T Y I G T W E T V C, (SEQ ID NO:128)

C T D T N W S W M F D C, (SEQ ID NO:129)

C T L E I G T W F V F C, (SEQ ID NO:130)

C K I A L F Q H F E V C, (SEQ ID NO:131)

C I K L Y G L G H M Y C, (SEQ ID NO:132)

C E M Q S I I P W W E C, (SEQ ID NO:133)

C V E K Y Y W D V L I C, (SEQ ID NO:134)

C P H G R Y S M F P C, (SEQ ID NO:135)

C N V R W T D T P Y W C, (SEQ ID NO:136)

C T Y D P I A D L L F C, (SEQ ID NO:137)

C M D W P N H R D C, (SEQ ID NO:138)

C F P I H L T M F C, (SEQ ID NO:139)

-continued

C Q T S F T N Y W C, (SEQ ID NO:140)

C M E F G P D D C, (SEQ ID NO:141)

C S W D P I F C, (SEQ ID NO: 142)

C A W D P L V C, (SEQ ID NO: 143)

C H I Y D W F C, (SEQ ID NO:144)

C L W D P M I C, (SEQ ID NO:145)

C S P P G K T C, (SEQ ID NO:146)

C T F W Q Y W C, (SEQ ID NO:147)

C M F E L P F C, (SEQ ID NO: 148)

C F S K P D Q C, (SEQ ID NO:149)

C F Y Q W W G C, (SEQ ID NO:150)

C T W D P I F C, (SEQ ID NO:151)

C W L Y D C, (SEQ ID NO:152)

C D K Y G C, and (SEQ ID NO:153)

C S K D T C. (SEQ ID NO: 154)

[0119] Additional examples of serum albumin-binding agents are polypeptides that include an amino acid sequence selected from the group consisting of:

A D F C E G K D M I D W V Y C R L Y, (SEQ ID NO:27)

F W F C D R I A W Y P Q H L C E F L, (SEQ ID NO:28)

F W F C D R I A W Y P Q H L C E F A, (SEQ ID NO:50)

F W F C D R I A W Y P Q H L C E A L, (SEQ ID NO:51)

F W F C D R I A W Y P Q H L C A F L, (SEQ ID NO:52)

F W F C D R I A W Y P Q H A C E F L, (SEQ ID NO:53)

F W F C D R I A W Y P Q A L C E F L, (SEQ ID NO:54)

F W F C D R I A W Y P A H L C E F L, (SEQ ID NO:55)

F W F C D R I A W Y A Q H L C E F L, (SEQ ID NO:56)

F W F C D R I A W A P Q H L C E F L, (SEQ ID NO:57)

F W F C D R I A A Y P Q H L C E F L, (SEQ ID NO:58)

F W F C D R A A W Y P Q H L C E F L, (SEQ ID NO:59)

F W F C D A I A W Y P Q H L C E F L, (SEQ ID NO:60)

F W F C A R I A W Y P Q H L C E F L, (SEQ ID NO:61)

F W A C D R I A W Y P Q H L C E F L, (SEQ ID NO:62)

F A F C D R I A W Y P Q H L C E F L, (SEQ ID NO:63)

A W F C D R I A W Y P Q H L C E F L, (SEQ ID NO:64)

D W D C V T R W A N R D Q Q C W G P, (SEQ ID NO:29)

D W D C V T R W A N R D Q Q C W A L, (SEQ ID NO:30)

D W D C V T D W A N R H Q H C W A L, (SEQ ID NO:31)

-continued

D W Q C V K D W A N R R R G C M A D, (SEQ ID NO:32)

R N M C K F S W I R S P A F C A R A, (SEQ ID NO:33)

L R D C Q T T W P F M M Q C P N N, (SEQ ID NO:155)

N R E C V T M W P F E Q I F C P W P, (SEQ ID NO:156)

L R S C F T Y Y P F T T F S C S P A, (SEQ ID NO:157)

L S H C W T K F P F D L V W C D S P, (SEQ ID NO:158)

L R M C V S Y W P H F V P V C E N P, (SEQ ID NO:159)

L R D C Y I S F P F D Q M Y C S H F, (SEQ ID NO:160)

F R H C S V Q Y P F E V V V C P A N, (SEQ ID NO:161)

L R N C W T Q Y P F D H S T C S P N, (SEQ ID NO:162)

D S M C I T W P F K R P W P C A N, (SEQ ID NO:163)

A F M C I S W P F E M P F H C S P D, (SEQ ID NO:164)

D S M C I T W P F K R P W P C A N P, (SEQ ID NO:165)

W D L C I T Y P F H E M F P C E D G, (SEQ ID NO:166)

G G E C I T W P F Q T S Y P C T N G, (SEQ ID NO:167)

R N M C K F S W I R S P A F C A R A, (SEQ ID NO:168)

F S L C W I V D E D G T K W C L P, (SEQ ID NO:169)

R W F C D S A Y W Q E I P A C A R D, (SEQ ID NO:170)

R W Y C L W D P M L C M S D, (SEQ ID NO:171)

A W Y C E H P Y W T E V D K C H S S, (SEQ ID NO:172)

S D F C D T P Y W R D L W Q C N S P, (SEQ ID NO:173)

L P W C Q L P Y M S T P E F C I R P, (SEQ ID NO:174)

Y H V C G R G F D K E S I Y C K F L, (SEQ ID NO:175)

S F C V T Y I G T W E T V C K R S, (SEQ ID NO:176)

N D G C T D T N W S W M F D C P P L, (SEQ ID NO:177)

W R D C T L E I G T W F V F C K G S, (SEQ ID NO:178)

S P Y C K I A L F Q H F E V C A A D, (SEQ ID NO:179)

R H W C I K L Y G L G H M Y C N R S, (SEQ ID NO:180)

D H A C E M Q S I I P W W E C Y P H, (SEQ ID NO:181)

P R S C V E K Y Y W D V L I C G F F, (SEQ ID NO:182)

F H T C P H G R Y S M F P C D Y W, (SEQ ID NO:183)

H G W C N V R W T D T P Y W C A F S, (SEQ ID NO:184)

Y R V C T Y D P I A D L L F C P F N, (SEQ ID NO:185)

R S F C M D W P N H R D C D Y S, (SEQ ID NO:186)

F W D C F P I H L T M F C D R F, (SEQ ID NO:187)

Y L Y C Q T S F T N Y W C A F H, (SEQ ID NO:188)

G L Y C M E F G P D D C A W H, (SEQ ID NO:189)

K N F C S W D P I F C G I H, (SEQ ID NO:190)

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K W Y C A W D P L V C E I F, (SEQ ID NO:191)

W T T C H I Y D W F C S S S, (SEQ ID NO:192)

Q W Y C L W D P M I C G L I, (SEQ ID NO:193)

Q T N C S P P G K T C D K N, (SEQ ID NO:194)

A I C T F W Q Y W C L E P, (SEQ ID NO:195)

F E W C M F E L P F C S W P, (SEQ ID NO:196)

Q E G C F S K P D Q C K V M, (SEQ ID NO:197)

L E Y C F Y Q W W G C P H A, (SEQ ID NO:198)

Y Q F C T W D P I F C G W H, (SEQ ID NO:199)

L W D C W L Y D C E G N, (SEQ ID NO:200)

V H S C D K Y G C V N A, (SEQ ID NO:201)

F E H C S K D T C S G N, (SEQ ID NO:202)

V A W C T I F L C L D V, (SEQ ID NO:203)

F K I C D Q W F C L M P, (SEQ ID NO:204)

-continued

H V G C N N A L C M Q Y, (SEQ ID NO:205)

W K V C D H F F C L S P, (SEQ ID NO:206)

N H G C W H F S C I W D, (SEQ ID NO:207)

F R N C E P W M L R F G C N P R, (SEQ ID NO:208)

A D F C E G K D M I D W V Y C R L Y, (SEQ ID NO:209)

F W F C D R I A W Y P Q H L C E F L D, (SEQ ID NO:210)

D W D C V T R W A N R D Q Q C W G P, (SEQ ID NO:211)

D W D C V T R W A N R D Q Q C W A L, (SEQ ID NO:212)

D W D C V T D W A N R H Q H C W A L, (SEQ ID NO:213)

D W Q C V K D W A N R R R G C M A D, (SEQ ID NO:214)

R N M C K F S W I R S P A F C A R A D P, (SEQ ID NO:215).

[0120] Additional examples of serum albumin-binding agents include polypeptides that comprising an amino acid sequence selected from the group consisting of:

A E G T G D A D F C E G K D M I D W V Y C R L Y D P E, (SEQ ID NO:34)

A E G T G D F W F C D R I A W Y P Q H L C E F L D P E, (SEQ ID NO:35)

A E G T G D F W F C D R I A W Y P Q H L C E F L A P E, (SEQ ID NO:65)

A E G T G D F W F C D R I A W Y P Q H L C E F A D P E, (SEQ ID NO:66)

A E G T G D F W F C D R I A W Y P Q H L C E A L D P E, (SEQ ID NO:67)

A E G T G D F W F C D R I A W Y P Q H L C A F L D P E, (SEQ ID NO:68)

A E G T G D F W F C D R I A W Y P Q H A C E F L D P E, (SEQ ID NO:69)

A E G T G D F W F C D R I A W Y P Q A L C E F L D P E, (SEQ ID NO:70)

A E G T G D F W F C D R I A W Y P A H L C E F L D P E, (SEQ ID NO:71)

A E G T G D F W F C D R I A W Y A Q H L C E F L D P E, (SEQ ID NO:72)

A E G T G D F W F C D R I A W A P Q H L C E F L D P E, (SEQ ID NO:73)

A E G T G D F W F C D R I A A Y P Q H L C E F L D P E, (SEQ ID NO:74)

A E G T G D F W F C D R A A W Y P Q H L C E F L D P E, (SEQ ID NO:75)

A E G T G D F W F C D A I A W Y P Q H L C E F L D P E, (SEQ ID NO:76)

A E G T G D F W F C A R I A W Y P Q H L C E F L D P E, (SEQ ID NO:77)

A E G T G D F W A C D R I A W Y P Q H L C E F L D P E, (SEQ ID NO:78)

A E G T G D F A F C D R I A W Y P Q H L C E F L D P E, (SEQ ID NO:79)

A E G T G D A W F C D R I A W Y P Q H L C E F L D P E, (SEQ ID NO:80)

A E G T G A F W F C D R I A W Y P Q H L C E F L D P E, (SEQ ID NO:81)

A E G T G D D W D C V T R W A N R D Q Q C W G P D P E, (SEQ ID NO:36)

A E G T G D D W D C V T R W A N R D Q Q C W A L D P E, (SEQ ID NO:37)

A E G T G D D W D C V T D W A N R H Q H C W A L D P E, (SEQ ID NO:38)

-continued

A E G T G D D W Q C V K D W A N R R R G C M A D D P E, (SEQ ID NO:39)
and

A E G T G D R N M C K F S W I R S P A F C A R A D P E. (SEQ ID NO:40)

[0121] Particular examples of a serum albumin-binding agents are polypeptides that include a compound of the formula:

[0122] AEGTGDFWFCDRIAWYPQHLCEFLD-PEGGGK(SEQ ID NO: 19). This polypeptide is designated DX-236.

[0123] DX-236 binds mammalian serum albumins and is useful under appropriate conditions as a "pan mammalian" serum albumin-binding agent. DX-236 variants that include between one and five amino acid changes (substitutions, insertions, or deletions), e.g., between one and three, or one or two,; or between one and six conservative amino acid substitutions, e.g., between one and four, one and three, or one and two; and that bind to a serum albumin can also be used. The following two DX-236 variants can be used: DX-236A which includes the peptide sequence: FWFCDRI-AWYPQHLCEFLD (SEQ ID NO: 210) and DX-236B which includes the peptide sequence:

[0124] CDRIAWYPQHLC (SEQ ID NO: 9)

[0125] DX-236 can also include additional chemical modifications, for example:

[0126] Ac-AEGTGDFWFCDRIAWYPQHLCE-FLDPEGGGK—NH_2 (SEQ ID NO: 19), wherein Ac indicates an N-terminal acetyl capping group and —NH_2 indicates a C-terminal amide capping group. Examples of DX-236 variants include compounds that include the following sequences:

[0127] AEGTGDFWFCDRIAWYPQHLCEFLA-PEGGGK—,

[0128] AEGTGDFWFCDRIAWYPQHLCEFAD-PEGGGK—,

[0129] AEGTGDFWFCDRIAWYPQHLCEALD-PEGGGK—,

[0130] AEGTGDFWFCDRIAWYPQHLCAFLD-PEGGGK—,

[0131] AEGTGDFWFCDRIAWYPQHACEFLD-PEGGGK—,

[0132] AEGTGDFWFCDRIAWYPQALCEFLD-PEGGGK—,

[0133] AEGTGDFWFCDRIAWYPAHLCEFLD-PEGGGK—,

[0134] AEGTGDFWFCDRIAWYAQHLCEFLD-PEGGGK—,

[0135] AEGTGDFWFCDRIAWAPQHLCEFLD-PEGGGK—,

[0136] AEGTGDFWFCDRIAAYPQHLCEFLD-PEGGGK—,

[0137] AEGTGDFWFCDRAAWYPQHLCE-FLDPEGGGK—,

[0138] AEGTGDFWFCDAIAWYPQHLCEFLD-PEGGGK—,

[0139] AEGTGDFWFCARIAWYPQHLCEFLD-PEGGGK—,

[0140] AEGTGDFWACDRIAWYPQHLCEFLD-PEGGGK—,

[0141] AEGTGDFAFCDRIAWYPQHLCEFLD-PEGGGK—,

[0142] AEGTGDAWFCDRIAWYPQHLCEFLD-PEGGGK—, and

[0143] AEGTGAFWFCDRIAWYPQHLCEFLD-PEGGGK—,

[0144] (SEQ ID NOs: 82 through 98, respectively). The variants can further include an N— or C-terminal modification. Exemplary variants have between one and six, one and five, one and four, or one and three amino acid substitutions, e.g., one or two amino acid substitutions. Other variants include one, two, three, or less than five amino acid insertions, deletions, or substitutions.

[0145] Additional serum albumin-binding agents include the following:

[0146] GDLRDCQTTWPFTMMQCPNND-PGGGK—,

[0147] GDNRECVTMWPFEQIFCPWPD-PGGGK—,

[0148] GDLRSCFTYYPFTTFSCSPADP GGGK—,

[0149] GDDSMCITWPFKRPWPCANDPGGGK—,

[0150] GDRNMCKFSWIRSPAFCARAD-PGGGK—,

[0151] GDFSLCWIVDEDGTKWCLPDPGGGK—,

[0152] GDRWFCDSAYWQEIPACARD-DPGGGK—,

[0153] GDSDFCDTPYWRDLWQCNSPD-PGGGK—,

[0154] GDSFCVTYIGTWETVCKRSDPGGGK—,

[0155] GDNDGCTDTNWSWMFDCPPLD-PGGGK—,

[0156] GDSPYCKIALFQHFEVCAAD-DPGGGK—,

[0157] GDPRSCVEKYYWDVLICGFFD-PGGGK—,

[0158] GSRSFCMDWPNHRDCDYSAPGGGK—,

[0159] AGKWYCAWDPLVCEIFGTGGGK—,

[0160] AGWTTCHIYDWFCSSSGTGGGK—,

[0161] AGLEYCFYQWWGCPHAGTGGGK—,

[0162] AGYQFCTWDPIFCGWHGTGGGK—, and

[0163] GSLWDCWLYDCEGNAPGGGK—,

[0164] (SEQ ID NOs: 216 through 233, respectively).

[0165] Another particular serum albumin-binding agent is a compound that includes: AEGTGDRNMCKFSWIRSPAF-CARADPE (SEQ ID NO: 20). This binding moiety is designated polypeptide compound DX-321. Dx-321 can also be modified, e.g., as follows:

[0166] Ac-AEGTGDRNMCKFSWIRSPAF-CARADPE-X—K—NH_2 (SEQ ID NO: 24), wherein Ac indicates an N-terminal acetyl capping group, X (above) indicates a polypeptide linked 6-aminohexanoic acid group, and —NH_2 indicates a C-terminal amide capping group. DX-321 preferentially binds human serum albumin (HSA) over serum albumins from other species under appropriate conditions. DX-321 is useful as a reagent to specifically detect or isolate HSA. In some embodiments, the compounds do not include the N-terminal acetyl capping group, and may or may not include a C-terminal amide capping group.

[0167] DX-321 variants that include between one and five amino acid changes (substitutions, insertions, or deletions), e.g., between one and three, or one or two,; or between one and six conservative amino acid substitutions, e.g., between one and four, one and three, or one and two; and that bind to a serum albumin can also be used. The following DX-321 variants can also be used: DX-321-A which includes the peptide sequence: RNMCKFSWIRSPAFCARA (SEQ ID NO: 430); and DX-321-B which includes the peptide sequence: CKFSWIRSPAFC (SEQ ID NO: 120).

[0168] Examples of specific immunoglobulin binding molecules (which bind the Fc region of immunoglobulin) include polypeptides comprising amino acid sequences of the following four general formulae:

Z1-X1-X2-X3-X4-W—C-Z2 (SEQ ID NO: 234); I.

[0169] wherein, Z1 is a polypeptide of at least 6 amino acids; X1 is G, H, N, R, or S;

[0170] X2 is A, D, E, F, I, M, or S; X3 is A, I, L, M, or V; X4 is I, M, T, or V; Z2 is a polypeptide of at least one amino acid or is absent; and Z1 contains at least one cysteine residue such that formation of a disulfide bond with the invariant cysteine residue forms a cyclic peptide of 12 amino acids.

Z1-X—W-Z2-W-Z3 (SEQ ID NO: 235) II.

[0171] wherein, Z1 is a polypeptide of at least one amino acid or is absent;

[0172] X is F or Y; Z2 is a tripeptide; and Z3 is a polypeptide of at least one amino acid; and

[0173] wherein at least two of the polypeptides Z1, Z2, and Z3 contain a cysteine residue, such that formation of a disulfide bond between such cysteine residues forms a cyclic peptide of 7-12 amino acids.

[0174] In the foregoing formula II polypeptides, Z2 can have the formula (IIA):

X1-X2-X3 (IIA),

[0175] wherein, X1 is A, C, F, K, P, R, W, or Y; X2 is C, D, E, G, H, K, M, N, Q, R, S, T, V, or Y; and X3 is A, E, F, H, I, K, L, Q, R, S, T, V, or Y; with the proviso that at most one of X1, X2 and X3 can be C. In some implementations, where X2 is C, then X1 is Y. In some implementations, X1 is C.

Z1-W-Z2-W—W-Z3 (SEQ ID NO: 236); III.

[0176] wherein, Z1 is a polypeptide of at least one amino acid; Z2 is a tripeptide; and Z3 is a polypeptide of at least one amino acid; wherein at least two of the polypeptides Z 1, Z2, and Z3 contain a cysteine residue, such that formation of a disulfide bond between such cysteine residues forms a cyclic peptide of 8-12 amino acids, with the proviso that where Z1 contains a cysteine, then Z2 does not contain a cysteine, and where Z2 contains a cysteine, it is the middle residue of the tripeptide and Z3 also contains a cysteine.

[0177] In some cases, for the polypeptides of formula III, when Z1 and Z3 each contain a cysteine residue, the cysteine of Z1 is adjacent the invariant tryptophan (W), the first amino acid of Z2 is lysine and the second amino acid of Z3 is aspartic acid (D).

Z1-P—X1-W—X2-C—X3-X4-X5 (SEQ ID NO: 237); IV.

[0178] wherein, Z1 is a polypeptide of at least one amino acid and includes a cysteine residue; X1 is A, E, R, S, or T; X2 is F, W, or Y; X3 is D, E, L, M, or Q; X4 is H, W, or Y;

[0179] X5 is F or Y; and wherein the cysteine residue in Z1 and the cysteine residue between X2 and X3 form a cyclic peptide of 10-12 amino acids.

[0180] Examples of immunoglobulin binding polypeptides include polypeptides comprising amino acid sequences selected from the group consisting of:

R-R-A-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:238)

W-G-E-C-T-V-T-S-Y-G-E-L-I-W-C-G-G-L (SEQ ID NO:239)

S-S-A-C-A-F-D-P-M-G-A-V-W-C-T-Y-D (SEQ ID NO:240)

L-L-E-C-A-Y-N-T-S-G-E-L-I-W-C-N-G-S (SEQ ID NO:241)

P-D-D-C-S-I-H-F-S-G-E-L-I-W-C-E-P-L (SEQ ID NO:242)

L-G-E-C-T-V-T-S-Y-G-E-L-I-W-C-G-G-L (SEQ ID NO:243)

W-G-E-C-T-V-T-S-Y-G-E-L-I-W-C-G-G-H (SEQ ID NO:244)

D-H-M-C-V-Y-T-T-W-G-E-L-I-W-C-D-D-H (SEQ ID NO:245)

W-G-E-C-T-V-T-S-Y-G-E-L-I-W-C-G-G-L (SEQ ID NO:246)

C-R-A-C-S-R-D-W-P-G-A-L-V-W-C-A-G-H (SEQ ID NO:247)

R-R-A-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:248)

L-H-A-C-A-F-D-P-M-G-A-V-I-W-C-T-Y-D (SEQ ID NO:249)

D-H-M-C-V-Y-T-T-W-G-E-L-M-W-C-D-N-H (SEQ ID NO:250)

P-P-T-C-T-W-D-W-Q-G-I-L-V-W-C-S-G-H (SEQ ID NO:251)

S-N-K-C-S-N-T-W-D-G-S-L-I-W-C-S-A-N (SEQ ID NO:252)

F-P-E-C-T-F-D-M-E-G-F-L-I-W-C-S-S-F (SEQ ID NO:253)

H-D-L-C-A-Q-A-P-F-G-D-A-T-W-C-D-L-R (SEQ ID NO:254)

P-N-H-C-S-Y-N-L-K-S-E-L-I-W-C-Q-D-L (SEQ ID NO:255)

P-L-D-C-A-R-D-I-H-N-S-L-I-W-C-S-L-G (SEQ ID NO:256)

-continued

G-S-E-C-S-W-T-S-L-N-E-L-I-W-C-A-H-W (SEQ ID NO:257)

W-P-D-C-S-F-T-V-Q-R-D-L-I-W-C-E-A-L (SEQ ID NO:258)

S-H-S-C-A-Y-D-Y-A-H-M-L-V-W-C-T-H-F (SEQ ID NO:259)

D-H-M-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:260)

R-P-N-C-T-F-A-A-S-G-E-L-I-W-C-M-H-Y (SEQ ID NO:261)

W-W-G-C-Q-F-D-W-R-G-E-L-V-W-C-P-Y-L (SEQ ID NO:262)

G-G-V-C-S-Y-S-G-M-G-E-I-V-W-C-R-W-F (SEQ ID NO:263)

A-L-M-C-S-H-D-M-W-G-S-L-I-W-C-K-H-F (SEQ ID NO:264)

W-W-N-C-H-N-G-W-T-W-T-G-G-W-C-W-W-F (SEQ ID NO:265)

Y-H-V-C-A-R-D-S-W-D-Q-L-I-W-C-E-A-F (SEQ ID NO:266)

N-Y-W-C-N-F-W-Q-L-P-T-C-D-N-L (SEQ ID NO:267)

Y-W-Y-C-K-W-F-S-E-S-A-S-C-S-S-R (SEQ ID NO:268)

Y-W-Y-C-K-W-F-E-D-K-H-P-C-D-S-S (SEQ ID NO:269)

Y-W-Y-C-S-W-F-P-D-R-P-D-C-P-L-Y (SEQ ID NO:270)

N-Y-W-C-N-V-W-L-L-G-D-V-C-R-S-H (SEQ ID NO:271)

L-Y-W-C-H-V-W-F-G-Q-H-A-W-Q-C-K-Y-P (SEQ ID NO:272)

Y-W-K-C-K-W-M-P-W-M-C-G-F-D (SEQ ID NO:273)

D-D-H-C-Y-W-F-R-E-W-F-N-S-E-C-P-H-G (SEQ ID NO:274)

N-Y-W-C-N-I-W-G-L-H--G-C-N-S-H (SEQ ID NO:275)

Y-W-F-C-Q-W-F-S-Q-N-H-T-C-F-R-D (SEQ ID NO:276)

H-Y-W-C-D-I-W-F-G-A-P-A-C-Q-F-R (SEQ ID NO:277)

S-G-D-C-G-F-W-P-R-I-W-G-L-C-M-D-N (SEQ ID NO:278)

F-W-Y-C-K-W-F-Y-E-D-A-Q-C-S-H-D (SEQ ID NO:279)

Y-Y-W-C-N-Y-W-G-L-C-P-D-Q (SEQ ID NO:280)

S-Y-W-C-K-I-W-D-V-C-P-Q-S (SEQ ID NO:281)

K-Y-W-C-N-L-W-G-V-C-P-A-N (SEQ ID NO:282)

Q-Y-W-C-Y-Q-W-G-L-C-G-A-N (SEQ ID NO:283)

K-Y-W-C-Q-Q-W-G-V-C-N-G-S (SEQ ID NO:284)

K-Y-W-C-V-Q-W-G-V-C-P-E-S (SEQ ID NO:285)

K-Y-W-C-M-Q-W-G-L-C-G-W-E (SEQ ID NO:286)

H-F-W-C-E-V-W-G-L-C-P-S-I (SEQ ID NO:287)

Q-Y-W-C-T-K-W-G-L-C-T-N-V (SEQ ID NO:288)

A-Y-W-C-K-V-W-G-L-C-Q-G-E (SEQ ID NO:289)

K-Y-W-C-N-L-W-G-V-C-P-A-N (SEQ ID NO:290)

Q-Y-W-C-N-V-W-G-V-C-L-P-S (SEQ ID NO:291)

H-Y-W-C-Q-Q-W-G-I-C-E-R-P (SEQ ID NO:292)

R-Y-W-C-N-I-W-D-V-C-P-E-Q (SEQ ID NO:293)

Q-Y-W-C-T-H-W-G-L-C-G-K-Y (SEQ ID NO:294)

-continued

T-Y-W-C-T-K-W-G-L-C-P-H-N (SEQ ID NO:295)

F-Y-W-C-G-Q-W-G-L-C-A-P-P (SEQ ID NO:296)

G-Y-W-C-N-V-W-G-L-C-S-T-E (SEQ ID NO:297)

R-Y-W-C-G-V-W-G-V-C-E-I-D (SEQ ID NO:298)

K-F-W-C-T-I-W-G-V-C-H-M-P (SEQ ID NO:299)

H-Y-W-C-Q-Q-W-G-I-C-E-R-P (SEQ ID NO:300)

R-Y-W-C-N-I-W-D-V-C-P-E-Q (SEQ ID NO:301)

F-Y-W-C-S-Q-W-G-L-C-K-Y-D (SEQ ID NO:302)

H-Y-W-C-E-K-W-G-L-C-L-M-S (SEQ ID NO:303)

H-Y-W-C-Q-K-W-G-V-C-P-T-D (SEQ ID NO:304)

H-Y-W-C-S-L-W-G-V-C-D-I-N (SEQ ID NO:305)

R-F-W-C-S-A-W-G-V-C-P-A (SEQ ID NO:306)

S-Y-W-C-K-I-W-D-V-C-P-Q-S (SEQ ID NO:307)

Q-Y-W-C-S-I-W-K-V-C-P-G-R (SEQ ID NO:308)

Y-W-Y-C-E-W-F-G-A-C-I-N-D (SEQ ID NO:309)

E-Y-W-C-K-Y-W-G-L-E-C-V-H-R (SEQ ID NO:310)

K-Y-W-C-T-Q-W-G-L-K-C-D-K-Q (SEQ ID NO:311)

K-Y-W-C-S-F-W-G-L-Q-C-K-T (SEQ ID NO:312)

R-Y-W-C-N-F-W-G-V-N-C-D-A-N (SEQ ID NO:313)

N-Y-W-C-T-H-W-G-V-M-C-L-D-H (SEQ ID NO:314)

Y-W-F-C-K-W-F-P-S-Q-C-Q-F-M (SEQ ID NO:315)

A-Y-W-C-K-Q-W-G-L-K-C-Q-L-G (SEQ ID NO:316)

K-Y-W-C-K-F-W-G-L-E-C-K-V-G (SEQ ID NO:317)

N-Y-W-C-T-E-W-G-L-N-C-N-N-K (SEQ ID NO:318)

S-Y-W-C-E-K-W-G-L-T-C-E-T-H (SEQ ID NO:319)

E-Y-W-C-R-I-W-G-L-Q-C-N-M-V (SEQ ID NO:320)

K-Y-W-C-K-K-W-G-V-N-C-D-F-N (SEQ ID NO:321)

K-Y-W-C-S-V-W-G-V-Q-C-P-H-S (SEQ ID NO:322)

F-Y-W-C-T-K-W-G-L-E-C-I-H-S (SEQ ID NO:323)

H-Y-W-C-Q-Q-W-G-L-M-C-F-E-T (SEQ ID NO:324)

K-Y-W-C-K-R-W-G-L-M-C-N-G-G (SEQ ID NO:325)

A-Y-W-C-M-T-W-G-V-P-C-I-S-W (SEQ ID NO:326)

K-Y-W-C-K-K-W-G-V-N-C-D-F-N (SEQ ID NO:327)

K-Y-W-C-S-V-W-G-V-Q-C-P-D-S (SEQ ID NO:328)

K-Y-W-C-S-V-W-G-V-Q-C-P-H-S (SEQ ID NO:329)

L-Y-W-C-T-K-W-G-V-T-C-Q-K-D (SEQ ID NO:330)

T-Y-W-C-H-K-W-G-V-K-C-A-T-T (SEQ ID NO:331)

T-Y-W-C-T-F-W-E-L-P-C-D-P-A (SEQ ID NO:332)

K-Y-W-C-T-K-W-Q-L-N-C-E-E-V (SEQ ID NO:333)

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N-Y-W-C-H-F-W-Q-V-P-C-L-E-Q (SEQ ID NO:334)

T-Y-W-C-V-V-W-N-V-P-C-S-T-D (SEQ ID NO:335)

N-F-W-C-H-T-W-G-L-Q-C-N-D-L (SEQ ID NO:336)

F-W-Y-C-Y-W-F-N-E-K-C-K-T-P (SEQ ID NO:337)

G-F-W-C-T-F-W-G-V-T-C-E-A-G (SEQ ID NO:338)

P-H-N-C-D-D-H-Y-W-Y-C-K-W-F (SEQ ID NO:339)

E-M-T-C-S-S-H-Y-W-Y-C-T-W-M (SEQ ID NO:340)

H-I-D-C-K-T-N-Y-W-W-C-R-W-T (SEQ ID NO:341)

E-M-R-C-G-Q-H-F-W-Y-C-E-W-F (SEQ ID NO:342)

N-Y-W-C-N-F-W-Q-L-P-T-C-D-N-L (SEQ ID NO:343)

Y-W-Y-C-Q-W-F-Q-E-V-N-K-C-F-N-S (SEQ ID NO:344)

Y-Y-W-C-R-H-W-F-P-D-F-D-C-V-H-S (SEQ ID NO:345)

Y-W-Y-C-S-W-F-P-D-R-P-D-C-P-L-Y (SEQ ID NO:346)

Y-W-Y-C-V-W-F-D-N-A-D-Q-C-V-H-H (SEQ ID NO:347)

A-A-T-C-S-T-S-Y-W-Y-Y-Q-W-F-C-T-D-S (SEQ ID NO:348)

Y-W-A-C-V-W-G-L-K-S-C-V-D-R (SEQ ID NO:349)

Y-W-R-C-V-W-F-P-A-S-C-P-T (SEQ ID NO:350)

D-W-Q-C-L-W-W-G-N-S-F-W-P-Y-C-A-N-L (SEQ ID NO:351)

F-W-R-C-H-W-W-P-E-R-C-P-V-D (SEQ ID NO:352)

N-P-M-C-W-K-K-S-W-W-E-D-A-Y-C-I-N-H (SEQ ID NO:353)

S-W-V-C-W-K-A-K-W-W-E-D-K-R-C-A-P-F (SEQ ID NO:354)

S-R-Q-C-W-K-E-L-W-W-T-D-Q-M-C-L-D-L (SEQ ID NO:355)

S-F-R-C-Q-S-S-F-P-S-W-Y-C-D-Y-Y (SEQ ID NO: 356)

S-W-H-C-Q-N-T-Y-P-E-W-Y-C-Q-W-Y (SEQ ID NO:357)

G-S-K-C-K-Q-T-G-F-P-R-W-W-C-E-H-Y (SEQ ID NO:358)

D-G-V-C-G-P-R-G-F-G-P-A-W-F-C-M-H-Y (SEQ ID NO:359)

Y-S-H-C-A-T-H-Y-P-T-W-Y-C-L-H-F (SEQ ID NO:360)

F-C-N-C-W-G-S-H-E-F-T-F-C-V-D-D (SEQ ID NO:361)

P-G-W-C-Y-S-D-I-W-G-F-K-H-F-C-N-L-D (SEQ ID NO:362)

D-S-S-C-I-K-H-H-N-K-V-T-C-F-F-P (SEQ ID NO:363)

R-W-S-C-W-G-V-W-G-C-V-W-V (SEQ ID NO:364)

P-V-D-C-K-H-H-F-W-W-C-Y-W-N (SEQ ID NO:365)

S-W-N-C-A-F-H-H-N-E-M-V-W-C-D-D-G (SEQ ID NO:366)

Y-W-Y-C-W-F-P-D-R-P-E-C-P-L-Y (SEQ ID NO:367)

N-P-M-C-W-R-A-S-W-W-E-D-A-Y-C-I-N-H (SEQ ID NO:409)

N-P-M-C-W-R-A-H-W-W-E-D-A-Y-C-I-N-H (SEQ ID NO:410)

E-H-M-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:411)

A-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:412)

-continued

T-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:413)

E-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:414)

V-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:415)

[Nle]-C-V-Y-T-T-W-G-E-L-I-W-C-D-N-H (SEQ ID NO:416)

S-R-A-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:417)

E-R-A-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:418)

A-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:419)

T-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:420)

E-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H (SEQ ID NO:421)

V-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H and (SEQ ID NO:422)

G-C-S-R-D-W-S-G-A-L-V-W-C-A-G-H. (SEQ ID NO:423)

[0181] N-terminal and/or C-terminal truncations of the above Fc-region binding polypeptides can also be used, particularly cyclic polypeptides that retain binding affinity for antibody Fc-regions.

[0182] Fc-region binding molecules according to the above formulae can include the following: polypeptides of formula I, in which X1 is G; X2 is A or E; X3 is L; and X4 is I or V; polypeptides of formula II, in which X is F or Y; and in the tripeptide of formula IIA, X1 is C or Y; X2 is C, K, N or T; and X3 is F, I, K, Q or V.

[0183] Particular examples of immunoglobulin binding molecules include proteins that include the following polypeptides:

RRACSRDWSGALVWCAGH; (SEQ ID NO:238)

DHMCVYTTWGELIWCDNH; (SEQ ID NO:260)

KYWCSFWGLQCKT; (SEQ ID NO:312)

PVDCKHHFWWCYWN; (SEQ ID NO:365)

DDHCYWFREWFNSECPHG; (SEQ ID NO:274)

YYWCNYWGLCPDQ; (SEQ ID NO:280)

PHNCDDHYWYCKWF; (SEQ ID NO:339)

SYWCKIWDVCPQS; (SEQ ID NO:281)

KYWCNLWGVCPAN; (SEQ ID NO:282)

AATCSTSYWYYQWFCTDS; (SEQ ID NO:348)

TYWCTFWELPCDPA; (SEQ ID NO:332)

YWYCWFPDRPECPLY; (SEQ ID NO:367)

SWVCWKAKWWEDKRCAPF; (SEQ ID NO:354)

NPMCWKKSWWEDAYCINH; and (SEQ ID NO:353)

SWNCAFHHNEMVWCDDG. (SEQ ID NO:366)

[0184] Still other exemplary polypeptides can have the following sequences, and may include optional amino-terminal (e.g., acetylation) and carboxy-tenninal modifications (e.g., amidation):

GDDHMCVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:368, designated DX249)

AGKYWCSFWGLQCKTGTPGPEGGGK; (SEQ ID NO:370, designated DX250)

AGPVDCKHHFWWCYWNGTPGPEGGGK; (SEQ ID NO:377, designated DX251)

GDDDHCYWFREWFNSECPHGEPGPEGGGK; (SEQ ID NO:378, designated DX252)

GDRRACSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:369, designated DX253)

AGYYWCNYWGLCPDQGTPGPEGGGK; (SEQ ID NO:379, designated DX254)

AGPHNCDDHYWYCKWFPGPEGGGK; (SEQ ID NO374, designated DX389)

AGSYWCKIWDVCPQSPGPEGGGK; (SEQ ID NO:371, designated DX392)

AGKYWCNLWGVCPANPGPEGGGK; (SEQ ID NO:372, designated DX395)

AGAATCSTSYWYYQWFCTDSPGPEGGGK; (SEQ ID NO:375, designated DX398)

AGTYWCTFWELPCDPAPGPEGGGK; (SEQ ID NO:373, designated DX404)

AGYWYCWFPDRPECPLYPGPEGGGK; (SEQ ID NO:376, designated DX413)

GDSWVCWKAKWWEDKRCAPFGTPGPEGGGK; (SEQ ID NO:380, designated DX595)

GDNPMCWKKSWWEDAYCINHGTPGPEGGGK; (SEQ ID NO:381, designated DX596)

GDSWNCAFHHNEMVWCDDGGTPGPEGGGK; (SEQ ID NO:382, designated DX597)

GDWGECTVTSYGELIWCGGLEPGPEGGGK; (SEQ ID NO:383, designated DX1070)

GDNPMCWRASWWEDAYCINHEPGPEGGGK; (SEQ ID NO:384, designated DX1071)

GDNPMCWRAHWWEDAYCINHEPGpPGGGK; (SEQ ID NO:385, designated DX1072)

GDDHMCVYTTWGELIWCDNHEPGPEG-J-NH2
(SEQ ID NO:386, designated DX877)

GDDHMCVYTTWGELIWCDNHEPG-J-Su-J-NH2
(SEQ ID NO:387, designated DX878)

GDDHMCVYTTWGELIWCDNHEPG-J-Z-J-NH2
(SEQ ID NO:388, designated DX905)

GDDHMCVYTTWGELIWCDNH-J-NH2 (SEQ ID
NO:389, designated DX907)

GDDHMCVYTTWGELIWCDNH-J-Su-J-NH2 (SEQ
ID NO:390, designated DX909)

GDDHMCVYTTWGELIWCDNH-J-Z-J-NH2 (SEQ
ID NO:391, designated DX911)

DHMCVYTTWGELIWCDNHEPEGGGK; (SEQ ID NO:392, designated DX1062)

EHMCVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:393, designated DX1063)

ACVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:394, designated DX1064)

TCVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:395, designated DX1065)

ECVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:396, designated DX1066)

VCVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:397, designated DX1067)

Ac-[Nle]CVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:398, designated DX1068)

CVYTTWGELIWCDNHEPGPEGGGK; (SEQ ID NO:399, designated DX1069)

SRACSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:400, designated DX1139)

RRACSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:401, designated DX1142)

ERACSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:402, designated DX1141)

ACSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:403, designated DX1142)

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TCSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:404, designated DX1143)

ECSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:405, designated DX1144)

VCSRDWSGALVWCAGHEPGPEGGGK; (SEQ ID NO:406, designated DX1145)

GCSRDWSGALVWCAGHEPGPEGGGK; and (SEQ ID NO:407, designated DX1146)

CSRDWSGALVWCAGHEPGPEGGGK-NH2. (SEQ ID NO:408, designated DX1147)

[0185] With respect to the foregoing polypeptides, the polypeptides can further include a chemical modification, e.g., N-terminal acetylation and/or C-terminal amidation: e.g., one of the following: -J-NH_2 denotes the C-terminal group —NH—$(CH_2CH_2O)_2$—CH_2CH_2—NH_2, -J-Su-J-NH_2 denotes the C-terminal group —NH—$(CH_2CH_2O)_2$—CH_2CH_2—NH—C:O—CH_2CH_2—C:O—NH$(CH_2CH_2O)_2$—CH_2CH_2—NH_2, -J-Z-J-NH_2 denotes the C-terminal group —NH—$(CH_2CH_2O)_2$—CH_2CH_2—NH—C:O—CH_2—O—$(CH_2CH_2O)_2$—CH_2—C:O NH—$(CH_2CH_2O)_2$—CH_2CH_2—NH_2, and [Nle] denotes norleucine.

[0186] The immunoglobulin binding polypeptides can have high affinity (e.g., K_D in the range 10 μM to 0.01 μM, more preferably in the range 1.0 μM to 0.01 μM) for human Fc polypeptides or particular IgG isotypes (e.g., IgGI, IgG2, IgG3 and/or IgG4). Some polypeptides also show species specificity (e.g., binding to human but not other mammalian IgGs). For example:

[0187] DX249 exhibits dissociation constants (K_D) for human IgGI of less than 0.1 μM at pH 5.7 and less than 0.5 μM at pH 7.4;

[0188] DX252 exhibits dissociation constants (K_D) for human IgG3 of less than 0.1 μM at pH 5.7 and in the range of 2.1 μM to 3.4 μM for IgGI, IgG2, IgG3, and IgG4 at pH 7.4;

[0189] DX253 exhibits quantitative binding of Fc protein (capture efficiency >90% of total load) from buffer solution and tobacco extract;

[0190] DX254 exhibits dissociation constants (K_D) for human IgG1 of less than 0.1 μM at pH 5.7, less than 2.0 μM at pH 7.4, and less than 1.0 μM at pH 9.3;

[0191] DX301 exhibits dissociation constants below about 10 μM for human Fe, IgG1, IgG2 and IgG4; and

[0192] DX300 exhibits a dissociation constant of 4.1±4.6 for human IgG3. Variants of the above peptides can also be used, including the segment DX249-A, DHMCVYTTWGELIWCDNH (SEQ ID NO: 260); the segment DX253-A, RRACSRDWSGALVWCAGH (SEQ ID NO: 238); and AATCSTSYWYYQWFCTDS (SEQ ID NO: 348).

[0193] The term "associated" refers to a direct or indirect physical attachment between compounds. Attachments can be mediated by a covalent or non-covalent interaction. An indirectly physical attachment refers to, for example, a case where two compounds are not in direct contact with each other, but each contact one or more intermediary compounds.

[0194] The term "polypeptide" refers to a polymer of three or more amino acids linked by a peptide bond. The polypeptide may include one or more unnatural amino acids. Typically, the polypeptide includes only natural amino acids. The term "peptide" refers to a polypeptide that is between three and thirty-two amino acids in length. A protein can include one or more polypeptide chains.

[0195] The term "antibody" as used herein refers to an immunoglobulin molecule or immunologically active portion thereof, i.e., an antigen-binding portion. An antibody can include at least one, and preferably two, heavy (H) chain variable regions (abbreviated herein as VH), and at least one and preferably two light (L) chain variable regions (abbreviated herein as VL). The VH and VL regions can be further subdivided into regions of hypervariability, termed "complementarity determining regions" ("CDR"), interspersed with regions that are more conserved, termed "framework regions" (FR). The extent of the framework region and CDR's has been precisely defined (see, Kabat, E. A., et al. (1991) *Sequences of Proteins of Immunological Interest, Fifth Edition*, U.S. Department of Health and Human Services, NIH Publication No. 91-3242, and Chothia, C. et al. (1987) J. Mol. Biol. 196:901-917). Each VH and VL is composed of three CDR's and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

[0196] As used herein, the term "immunoglobulin" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. Some human immunoglobulin genes include the kappa, lambda, alpha (IgA1 and IgA2), gamma (IgG1, IgG2, IgG3, IgG4), delta, epsilon and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Full-length immunoglobulin "light chains" (about 25 KDa or 214 amino acids) are encoded by a variable region gene at the NH_2-terminus (about 110 amino acids) and a kappa or lambda constant region gene at the COOH—terminus. Full-length immunoglobulin "heavy chains" (about 50 KDa or 446 amino acids), are similarly encoded by a variable region gene (about 116 amino acids) and one of the other aforementioned constant region genes, e.g., gamma (encoding about 330 amino acids).

[0197] The term "antigen-binding fragment" of an antibody (or simply "antibody portion," or "fragment"), as used herein, refers to one or more fragments of a full-length antibody that retain the ability to specifically bind to the antigen. Examples of antigen-binding fragments include, but are not limited to: (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region;

(iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) *Science* 242:423-426; and Huston et al (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883). Such single chain antibodies are also encompassed within the term "antigen-binding fragment" of an antibody. These antibody fragments are obtained using conventional techniques (including immunization, phage display, and CDR grafting) known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies.

[0198] An "isolated composition" refers to a composition that is removed from at least 90% of at least one component of a natural sample from which the isolated composition can be obtained.

[0199] The invention includes sequences and variants that include one or more substitutions, e.g., between one and six substitutions. Whether or not a particular substitution will be tolerated, i.e., will not adversely affect desired biological properties, such as binding activity can be determined as described in Bowie, et al. (1990) *Science* 247:1306-1310. One or more or all substitutions may be conservative. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. 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, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Still other substitutions may insert a non-naturally occurring amino acid.

[0200] All patent applications, patents, and references cited herein are incorporated by reference in their entirety. Accordingly, U.S. provisional applications Ser. No. 60/331,352 filed Mar. 9, 2001, Ser. No. 60/292,975 filed May 23, 2001, Ser. No. 60/284,534, filed Apr.18, 2001, Ser. No. 10/094,401, filed Mar. 8, 2002, and Ser. No. 10/125,869, filed Apr. 18, 2002, U.S. Published application 2003/0069395 are incorporated by reference for all purposes in their entirety.

BRIEF DESCRIPTION OF THE DRAWINGS

[0201] **FIG. 1** is an image of a two-dimensional gel of a proteins in a fraction of affinity-purified serum albumin and associated proteins.

DETAILED DESCRIPTION

[0202] Serum proteins are important components of the circulatory system and have wide spread function in physiology and the immune response, among other roles. Characterization of compounds associated with serum proteins provide useful indicia for studying, diagnosing, and monitoring a subject. Serum proteins can be isolated using an affinity reagent. Compounds covalently or non-covalently associated the isolated serum proteins are analyzed, e.g., to determine their identity and/or abundance.

[0203] Isolating Serum Albumin and Associated Compounds

[0204] In one implementation, human serum albumin (HSA) is isolated from a sample, e.g., blood, plasma, or serum. Compounds associated with the serum albumin are then analyzed.

[0205] 1. In a first example, a serum sample is applied to an insoluble matrix that includes one or more affinity ligands for HSA. Examples of affinity ligands include peptide ligands described below. The matrix is washed with a physiological-strength buffer (e.g., phosphate buffered saline), or more stringent buffers (e.g., including higher ionic strengths, detergents, chaotropes, and the like).

[0206] HSA and any compounds associated with it are eluted from the matrix, and recovered. Elution can be achieved, for example, by applying an appropriate buffer that favors the dissociation of HSA from the affinity ligand or by separating the affinity ligand from the insoluble matrix.

[0207] In the eluted material, serum albumin may represent a substantial fraction of the purified composition (see, e.g., **FIG. 1** and Example 1). Hence, the associated compounds may constitute less than 10% of the sample. At least some of the associated compounds may be proteinaceous, e.g., peptides, polypeptides, or protein complexes. For example, in the case of protein complexes, at least some of the associated compounds may be indirectly associated with HSA. Other compounds may be metabolites, small molecules (e.g., having a molecular weight of less than 5000 or 1000 Daltons),

[0208] 2. In a second example, a sample is applied to an insoluble matrix that includes one or more affinity ligands for HSA. The matrix is washed with a physiological-strength buffer (e.g., phosphate buffered saline), but not more stringent buffers.

[0209] HSA and any compounds associated with it are removed from the matrix by separating the affinity ligands from the matrix (e.g., the affinity ligands can be attached to the matrix by a covalent bond that is cleaved).

[0210] This preparation is then applied to an insoluble matrix that includes a thiol-reactive group, e.g., an activated maleimide or iodoacetamide (see also "Thiol Reactive Compounds," below). The activated maleimide, for example, reacts with the free cysteine of HSA, cysteine 34. Few other abundant proteins include a free cysteine when isolated from serum or from an oxidized sample. After reaction, the matrix is washed to remove proteins and other compounds that are not associated with HSA.

[0211] Compounds associated with HSA can be released from the matrix by one or more of following processes:

[0212] (a) HSA can be denatured with a chaotrope or other denaturing conditions. The denatured HSA remains covalently bound to the matrix, while non-

covalently associated compounds are released from the matrix. Denaturants can be applied to the matrix incrementally, e.g., in a step or continuous gradient.

[0213] Examples of chaotropes include guanidinium HCl (e.g., >4, 5, or 6M) or urea (e.g., >6 or 8M). Examples of other denaturing conditions include acid (e.g., phosphoric acid, pH 1), ionic detergents (e.g., 1% SDS, or greater), heat (e.g., >60° C.) boiling or an organic solvent (e.g., acetonitrile).

[0214] (b) Associated compounds can be eluted by competition using an affinity ligand that binds to HSA (e.g., an antibody, a peptide ligand, or a compound known to bind HSA, e.g., a long chain fatty acid, a drug, e.g., a drug listed in Table 1, or an endogenous compound, e.g., an endogenous compound listed in Table 2). This process may specifically elute compounds that associate with a particular epitope of HSA.

[0215] (c) Associated compounds can be separated from each other by selective elution, e.g., using a step or gradient elution, in which a solution parameter is altered (e.g., ionic strength, pH, chaotrope concentration). Fractions can be collected, and individually analyzed. This process, for example, can used to obtain preparations that include a subset of the associated compounds.

[0216] Fractions of eluted associated compounds can be subjected to additional purification steps, e.g., a preparative or analytic process described in Scopes (1994) Protein Purification: Principles and Practice, New York: Springer-Verlag.

[0217] The methods described herein can also be used to isolate serum albumins from other species, e.g., a non-human mammalian species and non-mammalian species.

[0218] Peptide Ligands that Bind Serum Albumin.

[0219] In some embodiments, peptide ligands are used to isolate a serum albumin and associated proteins. Provisional patent applications Ser. No. 60/331,352 filed Mar. 9, 2001 and Ser. No. 60/292,975 filed May 23, 2001 describe a number of exemplary peptide ligands that bind to serum albumin. Some exemplary peptide ligands include DX-321, DX-321-A, DX-321-B, DX-236, DX-236-A, and DX-236B.

[0220] DX-321 includes the peptide sequence:

[0221] AEGTGDRNMCKFSWIRSPAFCARADPE- (SEQ ID NO: 40). DX-321 binds to human serum albumin and is useful for isolating human serum albumin and associated compounds.

[0222] DX-321-A includes the peptide sequence:

[0223] RNMCKFSWIRSPAFCARA (SEQ ID NO: 215).

[0224] DX-321-B includes the peptide sequence:

[0225] CKFSWIRSPAFC (SEQ ID NO: 120)

[0226] DX-236 includes the peptide sequence:

[0227] AEGTGDFWFCDRIAWYPQHLCEFLD-PEGGGK(SEQ ID NO: 19). DX-236 binds at least to a number of mammalian serum albumins and is useful under appropriate conditions as a serum albumin-binding agent that binds to serum albumins from multiple species.

[0228] DX-236A includes the peptide sequence:

[0229] FWFCDRIAWYPQHLCEFLD (SEQ ID NO: 210)

[0230] DX-236B includes the peptide sequence:

[0231] CDRIAWYPQHLC (SEQ ID NO: 9)

[0232] In one implementation, an affinity matrix for purifying serum albumin includes a plurality of binding ligands, e.g., binding ligands having specificity for different epitopes on the serum albumin. For example, an affinity matrix for binding HSA can include two different species of HSA binding peptides, e.g., DX-236 and DX-321.

[0233] In addition to peptide ligands, larger polypeptide ligands can be used, e.g., protein that include at least one immunoglobulin domain, e.g., an antibody or antibody fragment.

[0234] Exemplary Serum Albumin Associated Compounds

[0235] A number of endogenous and exogenous compounds are known to associated with serum albumin. A method described herein can include determining whether one or more of such compounds (e.g., a compound in Table 1 or Table 2) is associated with an isolated serum albumin. Compounds other than serum albumin can also be evaluated.

TABLE 1

Drugs that bind to Serum Albumin

Salicylate	Sulfisoxazole
Warfarin	Phenylbutazone
Digitoxin	Indomethacin
Tolbutamide	Furosenmide
Phenytoin	Chlorpropamide
Chlorthiazide	Oxacillin
Benzylpenicilliln	Acetotrizoate
Phenol Red	Bromscesol green
Bromophenol Blue	Iophenoxate
Sulfobromophthalein	Methyl organge
Methyl Red	Evans blue
Diazepam (S)	Ibuprofen
Naproxen	Octanoate
Chlofibrate	Chlorpromazine
Imipramine	Quinidine

[0236]

TABLE 2

Endogenous compounds that bind Serum Albumin

Long-chain fatty acids	Eicosanoids
Bile acids	
Steroids	Cortisol
Progesterone	Testosterone
Aldosterone	
Hematin	Bilirubin
L-Thyroxine	L-Tryptophan
25-OH-Vitamin D_3	1,25-$(OH)_2$-Vitamin D_3
Aquocobalamin	Folate
Ascorbate	
Copper(II)	Zinc(II)
Calcium	Magnesium
Chloride	

[0237] Thiol Reactive Compounds

[0238] As described above, thiol reactive groups can be used to immobilize a serum protein that includes a free cysteine. In particular, serum albumin is an abundant serum protein that includes a free cysteine. For example, cysteine 34 of HSA is typically available for coupling. Exemplary thiol reactive groups include the following.

[0239] Halogen derivatives. Haloacetyl compounds and benzyl halides, particularly iodo and bromo derivatives, can be reacted with cysteines. For example, iodoacetate can be used to react with cysteines. The reaction is more specific if the iodoacetate is present in limiting quantities related to the number of available sulfhydryl and under alkaline pH.

[0240] Maleimides. The double bond of maleimides (maleic acid imides) can undergo an alkylation reaction with sulfhydryl groups, resulting in a thioether bond. Maleimides are particularly specific for sulfhydryls between pH 6.5 and 7.5.

[0241] Thiol-Disulfide Exchange Reagents. Cysteines can also be crosslinked using compounds that have a disulfide bond and undergo disulfide exchange with the free cysteine on the serum protein. Pyridyl disulfides, for example, can be generated by reaction of 2-iminothiolane with 4,4' dipyridyl disulfide.

[0242] Still other thiol reactive compounds include aziridines, acryloyl derivaties, and arylating reagents (such as 2,4 dinitrofluorobenzye). See also Hermanson (1996) "Section 2: Thiol-Reactive Chemical Reactions" of *Bioconjugate Techniques* Academic Press.

[0243] Peptide Ligands that Bind Immunoglobulins

[0244] In another implementation, a soluble immunoglobulin is isolated from a sample, e.g., blood, plasma, or serum. Compounds associated with the immunoglobulin are then analyzed.

[0245] A peptide ligand can be used to isolate the soluble immunoglobulin. WO 2002/086070 and provisional patent application 60/284,534, filed Apr. 18, 2001, describe a number of exemplary peptide ligands that bind to the Fc region of an immunoglobulin. For example:

[0246] DX249, GDDHMCVYTTWGELIWCDNHEPGPEGGGK (SEQ ID NO: 368) which exhibits dissociation constants (K_D) for human IgG1 of less than 0.1 μM at pH 5.7 and less than 0.5 μM at pH 7.4, the segment DX249-A, DHMCVYTTWGELIWCDNH (SEQ ID NO: 260), or the segment DX-249-B, CVYTTWGELIWC (SEQ ID NO: 427);

[0247] DX253, GDRRACSRDWSGALVWCAGHEPGPEGGGK (SEQ ID NO: 369), exhibits quantitative binding of Fc protein (capture efficiency >90% of total load), the segment DX253-A, RRACSRDWSGALVWCAGH (SEQ ID NO: 238), or the segment DX253-B, CSRDWSGALVWC (SEQ ID NO: 428);

[0248] DX398, AGAATCSTSYWYYQWFCTDSPGPEGGGK (SEQ ID NO: 375), DX398-A: AATCSTSYWYYQWFCTDS (SEQ ID NO: 348) or DX398-B: CSTSYWYYQWFC (SEQ ID NO: 429);

[0249] DX252, GDDDHCYWFREWFNSECPHGEPGPEGGGK (SEQ ID NO: 378), exhibits dissociation constants (K_D) for human IgG3 of less than 0.1 μM at pH 5.7 and in the range of ~2.1 μM to ~3.4 μM for IgG1, IgG2, IgG3, and IgG4 at pH 7.4; and

[0250] DX254, AGYYWCNYWGLCPDQGTPGPEGGGK (SEQ ID NO: 379), exhibits dissociation constants (K_D) for human IgG1 of less than 0.1 μM at pH 5.7, less than 2.0 μM at pH 7.4, and less than 1.0 μM at pH 9.3.

[0251] In one implementation, a sample is contacted to an affinity matrix that includes ligands that bind to immunoglobulins. Immunoglobulin and associated compounds are isolated. In one example, the isolated material is analyzed, e.g., to characterize antigens associated with immunoglobulin. In another example, the isolated material is cultured, e.g., to identify a pathogen bound by the immunoglobulin.

[0252] Analyzing Associated Compounds

[0253] A fraction of a serum protein and associated compounds can be analyzed by a number of processes. Exemplary methods for analyzing proteinaceous compounds associated with a serum protein include: sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), 2-D gel electrophoresis (iso-electric focusing and PAGE), HPLC, FPLC (ion-chromatography, size exclusion chromatography, hydrophobic interaction chromatography, and the like), immuno-analysis (e.g., immuno-blots, enzyme-linke.d immunosorbent assay (ELISA), immunoprecipitation, and the like), mass spectroscopy, and protein sequencing.

[0254] Exemplary methods for analyzing a non-proteinaceous compound associated with a serum protein include: mass spectroscopy (e.g., GC-mass spec or "GC/MS"), thin-layer chromatography, and other chemical detection methods.

[0255] 1D gels. SDS-PAGE can be used to separate proteins by their apparent/approximate molecular weight in an acrylamide gel. The concentration of acrylamide can be varied according to the expected size or a gradient of acrylamide concentration can be used. After electrophoresis, proteins can be stained using a variety of dyes, include Coomassie Blue, silver stains, and fluorescent dyes such as Sypro Red (Molecular Probes, Inc., Eugene, Oreg.). The acrylamide gel can be imaged, e.g., to determine relative concentration of resolved bands of proteins. The image can be stored in a computer database.

[0256] 2D gels. This method can be used to separate polypeptides according to two properties, isoelectric point (pI) and apparent molecular weight (MW). Proteins are first separated by PI (isoelectric focusing) and then separated according to apparent molecular weight by SDS-PAGE. The 2D gel is stained and imaged. The detected "spots" of proteins provide information about the identity, modification state, and relative abundance of each protein. Proteins can also be excised from spots and further characterized by mass spectroscopy or protein sequencing.

[0257] Isoelectric focusing for the first dimension can utilize immobilized pH gradient strips, e.g., in which polycarboxylic acid ampholytes are immobilized. Strips can be produced that focus within a desired pH range, both narrow and wide. A strip can be selected for the appropriate degree of resolution.

[0258] After isoelectric focusing, protein in the strip are denatured and reduced, e.g., using SDS and a thiol reductant. The strip is attached to an SDS-PAGE slab gel and proteins are separated by molecular weight.

[0259] Immuno-Detection. Antibodies, either characterized or uncharacterized, can be used to identify compounds associated with a serum protein. The antibodies can be applied to a separated sample (e.g., an electrophoresed sample, as in a Western blot) or to the sample as a whole (e.g., an ELISA). An antibody can also be used to immunoprecipitate the compound. The antibody can be coupled to a label or signal generator to enable detection of the compound. Antibody fragments and other derivatives can also be used.

[0260] Mass Spectroscopy. Time-of flight mass spectrometry (TOF-MS) and electrospray mass spectrometry can be used to characterize compounds associated with a serum protein. TOF-MS is sensitive, highly accurate, and rapid (R. J. Cotter, (1992) *Anal. Chem.* 64:1027. For example, TOF-MS can record a complete mass spectrum on a microsecond timescale.

[0261] One common TOF-MS method is matrix-assisted laser desorption/ionization (MALDI) (Karas and Hillenkamp, *Anal. Chem.* 60, 2299 (1988). This method is amenable to the mass spectrometry to oligonucleotides and nucleic acids. See generally, P. Limbach et al, "Characterization of oligonucleotides and nucleic acids by mass spectrometry", In *Current Opinion in Biotechnology,* 6, 96-102 (1995).

[0262] Mass spectroscopy can be combined with protease digestion to determine the precise molecular weight of proteolytic fragments of a protein. This information can be compared to a computer sequence database to infer the sequence of the protein. For example, the database can includes predicted protein sequences from genome sequence. See, e.g., Zhang and Chait (2000) *Anal. Chem.* 72:2482. Mass spectroscopy can also be used to determine the modification state of a protein (e.g., oxidation, glycosylation).

[0263] Exemplary proteases for mapping proteolytic fragments include: elastase, trypsin, chymotrypsin, pepsin, papain, and Glu-C. Certain chemical agents can also be used, e.g., formic acid and cyanogen bromide.

[0264] For matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS or MALDI-TOF), a proteolyzed sample is combined with a matrix (e.g., α-cyano-4-hydroxycinnamic acid), sinapinic acid, or gentisic acid), and dried on a mass spectroscopy plate. The plate is then placed in a mass spectrometer where the protein fragments are ionized, and then analyzed for their time of flight. Accurate molecular weights are determined from these measurements.

[0265] Protein Sequencing. The N-termini of a purified protein (e.g., 2 to 5 picomoles of the protein) can be sequenced by Edman degradation. This process can be automated. N-terminal sequence information can be combined with mass spectroscopy information and comprehensive databases to unambiguously identify a protein.

[0266] Peptide and Protein Arrays

[0267] In some implementations, an array of proteins and/or peptide ligands, at least some of which bind to serum proteins can be used. For example, the array can include one or more peptide ligands described herein. In a particular example, the array includes at least two different peptide ligands that bind to serum albumin.

[0268] In general, a sample is contacted to the array, and complexes within the sample are allowed to bind to ligands on the array, e.g., so that different complexes of a serum binding protein are isolated by the different ligands. Each discrete address can be evaluated separately.

[0269] Methods of producing polypeptide arrays are described, e.g., in De Wildt et al. (2000) *Nat. Biotechnol.* 18:989-994; Lueking et al. (1 999) *Anal. Biochem.* 270:103-111; Ge (2000) *Nucleic Acids Res.* 28, e3, I-VII; MacBeath and Schreiber (2000) *Science* 289:1760-1763; U.S. Pat. No. 2002-192,673 WO 01/98534, WO01/83827, WO02/12893, WO 00/63701, WO 01/40803 and WO 99/51773. In some implementations, polypeptides (including peptides) are spotted onto discrete addresses of the array, e.g., at high speed, e.g., using commercially available robotic apparati, e.g., from Genetic MicroSystems or BioRobotics. The array substrate can be, for example, nitrocellulose, plastic, glass, e.g., surface-modified glass. The array can also include a porous matrix, e.g., acrylamide, agarose, or another polymer.

[0270] Arrays of peptides can be similarly produced. In addition, peptides can be directly synthesized in an array format, e.g., according to U.S. Pat. No. 5,143,854. It may also be possible to use nucleic acid aptamers as ligands to isolate serum proteins and associated complexes.

[0271] Analysis of Altered or Abnormal States

[0272] The methods described herein can be used to characterize an altered or abnormal state of a subject. For example, a profile of compounds associated with one or more serum proteins can be determined for the subject at one or more instances. The subject can be a diseased subject, a genetically altered subject, a subject afflicted by a genetic disorder, a subject exposed to toxins (e.g., environmental toxins, narcotics, and so forth), or a subject receiving a treatment. For instance, in the case of monitoring a treatment of a subject, the profile can be determined prior to treatment, and at regular intervals after treatment. The profile may provide information about the pathology of the subject (e.g., if diseased), the abundance of an administered drug, or a drug by-product in the subject's serum, or the abundance of natural components whose levels might be affected by the treatment.

[0273] Drug Testing

[0274] The methods described herein can also be used to test the affinity of a test compound, e.g., a drug, for serum components. Information about whether a potential pharmaceutical interacts with a serum protein is useful for characterizing its efficacy and utility as a therapeutic agent.

[0275] For example, the test compound can be mixed with a biological sample, such as blood or serum or an at least partially purified preparation of a serum protein (e.g., a recombinant serum protein). After incubation, one or more serum proteins is isolated from the sample, e.g., using an

affinity reagent, e.g., a reagent that includes a peptide ligand described herein. Binding of the test compound to the isolated serum protein can be determined, e.g., by quantifying the amount of test compound that is isolated with the serum protein. The test compound can be unlabeled or labeled (e.g., using a radioactive label or fluorescent label). A labeled test compound can be directly detected, e.g., using a scintillation proximity assay or fluorescence assay.

[0276] Unlabeled compounds can also be detected. For example, mass spectrometry can be used for detecting with unlabeled compounds. In another example, unlabeled compounds can be detected in a competition assay. Unlabeled compounds bound to the serum protein are separated from the serum protein and added to a binding reaction, e.g., in a well of a microtitre plate. The binding reaction includes an antibody that binds to the unlabeled compound and a known quantity of labeled compound. The amount of unlabeled compound present is determined by measuring the amount of labeled compound bound by the antibody. Competition by the unlabeled compound reduces the amount of bound labeled compound.

[0277] A related method includes administering the test compound to a subject, e.g., an animal model. After one or more appropriate intervals, a blood or serum sample is extracted from the subject. The amount of test compound associated with a serum protein can be determined, e.g., as described above. If the subject is a non-human mammal, an affinity ligand that is not species specific can be used.

[0278] Compounds that Modulate Interactions with a Serum Protein

[0279] It is also possible to screen for modulator compounds that modulate the interaction of a serum-protein binding compound and a serum protein, e.g., serum albumin. For example, it is possible to use a high throughput screen for compounds that disrupt (or enhance) the interaction between a naturally-occurring protein and serum protein.

[0280] One method for screening includes: contacting a candidate modulator compound to a complex that includes the serum protein-binding compound and the serum protein; and evaluating the interaction between the serum protein-binding compound and the serum protein. In one implementation, the serum protein is bound to an affinity reagent (e.g., a peptide ligand) and isolated. The isolated material is analyzed to determine the presence and/or amount of the serum protein-binding compound. A modulator compound that disrupts the interaction between the serum protein-binding compound and the serum protein may reduce or prevent isolation of the serum protein-binding compound.

[0281] A related method for screening involves contacting the serum protein to the candidate modulator compound, and subsequently adding the serum protein-binding compound to determine if the candidate modulator impairs or enhances the interaction between the serum protein and the serum protein-binding compound. Likewise, all three components can be combined together and then analyzed.

[0282] Identifying Binding Ligands for Serum Proteins.

[0283] Ligands that bind to a serum protein can be identified by a variety of methods including screening a display library. For example, phage display can be used to screen a library of linear or cyclic peptides for peptides that bind to a given serum protein. In addition, ligands that include an immunoglobulin domain, e.g., antibodies, can be generated (e.g., by immunization, or display library screening).

[0284] Peptide ligands that bind to human serum albumin and the Fc region of immunoglobulin are described herein and in U.S. provisional applications Ser. No. 60/331,352 filed Mar. 9, 2001, Ser. No. 60/292,975 filed May 23, 2001, Ser. No. 60/284,534, filed Apr. 18, 2001. Similarly, ligands can be isolated that bind to a serum protein such as: transferrin, α macroglobulins, ferritin, apolipoproteins, transthyretin, a protease inhibitor found in serum, retinol binding protein, thiostatin, α-fetoprotein, vitamin-D binding protein, or afamin.

[0285] One method of identifying a binding ligand for a serum protein is to screen a display library. A display library is a collection of entities; each entity includes an accessible polypeptide component and a recoverable component that encodes or identifies the polypeptide component. The polypeptide component can be of any length, e.g. from three amino acids to over 300 amino acids. In a selection, the polypeptide component of each member of the library is probed with the serum protein and if the polypeptide component binds to the protein, the display library member is identified, typically by retention on a support.

[0286] The screening of display libraries is advantageous, in that very large numbers (e.g., 5×10^9) of potential binders can be tested, and successful binders isolated in a short period of time. Further, unlike immunization, ligands can be identified that bind to epitopes of serum proteins that are conserved among different species.

[0287] Retained display library members are recovered from the support and analyzed. The analysis can include amplification and a subsequent selection under similar or dissimilar conditions. For example, positive and negative selections can be alternated. The analysis can also include determining the amino acid sequence of the polypeptide component and purification of the polypeptide component for detailed characterization.

[0288] A variety of formats can be used for display libraries. Examples include the following.

[0289] Phage Display. One format utilizes viruses, particularly bacteriophages. This format is termed "phage display." The polypeptide component is typically covalently linked to a bacteriophage coat protein. The linkage results form translation of a nucleic acid encoding the polypeptide component fused to the coat protein. The linkage can include a flexible peptide linker, a protease site, or an amino acid incorporated as a result of suppression of a stop codon. Phage display is described, for example, in Ladner et al., U.S. Pat. No. 5,223,409; Smith (1985) *Science* 228:1315-1317; WO 92/18619; WO 91/17271; WO 92/20791; WO 92/15679; WO 93/01288; WO 92/01047; WO 92/09690; WO 90/02809; de Haard et al. (1999) *J. Biol. Chem* 274:18218-30; Hoogenboom et al. (1998) *Immunotechnology* 4:1-20; Hoogenboom et al. (2000) *Immunol Today* 2:371-8; Fuchs et al. (1991) *Bio/Technology* 9:1370-1372; Hay et al. (1992) *Hum Antibod Hybridomas* 3:81-85; Huse et al. (1989) *Science* 246:1275-1281; Griffiths et al. (1993) *EMBO J* 12:725-734; Hawkins et al. (1992) *J Mol Biol* 226:889-896; Clackson et al. (1991) *Nature* 352:624-628; Gram et al. (1992) *PNAS* 89:3576-3580; Garrard et al.

(1991) *Bio/Technology* 9:1373-1377; Rebar et al. (1996) *Methods Enzymol.* 267:129-49; Hoogenboom et al. (1991) *Nuc Acid Res* 19:4133-4137; and Barbas et al. (1991) *PNAS* 88:7978-7982.

[0290] Phage display systems have been developed for filamentous phage (phage fl, fd, and M13) as well as other bacteriophage (e.g. T7 bacteriophage and lambdoid phages; see, e.g., Santini (1998) *J. Mol Biol.* 282:125-135; Rosenberg et al. (1996) *Innovations* 6:1-6; Houshmet al. (1999) *Anal Biochem* 268:363-370). The filamentous phage display systems typically use fusions to a minor coat protein, such as gene III protein, and gene VIII protein, a major coat protein, but fusions to other coat proteins such as gene VI protein, gene VII protein, gene IX protein, or domains thereof can also been used (see, e.g., WO 00/71694). In a preferred embodiment, the fusion is to a domain of the gene III protein, e.g., the anchor domain or "stump," (see, e.g., U.S. Pat. No. 5,658,727 for a description of the gene III protein anchor domain).

[0291] The valency of the polypeptide component can also be controlled. Cloning of the sequence encoding the polypeptide component into the complete phage genome results in multivariant display since all replicates of the gene III protein are fused to the polypeptide component. For reduced valency, a phagemid system can be utilized. In this system, the nucleic acid encoding the polypeptide component fused to gene III is provided on a plasmid, typically of length less than 700 nucleotides. The plasmid includes a phage origin of replication so that the plasmid is incorporated into bacteriophage particles when bacterial cells bearing the plasmid are infected with helper phage, e.g. M13K01. The helper phage provides an intact copy of gene III and other phage genes required for phage replication and assembly. The helper phage has a defective origin such that the helper phage genome is not efficiently incorporated into phage particles relative to the plasmid that has a wild type origin.

[0292] Bacteriophage displaying the polypeptide component can be grown and harvested using standard phage preparatory methods, e.g. PEG precipitation from growth media.

[0293] After selection of individual display phages, the nucleic acid encoding the selected polypeptide components, by infecting cells using the selected phages. Individual colonies or plaques can be picked, the nucleic acid isolated and sequenced.

[0294] Cell-based Display. In still another format the library is a cell-display library. Proteins are displayed on the surface of a cell, e.g., a eukaryotic or prokaryotic cell. Exemplary prokaryotic cells include *E. coli* cells, *B. subtilis* cells, spores (see, e.g., Lu et al. (1995) *Biotechnology* 13:366). Exemplary eukaryotic cells include yeast (e.g., *Saccharomyces cerevisiae, Schizosaccharomyces pombe*, Hanseula, or *Pichia pastoris*). Yeast surface display is described, e.g., in Boder and Wittrup (1997) *Nat. Biotechnol.* 15:553-557 and WO03029456. This application describes a yeast display system that can be used to display immunoglobulin proteins such as Fab fragments, and the use of mating to generate combinations of heavy and light chains.

[0295] In one embodiment, variegate nucleic acid sequences are cloned into a vector for yeast display. The cloning joins the variegated sequence with a domain (or complete) yeast cell surface protein, e.g., Aga2, Aga1, Flo1, or Gas1. A domain of these proteins can anchor the polypeptide encoded by the variegated nucleic acid sequence by a transmembrane domain (e.g., Flo1) or by covalent linkage to the phospholipid bilayer (e.g., Gas1). The vector can be configured to express two polypeptide chains on the cell surface such that one of the chains is linked to the yeast cell surface protein. For example, the two chains can be immunoglobulin chains.

[0296] Ribosome Display. RNA and the polypeptide encoded by the RNA can be physically associated by stabilizing ribosomes that are translating the RNA and have the nascent polypeptide still attached. Typically, high divalent Mg^{2+} concentrations and low temperature are used. See, e.g., Mattheakis et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:9022 and Hanes et al (2000) *Nat Biotechnol.* 18:1287-92; Hanes et al. (2000) *Methods Enzymol.* 328:404-30. and Schaffitzel et al. (1999) *J Immunol Methods.* 231(1-2):119-35.

[0297] Peptide-Nucleic Acid Fusions. Another format utilizes peptide-nucleic acid fusions. Polypeptide-nucleic acid fusions can be generated by the in vitro translation of mRNA that include a covalently attached puromycin group, e.g., as described in Roberts and Szostak (1997) *Proc. Natl. Acad. Sci. USA* 94:12297-12302, and U.S. Pat. No. 6,207,446. The mRNA can then be reverse transcribed into DNA and crosslinked to the polypeptide.

[0298] Other Display Formats. Yet another display format is a non-biological display in which the polypeptide component is attached to a non-nucleic acid tag that identifies the polypeptide. For example, the tag can be a chemical tag attached to a bead that displays the polypeptide or a radiofrequency tag (see, e.g., U.S. Pat. No. 5,874,214).

[0299] Scaffolds. Scaffolds for display can include: antibodies (e.g., Fab fragments, single chain Fv molecules (scFV), single domain antibodies, camelid antibodies, and camelized antibodies); T-cell receptors; MHC proteins; extracellular domains (e.g., fibronectin Type III repeats, EGF repeats); protease inhibitors (e.g., Kunitz domains, ecotin, BPTI, and so forth); TPR repeats; trifoil structures; zinc finger domains; DNA-binding proteins; particularly monomeric DNA binding proteins; RNA binding proteins; enzymes, e.g., proteases (particularly inactivated proteases), RNase; chaperones, e.g., thioredoxin, and heat shock proteins; and intracellular signaling domains (such as SH2 and SH3 domains).

[0300] Another useful type of scaffolding domain is the immunoglobulin (Ig) domain. Methods using immunoglobulin domains for display are also known (see, e.g., Haard et al. (1999) *J. Biol. Chem* 274:18218-30; Hoogenboom et al. (1998) *Immunotechnology* 4:1-20. and Hoogenboom et al. (2000) *Immunol Today* 21:371-8).

[0301] Synthetic Peptides. The binding ligand can include a synthetic peptide, e.g., an artificial peptide of 30 amino acids or less. The synthetic peptide can include one or more disulfide bonds. Other synthetic peptides, so-called "linear peptides," are devoid of cysteines. Synthetic peptides may have little or no structure in solution (e.g., unstructured), heterogeneous structures (e.g., alternative conformations or "loosely structured), or a singular native structure (e.g.,

cooperatively folded). Some synthetic peptides adopt a particular structure when bound to a target molecule. Some exemplary synthetic peptides are so-called "cyclic peptides" that have at least disulfide bond, and, for example, a loop of about 4 to 12 non-cysteine residues.

[0302] Peptide sequences that bind a molecular target are selected from a phage-display library. After identification, such peptides can be produced synthetically or by recombinant means. The sequences can be incorporated (e.g., inserted, appended, or attached) into longer sequences.

[0303] Exemplary Phage Display Libraries for Identifying Binding Peptides

[0304] Display libraries exhibiting variegated heterologous peptides on the surface of recombinant phage or other genetic packages (bacteria, yeast, other host cells) may be prepared in any of several ways known in the art. See, e.g., Kay et al., *Phage Display of Peptides and Proteins: A Laboratory Manual* (Academic Press, Inc., San Diego 1996) and U.S. Pat. No. 5,223,409 (Ladner et al.).

[0305] The following are six exemplary phage libraries that can be screened to find at least some of the polypeptide ligands described herein. Each library displays a short, variegated exogenous peptide on the surface of M13 phage. The peptide display of five of the libraries was based on a parental domain having a segment of 4, 5, 6, 7, 8, or 10 amino acids, respectively, flanked by cysteine residues. The pairs of cysteines are believed to form stable disulfide bonds, yielding a cyclic display peptide. The cyclic peptides are displayed at the amino terminus of protein III on the surface of the phage. The libraries were designated TN6/6, TN8/9, TN9/4, TN10/9, and TN12/1. A phage library with a 20-amino acid linear display was also screened; this library was designated Lin20.

[0306] The TN6/6 library was constructed to display a single cyclic peptide contained in a 12-amino acid variegated template. The TN6/6 library utilized a template sequence of Xaa_1-Xaa_2-Xaa_3-Cys_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Cys_9-Xaa_{10}-Xaa_{11}-Xaa_{12} (SEQ ID NO: 21), where each variable amino acid position in the amino acid sequence of the template is indicated by a subscript integer. Each variable amino acid position (Xaa) in the template was varied, independently, to permit the following substitutions: residues Xaa_1 and Xaa_{12} were varied to contain any of the following 14 amino acids: Ala, Asp, Phe, Gly, His, Leu, Asn, Pro, Gln, Arg, Ser, Val, Trp, and Tyr; and residues Xaa_2, Xaa_3 Xaa_5, Xaa_6, Xaa_7, Xaa_8, Xaa_{10}, and Xaa_{11} were independently varied to contain any of the common α-amino acids, except cysteine (Cys). The number of potential designed sequences is 3.3×10^{12}; 2.0×10^8 independent transformants were included in the library.

[0307] The TN8/9 library was constructed to display a single binding loop contained in a 14-amino acid template. The TN8/9 library utilized a template sequence of Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Cys-Xaa_{12}-Xaa_{13}-Xaa_{14} (SEQ ID NO: 25). The amino acids at position 1, 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, and 14 in the template were varied to permit any amino acid except cysteine (Cys).

[0308] The TN9/4 library was constructed to display a single binding loop contained in a 15-amino acid template. The TN9/4 library utilized a template sequence Xaa_1-Xaa_2-Xaa_3-Cys-Xaa_5-Xaa_6-Xaa_7-Xaa_8 Xaa_9-Xaa_{10}-Xaa_{11}-Cys-Xaa_{13}-Xaa_{14}-Xaa_{15} (SEQ ID NO: 424 The amino acids at position 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 13, 14 and 15 in the template were varied to permit any amino acid except cysteine (Cys).

[0309] The TN10/9 library was constructed to display a single cyclic peptide contained in a 16-amino acid variegated template. The TN10/9 library utilized a template sequence Xaa_1-Xaa_2-Xaa_3-Cys_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_2-Cys_{13}-Xaa_{14}-Xaa_{15}-Xaa_{16} (SEQ ID NO: 22), where each variable amino acid position in the amino acid sequence of the template is indicated by a subscript integer. Each variable amino acid position (Xaa) was varied independently to permit the following substitutions. The amino acid positions Xaa_1, Xaa_2, Xaa_{15} and Xaa_{16} of the template were varied, independently, to permit each of the amino acids selected from a group of ten amino acids consisting of Asp, Phe, His, Leu, Asn, Pro, Arg, Ser, Trp, and Tyr; the amino acids at amino acid positions Xaa_3 and Xaa_{14} in the template were varied, independently, to permit each amino acid selected from the group of fourteen amino acids consisting of Ala, Asp, Glu, Phe, Gly, His, Leu, Asn, Pro, Arg, Ser, Val, Trp, and Tyr; the amino acids at amino acid positions Xaa_5, Xaa_6, Xaa_7, Xaa_8, Xaa_9, Xaa_{10}, Xaa_{11} and Xaa_{12} (i.e., between the invariant cysteine residues at positions 4 and 13 in the template) were varied, independently, to permit each of the common α-amino acids, except cysteine. The number of potential designed sequences is 3.0×10^{16}; and about 2.5×10^8 independent transformants were included in the library.

[0310] The TN12/1 library was constructed to display a single cyclic peptide contained in an 18-amino acid template. The TN12/1 library utilized a template sequence Xaa_1-Xaa_2-Xaa_3-Cys_4-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-Xaa_{13}-Xaa_{14}-Cys_{15}-Xaa_{16}-Xaa_{17}-Xaa_{18} (SEQ ID NO: 23), where each variable amino acid position in the amino acid sequence of the template is indicated by a subscript integer. The amino acid positions Xaa_1, Xaa_2, Xaa_{17} and Xaa_{18} of the template were varied, independently, to permit each amino acid selected from the group of 12 amino acids consisting of Ala, Asp, Phe, Gly, His, Leu, Asn, Pro, Arg, Ser, Trp, and Tyr. The amino acid positions Xaa_3, Xaa_5, Xaa_6, Xaa_7, Xaa_8, Xaa_9, Xaa_{10}, Xaa_{11}, Xaa_{12}, Xaa_{13}, Xaa_{14}, Xaa_{16}, of the the template were varied, independently, to permit each of the common (α-amino acids, except cysteine.

[0311] The Lin20 library was constructed to display a single linear peptide in a 20-amino acid template. The amino acids at each position in the template were varied to permit any amino acid except cysteine (Cys).

[0312] The techniques discussed in Kay et al., *Phage Display of Peptides and Proteins: A Laboratory Manual* (Academic Press, Inc., San Diego 1996) and U.S. Pat. No. 5,223,409 are useful for preparing a library of potential binders corresponding to the selected parental template. The libraries described above can be prepared according to such techniques, and screened for binding peptides against a serum protein, either immobilized on a solid surface or free in solution.

[0313] Screening Phage Display Libraries for Serum Protein Binding Peptides

[0314] In a typical screen, a phage library is contacted with and allowed to bind the target compound, e.g., a serum

protein of interest, or a particular fragment or subcomponent thereof. To facilitate separation of binders and non-binders in the screening process, it is often convenient to immobilize the target compound on a solid support, although it is also possible to first permit binding to the target compound in solution and then segregate binders from non-binders by coupling the target compound to a support. By way of illustration, when incubated in the presence of the target, phage bearing a target-binding moiety form a complex with the target compound immobilized on a solid support whereas non-binding phage remain in solution and may be washed away with buffer. Bound phage may then be liberated from the target by a number of means, such as changing the buffer to a relatively high acidic or basic pH (e.g., pH 2 or pH 10), changing the ionic strength of the buffer, adding denaturants, or other known means.

[0315] For example to identify HSA-binding ligands, HSA can be adsorbed (by passive immobilization) to a solid surface, such as the plastic surface of wells in a multi-well assay plate, and then an aliquot of a phage display library was added to a well under appropriate conditions that maintain the structure of the immobilized HSA and the phage, such as pH 6-7. Phage in the libraries that display peptide loop structures that bind the immobilized HSA are retained bound to the HSA adhering to the surface of the well and non-binding phage can be removed. Phage bound to the immobilized HSA may then be eluted by washing with a buffer solution having a relatively strong acid pH (e.g., pH 2) or an alkaline pH (e.g., pH 8-9). The solutions of recovered phage that are eluted from the HSA are then neutralized and may, if desired, be pooled as an enriched mixed library population of phage displaying serum albumin binding peptides. Alternatively the eluted phage from each library may be kept separate as a library-specific enriched population of HSA binders. Enriched populations of phage displaying serum albumin binding peptides may then be grown up by standard methods for further rounds of screening and/or for analysis of peptide displayed on the phage and/or for sequencing the DNA encoding the displayed binding peptide.

[0316] One of many possible alternative screening protocols uses HSA target molecules that are biotinylated and that can be captured by binding to streptavidin, for example, coated on particles. As is described in an example below, phage displaying HSA binding peptides were selected from a library in such a protocol in which phage displaying HSA binding peptides were bound to a caprylate-biotinylated-HSA in solution at pH 7.4 in phosphate buffered saline (PBS) supplemented with 0.1% Tween 20 nonionic detergent and also 0.1 % sodium caprylate, which is known to stabilize HSA against temperature-induced denaturation and proteolytic attack. The caprylate-biotinylated-HSA/phage complexes in solution were then captured on streptavidin-coated magnetic beads. Phage were subsequently eluted from the beads for further study.

[0317] Recovered phage may then be amplified by infection of bacterial cells, and the screening process may be repeated with the new pool of phage that is now depleted in non-HSA binders and enriched in HSA binders. The recovery of even a few binding phage is sufficient to carry the process to completion. After a few rounds of selection, the gene sequences encoding the binding moieties derived from selected phage clones in the binding pool are determined by conventional methods, revealing the peptide sequence that imparts binding affinity of the phage to the target. An increase in the number of phage recovered after each round of selection and the recovery of closely related sequences indicate that the screening is converging on sequences of the library having a desired characteristic.

[0318] After a set of binding polypeptides is identified, the sequence information may be used to design other, secondary libraries, biased for members having additional desired properties.

[0319] Display technology can also be used to obtain ligands, e.g., antibody ligands or peptide ligands, that bind to particular epitopes of a target. This can be done, for example, by using competing non-target molecules that lack the particular epitope or are mutated within the epitope, e.g., with alanine. Such non-target molecules can be used in a negative selection procedure as described below, as competing molecules when binding a display library to the target, or as a pre-elution agent, e.g., to capture in a wash solution dissociating display library members that are not specific to the target.

[0320] The binding properties of a ligand that binds a serum protein can be readily assessed using various assay formats. For example, the binding property of a ligand can be measured in solution by fluorescence anisotropy, which provides a convenient and accurate method of determining a dissociation constant (K_D) of a binding moiety for a serum albumin from one or more different species. In one such procedure, a binding moiety described herein is labeled with fluorescein. The fluorescein-labeled binding moiety may then be mixed in wells of a multi-well assay plate with various concentrations of a particular species of serum albumin. Fluorescence anisotropy measurements are then carried out using a fluorescence polarization plate reader. The binding interaction between a serum protein and a non-covalently associated compound can be similarly characterized. Other solution measures for studying binding properties include fluorescence resonance energy transfer (FRET) and NMR.

[0321] Binding properties can also be characterized using a method wherein one binding partner is immobilized. Such methods include ELISA and surface plasmon resonance.

[0322] Serum Binding Protein Ligand Variants

[0323] It is also possible to use a variant of a serum binding protein ligand described herein or isolated by a method described herein. A number of variants are possible. A variant can be prepared and then tested, e.g., using a binding assay described above (such as fluorescence anisotropy). If the variant is function, it can be used as an affinity reagent to isolate a serum protein and associated compounds.

[0324] One type of variant is a truncation of a ligand described herein or isolated by a method described herein. In this example, the variant is prepared by removing one or more amino acid residues of the ligand can be removed from the N or C terminus. In some cases, a series of such variants is prepared and tested. Information from testing the series is used to determine a region of the ligand that is essential for binding the serum protein. A series of internal deletions or insertions can be similarly constructed and tested.

[0325] Another type of variant is a substitution. In one example, the ligand is subjected to alanine scanning to identify residues that contribute to binding activity. In another example, a library of substitutions at one or more positions is constructed. The library may be unbiased or, particularly if multiple positions are varied, biased towards an original residue.

[0326] A related type of variant is a ligand that includes one or more non-naturally occurring amino acids. Such variant ligands can be produced by chemical synthesis. One or more positions can be substituted with a non-naturally occurring amino acid. In some cases, the substituted amino acid may be chemically related to the original naturally occurring residue (e.g., aliphatic, charged, basic, acidic, aromatic, hydrophilic) or an isostere of the original residue.

[0327] It may also be possible to include non-peptide linkages and other chemical modification. For example, part or all of the ligand may be synthesized as a peptidomimetic, e.g., a peptoid (see, e.g., Simon et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:9367-71 and Horwell (1995) Trends Biotechnol.13:132-4)

[0328] For example, variants of serum albumin-binding ligands (such as DX-321, DX-321-A, DX-321-B, DX-36, DX-236-A, and DX-236B) and immunoglobulin-binding ligands (such as DX249, DX249-A, DX253, DX-253-1, DX398, and DX398-A) can be used.

[0329] Sequences of Human Serum Proteins

[0330] The amino acid sequences of human serum proteins are well known and can be found in public sequence repositories, e.g., GenBank (National Center for Biotechnology Information, National Institutes of Health, Bethesda Md.). Further, in the human population, natural genetic variation can result in amino acid differences between serum proteins among individuals.

[0331] The following sequences are examples of at least some human serum protein amino acid sequences from particular individuals.

[0332] In many individuals, HSA has the amino acid sequence listed in SwissProt entry: P02768 and/or the following mature

[0333] Examples of human serum albumin variants include H27Q, H27Y, E106K, R122S, E378K, E400K, and E529K (numbered using the unprocessed sequence, wherein the initial D of SEQ ID NO: 26 corresponds to residue 25 of the unprocessed sequence).

[0334] Automated Methods and Information Management

[0335] Any and all aspects of the serum protein analysis platform can be automated. Automation, for example, can be used to process multiple different samples automatically. Liquid handling units can be used to isolate compounds associated with a serum protein from the sample and can automatically subject the isolated compounds to analytical methods such as electrophoresis and/or mass spectroscopy.

[0336] Equipment. Various robotic devices can be employed in the automation process. These include multi-well plate conveyance systems, magnetic bead particle processors, and liquid handling units. These devices can be built on custom specifications or purchased from commercial sources, such as Autogen (Framingham Mass.), Beckman Coulter (USA), Biorobotics (Woburn Mass.), Genetix (New Milton, Hampshire UK), Hamilton (Reno Nev.), Hudson (Springfield N.J.), Labsystems (Helsinki, Finland), Packard Bioscience (Meriden Conn.), and Tecan (Mannedorf, Switzerland).

[0337] Information Management. Information generated by the platform can be stored in a computer database (e.g., in digital form). Information, including information that describes the characterization of compounds associated with a serum protein, is stored in a central database. For example, the database can include information that describes a property of an associated compound (e.g., protein sequence, chemical structure, abundance, modification state, etc. and information that describes the sample (e.g., identity of its source, date, processing method, pathology, treatment, etc.). These items of information can be associated with each other. For example, a query about a particular state, e.g., a particular disease or treatment, can be used to identify properties of associated compounds found in that state. Likewise, a particular property of one or more associated compounds can be used as a query to identify states with which the property is prevalent.

DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEF (SEQ ID NO:26)

AKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFL

QHKDDNPNLPRLVRPEVDVMCTAYHDNEETFLKKYLYELARRHPYFYAYELLFF

AKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERA

FKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY

ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKN

YAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYA

KVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEV

SRNLGKVGSKCCKITPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTE

SLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVK

HKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL.

[0338] The database can also include a profile, e.g., a description of a plurality of associated compounds from a sample in a particular state. Software can be used to compare profiles, e.g., to evaluate a given sample by comparison to the collection of profiles. One or more similar profiles can be used to infer information about the sample (e.g., to generate a diagnosis).

[0339] The database server can also be configured to communicate with each device using commands and other signals that are interpretable by the device. The computer-based aspects of the system can be implemented in digital electronic circuitry, or in computer hardware, firmware, software, or in combinations thereof. An apparatus of the invention, e.g., the database server, can be implemented in a computer program product tangibly embodied in a machine-readable storage device for execution by a programmable processor; and method actions can be performed by a programmable processor executing a program of instructions to perform functions described herein by operating on input data and generating output. One non-limiting example of an execution environment includes computers running Windows NT 4.0 (Microsoft) or better or Solaris 2.6 or better (Sun Microsystems) operating systems

[0340] The database server can also be interface with a network (e.g., an intranet or the Internet). The server can receive queries from a remote system and send information (e.g., about a profile of compounds associated with a serum protein) to the requesting system.

[0341] A query can be used to filter the database to identify records that compare favorably with a given tolerance to the query. For example, a set of mass spectroscopy peaks can be used to formulate a query. The filter can locate (and optionally display) records that include one or more (e.g., all) the peaks that are present in the query.

[0342] Peptide Immobilization on NHS-Sepharose Resin

[0343] One method for producing a matrix having an immobilized peptide is as follows.

[0344] Five micromoles of each peptide were dissolved in DMSO in a minimal volume and then added to 1 ml of NHS-sepharose affinity chromatography resin (Amersham Pharmacia Biotech, Piscataway, N.J.), which had been washed once with dimethyl sulfoxide (DMSO). The immobilization reaction was initiated by the addition of diisopropylethylamine to 2% (vol/vol). After 4 hours of slow mixing on a shaker table at room temperature, the reaction was quenched by the addition of an equal volume of 0.5 M hydroxylamine, pH 8, in water. For those peptides with ivDde-protected internal lysines, the hydroxylamine quench treatment also removed the ivDde-protecting group. To allow for complete protecting group removal, the quenched reaction was allowed to incubate overnight at room temperature. Once quenched and deprotected, the immobilized peptide-Sepharose resin was washed at least 3 times with water to remove solvent and unbound peptide. Non-specifically bound peptide was eluted off the resin by washing the resin at least three times in 30 mM phosphoric acid, pH 2. Since the NHS-Sepharose resin surface becomes negatively charged after hydrolysis, an acidic wash neutralizes the surface and removes any peptides bound non-covalently to the surface via electrostatic interactions. After washing, the resin was resuspended in water as a 50% v/v mixture. A 50 μl aliquot was used to determine the ligand density on the resin by quantitative amino acid analysis. Finally, the resin slurry was packed into 0.35 ml OMNIFIT™ glass columns (3 mm×50 mm) for analytical testing.

[0345] For larger preparative columns, the amounts of peptide and Sepharose were scaled up proportionally, and the final peptide Sepharose batches were packed into larger 10 ml Omnifit columns (10 mm diameter).

EXAMPLE 1

[0346] Purification of HSA from Serum

[0347] A human serum sample was contacted to an HSA-binding peptide matrix that included the peptide ligands DX-236 and DX-321. The matrix was washed extensively with PBS, and eluted with a basic solution, 100 mM Tris, pH 9.1. Eluted material was rapidly neutralized with a buffer. An aliquot of this material was analyzed. **FIG. 1** is a 2-D gel that separates this material.

[0348] Another aliquot of this material can be contacted to a chromatography resin that includes activated maleimide. The fraction that does not react with the resin may include compounds that dissociate from HSA during the elution at pH 9.1. The maleimide reacts with the free cysteine on HSA and covalently couples the HSA to the resin. The resin is treated with denaturants (e.g., 8M urea), and the eluant is collected and analyzed.

[0349] In particular the eluant can be separated by 2-D electrophoresis by pI and apparent molecular weight. The 2-D gel is stained and individual protein-staining spots are excised, digested with protease, and analyzed by MALDI-MS. The analysis of each spot is stored in a database.

EXAMPLE 2

[0350] Purification of HSA from Serum

[0351] HSA was purified from blood serum using a preparative DX-236-Sepharose column (10 ml, 0.3 μmol/ml). Both the column and the serum sample were exchanged into 3 mM sodium phosphate, 20 mM NaCl, 0.1% Tween-20, pH 6.2. The 20 mM NaCl was added to the binding buffer to minimize nonspecific protein binding to the column. A 100 μl aliquot (approximately 5 mg HSA) was applied to the DX-236-Sepharose column previously equilibrated in the same buffer used for dialysis. A salt gradient between 20 and 44 mM was run, and then HSA was eluted with 100 mM Tris, pH 9.1. The results of the purification process are shown in Table 3.

TABLE 3

Purification of HSA Using DX-236 Sepharose Affinity Column

Fraction	μg HSA	% Initial
Initial Load	4805	100
Flowthrough	565	12
Wash/Gradient	88	1.8
Elution	4003	83
Total	4656	96.8

[0352] As shown in Table 6, the column bound essentially all the HSA in a 0.1 ml serum injection (~5 mg HSA total) and released essentially all the bound HSA with a 100 mM Tris, pH 9.1 wash (Table 6).

EXAMPLE 3

[0353] HSA-binding Matrices

[0354] DX-232, DX-236, and DX-321 binding peptides were used for affinity chromatography development. Each peptide was immobilized at high density on NHS-Sepharose resin using the procedure outlined above. The peptides were immobilized via a C-terminal lysine. As determined by quantitative amino acid analysis, the ligand densities for DX-321 -Sepharose, DX-236-Sepharose, and DX-232-Sepharose columns were 3.2, 0.8, and 2.4 μmol/ml, respectively. Each column was tested for HSA binding (1 mg injection) in binding buffer—3 mM sodium phosphate, 0.1% Tween-20 detergent, pH 6.2. Since some of the peptides showed a sharp increase in K_D as the pH was increased to 9.1, a 100 mM Tris, pH 9.1 buffer can be used to elute HSA from these columns.

[0355] For analytical affinity column testing, albumin was dissolved at 1 mg/ml concentration in 3 mM sodium phosphate, pH 6.2, 0.01% Tween-20 non-ionic detergent (equilibration buffer). One milliliter of albumin solution was passed through each column (0.35 ml) previously equilibrated in equilibration buffer. The columns were washed with the same equilibration buffer and then eluted with 100 mM Tris, pH 9.1 (flow rate, 0.5 ml/min for all steps). The column chromatography was carried out using a BIO-RAD BIOLOGIC™ monitoring system (Hercules, Calif.) throughout this testing with absorbance monitoring at 280 nm.

[0356] For preparative DX-236-Sepharose affinity column (10 ml) testing, human serum was dialyzed against 3 mM phosphate, pH 6.2, 20 mM NaCl, 0.01% Tween-20 non-ionic detergent (equilibration buffer). One hundred microliters (100 μl) of dialyzed serum were injected onto the preparative DX-236-Sepharose chromatography column, which was previously equilibrated with buffer. The column was washed with the same buffer, followed by a gradient between 20 and 44 mM NaCl, and finally the HSA was eluted with 100 mM Tris, pH 9.1. For all steps, the flow rates were 5 ml/min.

[0357] Each column performed differently in the initial HSA binding tests. Although soluble peptide DX-232 bound HSA with the highest affinity, immobilized DX-232 on a sepharose column captured no detectable HSA. DX-236-Sepharose, on the other hand, was the best performer and quantitatively bound the entire 1 mg injection (total capacity ≧2.7 mg/ml) (see, Table 4, below).

TABLE 4

Analysis of HSA Affinity Columns

Peptide in Affinity Column	Fraction	μg HSA	% Initial Load	Total Capacity
DX-321	Flow through	554	55.4	
	Elution	370	37.0	>1.1 mg/ml
DX-236	Flow through	0	0	
	Elution	947	94.7	>2.7 mg/ml

[0358] At higher HSA loads, the same DX-236 column was capable of binding at least 4 mg HSA, which corresponds to a total capacity of greater than 11 mg/ml. DX-321-Sepharose was an intermediate performer and bound a fraction of the total material (total capacity >1.1 mg/ml). The Tris elution buffer eluted all of the bound HSA from both DX-236- and DX-321-Sepharose columns.

EXAMPLE 4

[0359] Species Specificity of Isolated HSA Binders

[0360] To test the binding specificity of DX-236 and DX-321 for HSA over other albumins, their dissociation constants (K_D) were determined against a panel of mammalian albumins both in 3 mM sodium phosphate, pH 6.2, and in PBS (10 mM sodium phosphate, 140 mM NaCl, pH 7.4). The results are set forth in Table 5.

TABLE 5

Species Specificity Data for Affinity Columns

Species	pI	% Identity to Human	DX-236 phosphate, pH 6.2, O M NaCl K_D (μM)	DX-236 PBS, pH 7.4, 0.14 M NaCl K_D (μM)	DX-321 phosphate, pH 6.2, O M NaCl K_D (μM)	DX-321 PBS, pH 7.4, 0.14 M NaCl K_D (μM)
Human	5.67	100	1.9	11.0	0.9	84
Rhesus	5.67	93.2	1.1	23	38	82
Bovine	5.60	75.6	1.1	13.3	21	>200
Goat	N.D.	N.D.	1.6	23	95	83
Pig	5.75	75.0	0.5	12	21	>200
Rabbit	5.65	75.0	0.5	18	32	>200
Rat	5.80	73.2	1.6	25	23	117
Mouse	5.53	72.0	5.5	32	>200	>200
Chicken (egg)	5.19	N.D.	>200	>200	>200	>200

N.D. = not determined

[0361] In the 3 mM phosphate, pH 6.2 buffer, labeled DX-236 bound to all the albumins tested with high affinity, except for murine serum albumin (MSA). In PBS, the same affinity trend appeared with DX-236, except all the K_D values were higher than for the low salt, pH 6.2 condition.

[0362] Labeled DX-321 bound each mammalian albumin with a substantially higher K_D compared to HSA in the low salt, pH 6.2 buffer. In particular, MSA bound DX-321 with a K_D greater than 200 μM compared to HSA, which bound DX-321 with a submicromolar K_D. All of the other non-human albumins also bound weakly to DX-321 and had K_D values at least 10 times greater than for HSA. In PBS, however, the DX-321 affinity differences between HSA and the others were less pronounced compared to the pH 6.2 results. As a negative control, each peptide (DX-236 and DX-321) was also tested for binding to chicken ovalbumin in both sets of buffers and found that neither peptide showed any significant binding (Table 4). Chicken ovalbumin is not homologous to HSA as determined by sequence alignment analysis. This analysis indicated that immobilized DX-236 can be used to purify other mammalian albumins.

[0363] To demonstrate this property, the same DX-236- and DX-321-Sepharose columns were tested against bovine serum albumin (BSA), goat serum albumin (GSA), and murine serum albumin (MSA) in the pH 6.2 buffer. One mg of each type of albumin was injected onto each column (0.35 ml) previously equilibrated in 3 mM Phosphate, pH 6.2, 0.01% Tween-20. The columns were washed with equilibration buffer and then eluted with 100 mM Tris, pH 9.1 (flow rate, 1 ml/min). As shown in Table 6 below, DX-236-Sepharose quantitatively captured all three albumins like HSA.

TABLE 6

Mammalian Serum Albumin Testing with DX-236 and DX-321

		DX-236 Column		DX-321 Column	
Albumin	Protein Load	FT (mg)	Elution (mg)	FT (mg)	Elution (mg)
Bovine	1 mg	0	0.72	0.86	0.15
Goat	1 mg	0	0.79	0.93	0.11
Mouse	0.5 mg	0.05	0.59	0.49	0.13

FT = flowthrough

[0364] DX-236-Sepharose can be used as a "pan-albumin" binder for the affinity purification of nearly any mammalian albumin from serum. These results indicate that DX-236 could also be used to deplete albumin from serum samples prior to other analyses.

[0365] The data in Table 6 also show that DX-321-Sepharose captures the three non-human albumins poorly, as is expected based on the solution affinity data shown in Table 4. Of the three non-human albumins, BSA was captured most effectively by the DX-321-Sepharose resin. About 15% of the BSA present in the starting material was captured and subsequently eluted under the same chromatography conditions that allowed quantitative capture of DX-236-Sepharose resin. Goat serum albumin (GSA) and mouse serum albumin (MSA) were even less effectively captured by the DX-321-Sepharose column than with BSA. Thus, the DX-321-Sepharose column may be advantageously used to purify HSA from solutions containing non-human serum albumins.

EXAMPLE 5

[0366] Immunoglobulin Binding Peptides

[0367] Dissociation constants were determined for the following immunoglobulin-binding peptides, which were prepared using the Fc-region binding peptides of SEQ ID NOS: B57, B58, B108, B115, B124, and B143, respectively:

Ac-AGSYWCKIWDVCPQSPGPEGGGK-NH_2; (SEQ ID NO:371, designated DX392)

Ac-AGKYWCNLWGVCPANPGPEGGGK-NH_2 ; (SEQ ID NO:372, designated DX395)

Ac-AGTYWCTFWELPCDPAPGPEGGGK-NH_2 ; (SEQ ID NO:373, designated DX404)

Ac-AGPHNCDDHYWYCKWFPGPEGGGK-NH_2 ; (SEQ ID NO:374, designated DX389)

Ac-AGAATCSTSYWYYQWFCTDSPGPEGGGK-NH_2 ; and (SEQ ID NO:375, designated DX398)

Ac-AGYWYCWFPDRPECPLYPGPEGGGK-NH_2 . (SEQ ID NO:376, designated DX413)

[0368] Peptides were synthesized by BACHEM and then Oregon Green labeled and HPLC purified. Binding studies were performed using human plasma IgG isoforms: IgG1, IgG2, IgG3, and IgG4, obtained from Calbiochem.

[0369] Binding studies were carried out at either pH 4.0, 7.5, or 9.5, with or without salt in the following buffers:

[0370] 1) 10 mM Sodium Citrate, 0.01 % Tween 20, pH 4.0;

[0371] 2) 10 mM Sodium Citrate, 500 mM Sodium Chloride, 0.01 % Tween 20, pH 4.0;

[0372] 3) 10 mM Tris-HCl, 0.01 % Tween 20, pH 7.5;

[0373] 4) 10 mM Tris-HCl, 500 mM Sodium Chloride, 0.01 % Tween 20, pH 7.5;

[0374] 5) 10 mM Sodium Bicarbonate, 0.01 % Tween 20, pH 9.5;

[0375] 6) 10 mM Sodium Bicarbonate, 500 mM Sodium Chloride, 0.01 % Tween 20, pH 9.5; or

[0376] 7) TBS, 0.01 % Tween 20, pH 7.5.

TABLE 7

Summary of KD values for the IgG binding Oregon Green Labeled Peptides

		K_D(μM)						
Peptide	IgG isoform	pH 4.0 − salt	pH 4.0 + salt	pH 7.5 − salt	pH 7.5 + salt	pH 9.5 − salt	pH 9.5 + salt	TBS
DX389	IgG1	nb*	nb	nb	nb	nb	nb	nb
	IgG2	nb	nb	nb	binds$^{\Phi}$	nb	nb	nb
	IgG3	2.5 ± 1.0	1.8 ± 1.4	nb	binds	nb	nb	nb
	IgG4	nb	nb	nb	nb	nb	nb	nb
DX392	IgG1	nb	nb	nb	nb	nb	nb	nb
	IgG2	nb	nb	nb	nb	nb	nb	nb
	IgG3	0.32 ± 0.08	0.6 ± 0.2	nb	binds	nb	binds	nb
	IgG4	nb	nb	nb	nb	nb	nb	nb
DX395	IgG1	nb	nb	nb	nb	nb	nb	nb
	IgG2	nb	nb	nb	nb	nb	nb	nb
	IgG3	1.0 ± 0.26	1.8 ± 1	nb	1.9 ± 0.9	nb	binds	nb
	IgG4	nb	nb	binds	nb	nb	nb	nb
DX398	IgG1	2.4 ± 3.3	nb	4.6 ± 1.2	nb	nb	nb	nb
	IgG2	1.8 ± 1.2	nb	nb	nb	binds	nb	nb
	IgG3	0.02 ± 1.0	0.04 ± 0.01	nb	0.3 ± 0.03	binds	0.3 ± 0.1	binds
	IgG4	1.6 ± 1.5	nb	3.5 ± 0.8	nb	nb	nb	nb
DX404	IgG1	1.5 ± 0.8	2.0 ± 1.7	8.8 ± 4.0	nb	nb	nb	nd
	IgG2	1 ± 0.4	2.0 ± 1	8.6 +3.5	nb	nb	nb	nd
	IgG3	0.01 ± 0.01	0.20 ± 0.06	11 ± 5.4	3.7 ± 0.8	nb	binds	nd
	IgG4	nb	nb	nb	nb	nb	nb	nd#
DX413	IgG1	nb	nb	nb	nb	nb	nb	nd
	IgG2	nb	nb	nb	nb	nb	nb	nd
	IgG3	0.84 ± 0.08	1.1 ± 0.2	nb	nb	nb	nb	nd
	IgG4	nb	nb	nb	nb	nb	nb	nd

*nb: no significant binding observed

$^{\Phi}$binds: peptide appears to bind but the signal change could not be fit to obtain a reliable estimate of the K_D The K_D is estimated to be greater than 10 μM.

#nd: not determined.

[0378] The results shown in Table 7 demonstrate that DX389 specifically binds IgG3 at pH 4.0 in either the presence or absence of salt with moderate affinity (K_D≅2 μM). This interaction was not observed in the presence or absence of salt either at pH 7.5 or 9.5.

[0379] Peptide DX392 bound IgG3 specifically at pH 4.0 both in the presence and absence of salt and with a high affinity (K_D≅0.3-0.6 μM). This interaction was lower at pH 7.5 and pH 9.5 in the presence of salt and was not observed at either pH in the absence of salt.

[0380] Peptide DX395 bound IgG3 specifically at pH 4.0 in either the presence or absence of salt at moderate affinity (K_D≅1-2 μM). The affinity was approximately the same (K_D≅1.9 μM) in the presence of salt. This interaction was diminished at pH 9.5 in the presence of salt and was not observed at pH 7.5 or 9.5 in the absence of salt.

[0381] Peptide DX398 bound all four IgG isoforms at pH 4.0 in the absence of salt with moderate affinity (K_D≅2 μM) for IgG1, IgG2, and IgG4, and high affinity (K_D≅0.02 μM) for IgG3. At pH 4.0 in the presence of salt, peptide DX398 maintained a high affinity for IgG3 but did not interact with IgG, IgG2, or IgG4.

[0382] At pH 7.5, DX398 bound IgG1 and IgG4 only in the absence of salt and in the presence of salt, only bound IgG3. At pH 9.5, this peptide only bound IgG3 and the interaction was favored by increasing ionic strength.

[0383] Peptide DX404 bound IgG1 and IgG2 at pH 4.0 in the presence or absence of salt with moderate affinity (K_D≅2 μM) and had a higher affinity for IgG3 (K_D≅0,01 μM). In the presence of salt, the affinity for IgG3 increased to 0.2 μM. The affinity for IgG1 and IgG2 was reduced at pH 7.5 in the absence of salt and not observed in the presence of salt or at pH 9.5. IgG3 binding at pH 7.5 and 9.5 was favored in the presence of salt.

[0384] Peptide DX413 bound only to IgG3 at pH 4.0 in the presence or absence of salt with moderate affinity (K_D≅1.0 μM).

[0385] The data in Table 7 indicate that the peptides bind IgG with varying isoform specificities in a pH and salt-dependent manner. In general, the peptides in Table 8 can be grouped into two "classes" based on their specificity and mode of interaction:

[0386] Class 1 includes DX389, DX392, DX395 and DX413. Essentially these peptides all appear to exhibit primary specificity for IgG3. In addition, the interaction appears to be favored by low pH and high ionic strength. Binding is weakest at high pH and low salt.

[0387] Class 2 includes DX398. This peptide exhibits isoform specificity that is alterable by ionic strength. At low pH in the absence of salt, this peptide binds all IgG isoforms but in the presence of salt, it only binds IgG3 with very high affinity (K_D≅0.04-0.3 μM) at pH 4.0, 7.5, and 9.5 (See Table 7). DX404 is similar to DX398, however this peptide, unlike DX398, does not exhibit the salt-dependent IgG3 specificity at pH 4.0 but does exhibit salt-dependent IgG3 specificity at pH 7.5 and 9.5.

[0388] Other embodiments are within the following claims.

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5-12
<223> OTHER INFORMATION: Xaa = any common alfa-amino acids, except cysteine

<400> SEQUENCE: 22

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
1 5 10 15

<210> SEQ ID NO 23
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: template sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1, 2, 17, 18
<223> OTHER INFORMATION: Xaa = Ala, Asp, Phe, Gly, His, Leu, Asn, Pro, Arg, Ser, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3, 5-14, 16
<223> OTHER INFORMATION: Xaa = common alfa-amino acids, except cysteine

<400> SEQUENCE: 23

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

<210> SEQ ID NO 24
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: modified serum albumin-binding agent
<220> FEATURE:
<221> NAME/KEY: ACETYLATION
<222> LOCATION: 1
<223> OTHER INFORMATION: acetyl capping group
<220> FEATURE:
<221> NAME/KEY: AMIDATION
<222> LOCATION: 29
<223> OTHER INFORMATION: amide capping group
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 23
<223> OTHER INFORMATION: Xaa = 6-aminohexanoic acid group

<400> SEQUENCE: 24

Ala Glu Gly Thr Gly Asp Arg Asn Met Cys Lys Phe Ser Trp Ile Arg
 1   5   10   15
Ser Pro Ala Phe Cys Ala Arg Ala Asp Pro Glu Xaa Lys
            20   25

<210> SEQ ID NO 25
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: template sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1-3, 5-10, 12-14
<223> OTHER INFORMATION: Xaa = any amino acid except cysteine (Cys)

<400> SEQUENCE: 25

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1   5   10

<210> SEQ ID NO 26
<211> LENGTH: 585
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560
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Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> SEQ ID NO 27
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 27

Ala Asp Phe Cys Glu Gly Lys Asp Met Ile Asp Trp Val Tyr Cys Arg
1 5 10 15

Leu Tyr

<210> SEQ ID NO 28
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 28

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 29
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 29

Asp Trp Asp Cys Val Thr Arg Trp Ala Asn Arg Asp Gln Gln Cys Trp
1 5 10 15

Gly Pro

<210> SEQ ID NO 30
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 30

Asp Trp Asp Cys Val Thr Arg Trp Ala Asn Arg Asp Gln Gln Cys Trp
1 5 10 15

Ala Leu

<210> SEQ ID NO 31
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 31

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Asp Trp Asp Cys Val Thr Asp Trp Ala Asn Arg His Gln His Cys Trp
1 5 10 15

Ala Leu

<210> SEQ ID NO 32
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 32

Asp Trp Gln Cys Val Lys Asp Trp Ala Asn Arg Arg Arg Gly Cys Met
1 5 10 15

Ala Asp

<210> SEQ ID NO 33
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 33

Arg Asn Met Cys Lys Phe Ser Trp Ile Arg Ser Pro Ala Phe Cys Ala
1 5 10 15

Arg Ala

<210> SEQ ID NO 34
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 34

Ala Glu Gly Thr Gly Asp Ala Asp Phe Cys Glu Gly Lys Asp Met Ile
1 5 10 15

Asp Trp Val Tyr Cys Arg Leu Tyr Asp Pro Glu
20 25

<210> SEQ ID NO 35
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 35

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
20 25

<210> SEQ ID NO 36
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 36

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Ala Glu Gly Thr Gly Asp Asp Trp Asp Cys Val Thr Arg Trp Ala Asn
1 5 10 15

Arg Asp Gln Gln Cys Trp Gly Pro Asp Pro Glu
20 25

<210> SEQ ID NO 37
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 37

Ala Glu Gly Thr Gly Asp Asp Trp Asp Cys Val Thr Arg Trp Ala Asn
1 5 10 15

Arg Asp Gln Gln Cys Trp Ala Leu Asp Pro Glu
20 25

<210> SEQ ID NO 38
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 38

Ala Glu Gly Thr Gly Asp Asp Trp Asp Cys Val Thr Asp Trp Ala Asn
1 5 10 15

Arg His Gln His Cys Trp Ala Leu Asp Pro Glu
20 25

<210> SEQ ID NO 39
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 39

Ala Glu Gly Thr Gly Asp Asp Trp Gln Cys Val Lys Asp Trp Ala Asn
1 5 10 15

Arg Arg Arg Gly Cys Met Ala Asp Asp Pro Glu
20 25

<210> SEQ ID NO 40
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 40

Ala Glu Gly Thr Gly Asp Arg Asn Met Cys Lys Phe Ser Trp Ile Arg
1 5 10 15

Ser Pro Ala Phe Cys Ala Arg Ala Asp Pro Glu
20 25

<210> SEQ ID NO 41
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 41

Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Ala Cys
1 5 10

<210> SEQ ID NO 42
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 42

Cys Asp Arg Ile Ala Trp Tyr Pro Gln Ala Leu Cys
1 5 10

<210> SEQ ID NO 43
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 43

Cys Asp Arg Ile Ala Trp Tyr Pro Ala His Leu Cys
1 5 10

<210> SEQ ID NO 44
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 44

Cys Asp Arg Ile Ala Trp Tyr Ala Gln His Leu Cys
1 5 10

<210> SEQ ID NO 45
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 45

Cys Asp Arg Ile Ala Trp Ala Pro Gln His Leu Cys
1 5 10

<210> SEQ ID NO 46
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 46

Cys Asp Arg Ile Ala Ala Tyr Pro Gln His Leu Cys
1 5 10

<210> SEQ ID NO 47
<211> LENGTH: 12

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 47

Cys Asp Arg Ala Ala Trp Tyr Pro Gln His Leu Cys
1 5 10

<210> SEQ ID NO 48
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 48

Cys Asp Ala Ile Ala Trp Tyr Pro Gln His Leu Cys
1 5 10

<210> SEQ ID NO 49
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 49

Cys Ala Arg Ile Ala Trp Tyr Pro Gln His Leu Cys
1 5 10

<210> SEQ ID NO 50
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 50

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Ala

<210> SEQ ID NO 51
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 51

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Ala Leu

<210> SEQ ID NO 52
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 52

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Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Ala
1 5 10 15

Phe Leu

<210> SEQ ID NO 53
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 53

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Ala Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 54
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 54

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln Ala Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 55
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 55

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Ala His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 56
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 56

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Ala Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 57
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 57

Phe Trp Phe Cys Asp Arg Ile Ala Trp Ala Pro Gln His Leu Cys Glu

-continued

1 5 10 15

Phe Leu

<210> SEQ ID NO 58
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 58

Phe Trp Phe Cys Asp Arg Ile Ala Ala Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 59
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 59

Phe Trp Phe Cys Asp Arg Ala Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 60
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 60

Phe Trp Phe Cys Asp Ala Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 61
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 61

Phe Trp Phe Cys Ala Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 62
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 62

Phe Trp Ala Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

-continued

Phe Leu

<210> SEQ ID NO 63
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 63

Phe Ala Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 64
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 64

Ala Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu

<210> SEQ ID NO 65
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 65

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Ala Pro Glu
20 25

<210> SEQ ID NO 66
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 66

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Ala Asp Pro Glu
20 25

<210> SEQ ID NO 67
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 67

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr

-continued

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 1               5                  10                  15

Pro Gln His Leu Cys Glu Ala Leu Asp Pro Glu
            20                  25


<210> SEQ ID NO 68
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 68

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Pro Gln His Leu Cys Ala Phe Leu Asp Pro Glu
            20                  25


<210> SEQ ID NO 69
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 69

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Pro Gln His Ala Cys Glu Phe Leu Asp Pro Glu
            20                  25


<210> SEQ ID NO 70
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 70

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Pro Gln Ala Leu Cys Glu Phe Leu Asp Pro Glu
            20                  25


<210> SEQ ID NO 71
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 71

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Pro Ala His Leu Cys Glu Phe Leu Asp Pro Glu
            20                  25


<210> SEQ ID NO 72
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
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<400> SEQUENCE: 72

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Ala Gln His Leu Cys Glu Phe Leu Asp Pro Glu
20 25

<210> SEQ ID NO 73
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 73

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Ala
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
20 25

<210> SEQ ID NO 74
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 74

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Ala Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
20 25

<210> SEQ ID NO 75
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 75

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ala Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
20 25

<210> SEQ ID NO 76
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 76

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Ala Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
20 25

<210> SEQ ID NO 77
<211> LENGTH: 27

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 77

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Ala Arg Ile Ala Trp Tyr
 1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
 20 25

<210> SEQ ID NO 78
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 78

Ala Glu Gly Thr Gly Asp Phe Trp Ala Cys Asp Arg Ile Ala Trp Tyr
 1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
 20 25

<210> SEQ ID NO 79
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 79

Ala Glu Gly Thr Gly Asp Phe Ala Phe Cys Asp Arg Ile Ala Trp Tyr
 1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
 20 25

<210> SEQ ID NO 80
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 80

Ala Glu Gly Thr Gly Asp Ala Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
 20 25

<210> SEQ ID NO 81
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 81

Ala Glu Gly Thr Gly Ala Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu
 20 25

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<210> SEQ ID NO 82
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 82

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Ala Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 83
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 83

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Ala Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 84
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 84

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Ala Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 85
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 85

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Ala Phe Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 86
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 86

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr

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 1               5                  10                  15

Pro Gln His Ala Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20                  25                  30


<210> SEQ ID NO 87
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 87

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Pro Gln Ala Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20                  25                  30


<210> SEQ ID NO 88
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 88

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Pro Ala His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20                  25                  30


<210> SEQ ID NO 89
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 89

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1               5                  10                  15

Ala Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20                  25                  30


<210> SEQ ID NO 90
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 90

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Trp Ala
 1               5                  10                  15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20                  25                  30


<210> SEQ ID NO 91
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
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<400> SEQUENCE: 91

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ile Ala Ala Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 92
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 92

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Arg Ala Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 93
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 93

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Asp Ala Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 94
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 94

Ala Glu Gly Thr Gly Asp Phe Trp Phe Cys Ala Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 95
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 95

Ala Glu Gly Thr Gly Asp Phe Trp Ala Cys Asp Arg Ile Ala Trp Tyr
1 5 10 15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 96
<211> LENGTH: 31

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 96

Ala Glu Gly Thr Gly Asp Phe Ala Phe Cys Asp Arg Ile Ala Trp Tyr
 1   5   10   15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20   25   30

<210> SEQ ID NO 97
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 97

Ala Glu Gly Thr Gly Asp Ala Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1   5   10   15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20   25   30

<210> SEQ ID NO 98
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 98

Ala Glu Gly Thr Gly Ala Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr
 1   5   10   15

Pro Gln His Leu Cys Glu Phe Leu Asp Pro Glu Gly Gly Gly Lys
            20   25   30

<210> SEQ ID NO 99
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Ala, Gln, Leu, Lys, Phe, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Asn, Gln, Glu, Ile, Thr, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Asn, Gly, Phe, Thr, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Ala, Leu, His, Met, Phe, Ser, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa = Ile, Phe, Pro, Ser, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gln, Glu, Lys, Pro, Trp, or Tyr

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gln, Gly, Leu, Pro, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Ile, Leu, Lys, Met, Pro, Trp or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(0)
<223> OTHER INFORMATION: Xaa = Gln, Gly, Ile, Phe, Thr, Trp, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Glu, Gly, Leu, Lys, Pro, or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(0)
<223> OTHER INFORMATION: Xaa = Glu, His, Ile, Leu, Lys, Ser, Trp, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Asn, His, Ile, Met, Phe, Pro, or Ser

<400> SEQUENCE: 99

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1   5   10

<210> SEQ ID NO 100
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Ala, Gln, Leu, Lys, Phe, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Asn, Gln, Glu, Ile, Thr, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Asn, Gly, Phe, Thr, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 7
<223> OTHER INFORMATION: Xaa = Ala, Leu, His, Met, Phe, Ser, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 8
<223> OTHER INFORMATION: Xaa = Ile, Phe, Pro, Ser, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gln, Glu, Lys, Pro, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gln, Gly, Leu, Pro, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Ile, Leu, Lys, Met, Pro, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(0)
<223> OTHER INFORMATION: Xaa = Gln, Gly, Ile, Phe, Thr, Trp, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(0)

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<223> OTHER INFORMATION: Xaa = Asp, Glu, Gly, Leu, Lys, Pro, or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (15)...(0)
<223> OTHER INFORMATION: Xaa = Glu, His, Ile, Leu, Lys, Ser, Trp, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Asn, His, Ile, Met, Phe, Pro, or Ser

<400> SEQUENCE: 100

Ala Gly Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1 5 10 15

Gly Thr

<210> SEQ ID NO 101
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Gln, Glu, Phe, or Met
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Asp, Pro, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Ile, Ser, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = His, Met, Phe or Pro
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa = Asn, Leu, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Asn, His, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Met, Phe, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gly, Phe, or Trp

<400> SEQUENCE: 101

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 1 5 10

<210> SEQ ID NO 102
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Arg, Phe, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2

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<223> OTHER INFORMATION: Xaa = Arg, Leu, Ser, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Asn, Asp, Phe, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Gln, Glu, Phe, or Met
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa = Asp, Pro, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(0)
<223> OTHER INFORMATION: Xaa = Ile, Ser, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(0)
<223> OTHER INFORMATION: Xaa = His, Met, Phe or Pro
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(0)
<223> OTHER INFORMATION: Xaa = Asn, Leu, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Asn, His, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Met, Phe or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gly, Phe, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Asn, or Asp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (15)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Phe, Pro, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(0)
<223> OTHER INFORMATION: Xaa = Arg, His, Phe, or Ser

<400> SEQUENCE: 102

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1   5   10   15

<210> SEQ ID NO 103
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Arg, Phe, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Arg, Leu, Ser, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Asn, Asp, Phe, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT

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<222> LOCATION: 7
<223> OTHER INFORMATION: Xaa = Gln, Glu, Phe, or Met
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 8
<223> OTHER INFORMATION: Xaa = Asp, Pro, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(0)
<223> OTHER INFORMATION: Xaa = Ile, Ser, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(0)
<223> OTHER INFORMATION: Xaa = His, Met, Phe or Pro
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)...(0)
<223> OTHER INFORMATION: Xaa = Asn, Leu, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Asn, His, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Met, Phe, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Gly, Phe, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Asn, or Asp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (17)...(0)
<223> OTHER INFORMATION: Xaa = Arg, Phe, Pro, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (18)...(0)
<223> OTHER INFORMATION: Xaa = Arg, His, Phe, or Ser

<400> SEQUENCE: 103

Gly Ser Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 1   5   10   15

Xaa Xaa Ala Pro
            20

<210> SEQ ID NO 104
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 104

Pro Thr Val Val Gln Pro Lys Phe His Ala Phe Thr His Glu Asp Leu
 1   5   10   15

Leu Trp Ile Phe
            20

<210> SEQ ID NO 105
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 105

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

Gln His Glu Leu
20

<210> SEQ ID NO 106
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 106

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

Ile Tyr Met Phe
20

<210> SEQ ID NO 107
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 107

Cys Gln Thr Thr Trp Pro Phe Thr Met Met Gln Cys
1 5 10

<210> SEQ ID NO 108
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 108

Cys Val Thr Met Trp Pro Phe Glu Gln Ile Phe Cys
1 5 10

<210> SEQ ID NO 109
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 109

Cys Phe Thr Tyr Tyr Pro Phe Thr Thr Phe Ser Cys
1 5 10

<210> SEQ ID NO 110
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 110

Cys Trp Thr Lys Phe Pro Phe Asp Leu Val Trp Cys
1 5 10

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<210> SEQ ID NO 111
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 111

Cys Val Ser Tyr Trp Pro His Phe Val Pro Val Cys
1 5 10

<210> SEQ ID NO 112
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 112

Cys Tyr Ile Ser Phe Pro Phe Asp Gln Met Tyr Cys
1 5 10

<210> SEQ ID NO 113
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 113

Cys Ser Val Gln Tyr Pro Phe Glu Val Val Val Cys
1 5 10

<210> SEQ ID NO 114
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 114

Cys Trp Thr Gln Tyr Pro Phe Asp His Ser Thr Cys
1 5 10

<210> SEQ ID NO 115
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 115

Cys Ile Thr Trp Pro Phe Lys Arg Pro Trp Pro Cys
1 5 10

<210> SEQ ID NO 116
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 116

Cys Ile Ser Trp Pro Phe Glu Met Pro Phe His Cys
1 5 10

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<210> SEQ ID NO 117
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 117

Cys Ile Thr Trp Pro Phe Lys Arg Pro Trp Pro Cys
1 5 10

<210> SEQ ID NO 118
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 118

Cys Ile Thr Tyr Pro Phe His Glu Met Phe Pro Cys
1 5 10

<210> SEQ ID NO 119
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 119

Cys Ile Thr Trp Pro Phe Gln Thr Ser Tyr Pro Cys
1 5 10

<210> SEQ ID NO 120
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 120

Cys Lys Phe Ser Trp Ile Arg Ser Pro Ala Phe Cys
1 5 10

<210> SEQ ID NO 121
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 121

Cys Trp Ile Val Asp Glu Asp Gly Thr Lys Trp Cys
1 5 10

<210> SEQ ID NO 122
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 122

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Cys Asp Ser Ala Tyr Trp Gln Glu Ile Pro Ala Cys
1 5 10

<210> SEQ ID NO 123
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 123

Cys Leu Trp Asp Pro Met Leu Cys
1 5

<210> SEQ ID NO 124
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 124

Cys Glu His Pro Tyr Trp Thr Glu Val Asp Lys Cys
1 5 10

<210> SEQ ID NO 125
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 125

Cys Asp Thr Pro Tyr Trp Arg Asp Leu Trp Gln Cys
1 5 10

<210> SEQ ID NO 126
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 126

Cys Gln Leu Pro Tyr Met Ser Thr Pro Glu Phe Cys
1 5 10

<210> SEQ ID NO 127
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 127

Cys Gly Arg Gly Phe Asp Lys Glu Ser Ile Tyr Cys
1 5 10

<210> SEQ ID NO 128
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

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<400> SEQUENCE: 128

Cys Val Thr Tyr Ile Gly Thr Trp Glu Thr Val Cys
1 5 10

<210> SEQ ID NO 129
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 129

Cys Thr Asp Thr Asn Trp Ser Trp Met Phe Asp Cys
1 5 10

<210> SEQ ID NO 130
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 130

Cys Thr Leu Glu Ile Gly Thr Trp Phe Val Phe Cys
1 5 10

<210> SEQ ID NO 131
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 131

Cys Lys Ile Ala Leu Phe Gln His Phe Glu Val Cys
1 5 10

<210> SEQ ID NO 132
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 132

Cys Ile Lys Leu Tyr Gly Leu Gly His Met Tyr Cys
1 5 10

<210> SEQ ID NO 133
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 133

Cys Glu Met Gln Ser Ile Ile Pro Trp Trp Glu Cys
1 5 10

<210> SEQ ID NO 134
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 134

Cys Val Glu Lys Tyr Tyr Trp Asp Val Leu Ile Cys
1 5 10

<210> SEQ ID NO 135
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 135

Cys Pro His Gly Arg Tyr Ser Met Phe Pro Cys
1 5 10

<210> SEQ ID NO 136
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 136

Cys Asn Val Arg Trp Thr Asp Thr Pro Tyr Trp Cys
1 5 10

<210> SEQ ID NO 137
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 137

Cys Thr Tyr Asp Pro Ile Ala Asp Leu Leu Phe Cys
1 5 10

<210> SEQ ID NO 138
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 138

Cys Met Asp Trp Pro Asn His Arg Asp Cys
1 5 10

<210> SEQ ID NO 139
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 139

Cys Phe Pro Ile His Leu Thr Met Phe Cys
1 5 10

<210> SEQ ID NO 140
<211> LENGTH: 10
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 140

Cys Gln Thr Ser Phe Thr Asn Tyr Trp Cys
1 5 10

<210> SEQ ID NO 141
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 141

Cys Met Glu Phe Gly Pro Asp Asp Cys
1 5

<210> SEQ ID NO 142
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 142

Cys Ser Trp Asp Pro Ile Phe Cys
1 5

<210> SEQ ID NO 143
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 143

Cys Ala Trp Asp Pro Leu Val Cys
1 5

<210> SEQ ID NO 144
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 144

Cys His Ile Tyr Asp Trp Phe Cys
1 5

<210> SEQ ID NO 145
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 145

Cys Leu Trp Asp Pro Met Ile Cys
1 5

<210> SEQ ID NO 146

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 146

Cys Ser Pro Pro Gly Lys Thr Cys
1 5

<210> SEQ ID NO 147
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 147

Cys Thr Phe Trp Gln Tyr Trp Cys
1 5

<210> SEQ ID NO 148
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 148

Cys Met Phe Glu Leu Pro Phe Cys
1 5

<210> SEQ ID NO 149
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 149

Cys Phe Ser Lys Pro Asp Gln Cys
1 5

<210> SEQ ID NO 150
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 150

Cys Phe Tyr Gln Trp Trp Gly Cys
1 5

<210> SEQ ID NO 151
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 151

Cys Thr Trp Asp Pro Ile Phe Cys
1 5

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<210> SEQ ID NO 152
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 152

Cys Trp Leu Tyr Asp Cys
1 5

<210> SEQ ID NO 153
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 153

Cys Asp Lys Tyr Gly Cys
1 5

<210> SEQ ID NO 154
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 154

Cys Ser Lys Asp Thr Cys
1 5

<210> SEQ ID NO 155
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 155

Leu Arg Asp Cys Gln Thr Thr Trp Pro Phe Met Met Gln Cys Pro Asn
1 5 10 15

Asn

<210> SEQ ID NO 156
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 156

Asn Arg Glu Cys Val Thr Met Trp Pro Phe Glu Gln Ile Phe Cys Pro
1 5 10 15

Trp Pro

<210> SEQ ID NO 157
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

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<400> SEQUENCE: 157

Leu Arg Ser Cys Phe Thr Tyr Tyr Pro Phe Thr Thr Phe Ser Cys Ser
1 5 10 15

Pro Ala

<210> SEQ ID NO 158
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 158

Leu Ser His Cys Trp Thr Lys Phe Pro Phe Asp Leu Val Trp Cys Asp
1 5 10 15

Ser Pro

<210> SEQ ID NO 159
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 159

Leu Arg Met Cys Val Ser Tyr Trp Pro His Phe Val Pro Val Cys Glu
1 5 10 15

Asn Pro

<210> SEQ ID NO 160
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 160

Leu Arg Asp Cys Tyr Ile Ser Phe Pro Phe Asp Gln Met Tyr Cys Ser
1 5 10 15

His Phe

<210> SEQ ID NO 161
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 161

Phe Arg His Cys Ser Val Gln Tyr Pro Phe Glu Val Val Val Cys Pro
1 5 10 15

Ala Asn

<210> SEQ ID NO 162
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

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<400> SEQUENCE: 162

Leu Arg Asn Cys Trp Thr Gln Tyr Pro Phe Asp His Ser Thr Cys Ser
1 5 10 15

Pro Asn

<210> SEQ ID NO 163
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 163

Asp Ser Met Cys Ile Thr Trp Pro Phe Lys Arg Pro Trp Pro Cys Ala
1 5 10 15

Asn

<210> SEQ ID NO 164
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 164

Ala Phe Met Cys Ile Ser Trp Pro Phe Glu Met Pro Phe His Cys Ser
1 5 10 15

Pro Asp

<210> SEQ ID NO 165
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 165

Asp Ser Met Cys Ile Thr Trp Pro Phe Lys Arg Pro Trp Pro Cys Ala
1 5 10 15

Asn Pro

<210> SEQ ID NO 166
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 166

Trp Asp Leu Cys Ile Thr Tyr Pro Phe His Glu Met Phe Pro Cys Glu
1 5 10 15

Asp Gly

<210> SEQ ID NO 167
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 167

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Gly Gly Glu Cys Ile Thr Trp Pro Phe Gln Thr Ser Tyr Pro Cys Thr
1 5 10 15

Asn Gly

<210> SEQ ID NO 168
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 168

Arg Asn Met Cys Lys Phe Ser Trp Ile Arg Ser Pro Ala Phe Cys Ala
1 5 10 15

Arg Ala

<210> SEQ ID NO 169
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 169

Phe Ser Leu Cys Trp Ile Val Asp Glu Asp Gly Thr Lys Trp Cys Leu
1 5 10 15

Pro

<210> SEQ ID NO 170
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 170

Arg Trp Phe Cys Asp Ser Ala Tyr Trp Gln Glu Ile Pro Ala Cys Ala
1 5 10 15

Arg Asp

<210> SEQ ID NO 171
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 171

Arg Trp Tyr Cys Leu Trp Asp Pro Met Leu Cys Met Ser Asp
1 5 10

<210> SEQ ID NO 172
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 172

Ala Trp Tyr Cys Glu His Pro Tyr Trp Thr Glu Val Asp Lys Cys His
1 5 10 15

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Ser Ser

<210> SEQ ID NO 173
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 173

Ser Asp Phe Cys Asp Thr Pro Tyr Trp Arg Asp Leu Trp Gln Cys Asn
1 5 10 15

Ser Pro

<210> SEQ ID NO 174
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 174

Leu Pro Trp Cys Gln Leu Pro Tyr Met Ser Thr Pro Glu Phe Cys Ile
1 5 10 15

Arg Pro

<210> SEQ ID NO 175
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 175

Tyr His Val Cys Gly Arg Gly Phe Asp Lys Glu Ser Ile Tyr Cys Lys
1 5 10 15

Phe Leu

<210> SEQ ID NO 176
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agents

<400> SEQUENCE: 176

Ser Phe Cys Val Thr Tyr Ile Gly Thr Trp Glu Thr Val Cys Lys Arg
1 5 10 15

Ser

<210> SEQ ID NO 177
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 177

Asn Asp Gly Cys Thr Asp Thr Asn Trp Ser Trp Met Phe Asp Cys Pro
1 5 10 15

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Pro Leu

<210> SEQ ID NO 178
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 178

Trp Arg Asp Cys Thr Leu Glu Ile Gly Thr Trp Phe Val Phe Cys Lys
1 5 10 15

Gly Ser

<210> SEQ ID NO 179
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 179

Ser Pro Tyr Cys Lys Ile Ala Leu Phe Gln His Phe Glu Val Cys Ala
1 5 10 15

Ala Asp

<210> SEQ ID NO 180
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 180

Arg His Trp Cys Ile Lys Leu Tyr Gly Leu Gly His Met Tyr Cys Asn
1 5 10 15

Arg Ser

<210> SEQ ID NO 181
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 181

Asp His Ala Cys Glu Met Gln Ser Ile Ile Pro Trp Trp Glu Cys Tyr
1 5 10 15

Pro His

<210> SEQ ID NO 182
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 182

Pro Arg Ser Cys Val Glu Lys Tyr Tyr Trp Asp Val Leu Ile Cys Gly
1 5 10 15

Phe Phe

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<210> SEQ ID NO 183
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 183

Phe His Thr Cys Pro His Gly Arg Tyr Ser Met Phe Pro Cys Asp Tyr
1 5 10 15

Trp

<210> SEQ ID NO 184
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 184

His Gly Trp Cys Asn Val Arg Trp Thr Asp Thr Pro Tyr Trp Cys Ala
1 5 10 15

Phe Ser

<210> SEQ ID NO 185
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 185

Tyr Arg Val Cys Thr Tyr Asp Pro Ile Ala Asp Leu Leu Phe Cys Pro
1 5 10 15

Phe Asn

<210> SEQ ID NO 186
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 186

Arg Ser Phe Cys Met Asp Trp Pro Asn His Arg Asp Cys Asp Tyr Ser
1 5 10 15

<210> SEQ ID NO 187
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 187

Phe Trp Asp Cys Phe Pro Ile His Leu Thr Met Phe Cys Asp Arg Phe
1 5 10 15

<210> SEQ ID NO 188
<211> LENGTH: 16
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 188

Tyr Leu Tyr Cys Gln Thr Ser Phe Thr Asn Tyr Trp Cys Ala Phe His
 1 5 10 15

<210> SEQ ID NO 189
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 189

Gly Leu Tyr Cys Met Glu Phe Gly Pro Asp Asp Cys Ala Trp His
 1 5 10 15

<210> SEQ ID NO 190
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 190

Lys Asn Phe Cys Ser Trp Asp Pro Ile Phe Cys Gly Ile His
 1 5 10

<210> SEQ ID NO 191
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 191

Lys Trp Tyr Cys Ala Trp Asp Pro Leu Val Cys Glu Ile Phe
 1 5 10

<210> SEQ ID NO 192
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 192

Trp Thr Thr Cys His Ile Tyr Asp Trp Phe Cys Ser Ser Ser
 1 5 10

<210> SEQ ID NO 193
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 193

Gln Trp Tyr Cys Leu Trp Asp Pro Met Ile Cys Gly Leu Ile
 1 5 10

<210> SEQ ID NO 194

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<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 194

Gln Thr Asn Cys Ser Pro Pro Gly Lys Thr Cys Asp Lys Asn
1 5 10

<210> SEQ ID NO 195
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 195

Ala Ile Cys Thr Phe Trp Gln Tyr Trp Cys Leu Glu Pro
1 5 10

<210> SEQ ID NO 196
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 196

Phe Glu Trp Cys Met Phe Glu Leu Pro Phe Cys Ser Trp Pro
1 5 10

<210> SEQ ID NO 197
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 197

Gln Glu Gly Cys Phe Ser Lys Pro Asp Gln Cys Lys Val Met
1 5 10

<210> SEQ ID NO 198
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 198

Leu Glu Tyr Cys Phe Tyr Gln Trp Trp Gly Cys Pro His Ala
1 5 10

<210> SEQ ID NO 199
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 199

Tyr Gln Phe Cys Thr Trp Asp Pro Ile Phe Cys Gly Trp His
1 5 10

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<210> SEQ ID NO 200
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 200

Leu Trp Asp Cys Trp Leu Tyr Asp Cys Glu Gly Asn
1 5 10

<210> SEQ ID NO 201
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 201

Val His Ser Cys Asp Lys Tyr Gly Cys Val Asn Ala
1 5 10

<210> SEQ ID NO 202
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 202

Phe Glu His Cys Ser Lys Asp Thr Cys Ser Gly Asn
1 5 10

<210> SEQ ID NO 203
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 203

Val Ala Trp Cys Thr Ile Phe Leu Cys Leu Asp Val
1 5 10

<210> SEQ ID NO 204
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 204

Phe Lys Ile Cys Asp Gln Trp Phe Cys Leu Met Pro
1 5 10

<210> SEQ ID NO 205
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 205

His Val Gly Cys Asn Asn Ala Leu Cys Met Gln Tyr

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1 5 10

<210> SEQ ID NO 206
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 206

Trp Lys Val Cys Asp His Phe Phe Cys Leu Ser Pro
1 5 10

<210> SEQ ID NO 207
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 207

Asn His Gly Cys Trp His Phe Ser Cys Ile Trp Asp
1 5 10

<210> SEQ ID NO 208
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 208

Phe Arg Asn Cys Glu Pro Trp Met Leu Arg Phe Gly Cys Asn Pro Arg
1 5 10 15

<210> SEQ ID NO 209
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 209

Ala Asp Phe Cys Glu Gly Lys Asp Met Ile Asp Trp Val Tyr Cys Arg
1 5 10 15

Leu Tyr

<210> SEQ ID NO 210
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 210

Phe Trp Phe Cys Asp Arg Ile Ala Trp Tyr Pro Gln His Leu Cys Glu
1 5 10 15

Phe Leu Asp

<210> SEQ ID NO 211
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 211

Asp Trp Asp Cys Val Thr Arg Trp Ala Asn Arg Asp Gln Gln Cys Trp
 1   5   10   15

Gly Pro

<210> SEQ ID NO 212
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 212

Asp Trp Asp Cys Val Thr Arg Trp Ala Asn Arg Asp Gln Gln Cys Trp
 1   5   10   15

Ala Leu

<210> SEQ ID NO 213
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 213

Asp Trp Asp Cys Val Thr Asp Trp Ala Asn Arg His Gln His Cys Trp
 1   5   10   15

Ala Leu

<210> SEQ ID NO 214
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 214

Asp Trp Gln Cys Val Lys Asp Trp Ala Asn Arg Arg Arg Gly Cys Met
 1   5   10   15

Ala Asp

<210> SEQ ID NO 215
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: example of serum albumin-binding agent

<400> SEQUENCE: 215

Arg Asn Met Cys Lys Phe Ser Trp Ile Arg Ser Pro Ala Phe Cys Ala
 1   5   10   15

Arg Ala Asp Pro
            20

<210> SEQ ID NO 216
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 216

Gly Asp Leu Arg Asp Cys Gln Thr Thr Trp Pro Phe Thr Met Met Gln
1 5 10 15

Cys Pro Asn Asn Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 217
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 217

Gly Asp Asn Arg Glu Cys Val Thr Met Trp Pro Phe Glu Gln Ile Phe
1 5 10 15

Cys Pro Trp Pro Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 218
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 218

Gly Asp Leu Arg Ser Cys Phe Thr Tyr Tyr Pro Phe Thr Thr Phe Ser
1 5 10 15

Cys Ser Pro Ala Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 219
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 219

Gly Asp Asp Ser Met Cys Ile Thr Trp Pro Phe Lys Arg Pro Trp Pro
1 5 10 15

Cys Ala Asn Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 220
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 220

Gly Asp Arg Asn Met Cys Lys Phe Ser Trp Ile Arg Ser Pro Ala Phe
1 5 10 15

Cys Ala Arg Ala Asp Pro Gly Gly Gly Lys
20 25

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<210> SEQ ID NO 221
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 221

Gly Asp Phe Ser Leu Cys Trp Ile Val Asp Glu Asp Gly Thr Lys Trp
1 5 10 15

Cys Leu Pro Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 222
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 222

Gly Asp Arg Trp Phe Cys Asp Ser Ala Tyr Trp Gln Glu Ile Pro Ala
1 5 10 15

Cys Ala Arg Asp Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 223
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 223

Gly Asp Ser Asp Phe Cys Asp Thr Pro Tyr Trp Arg Asp Leu Trp Gln
1 5 10 15

Cys Asn Ser Pro Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 224
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 224

Gly Asp Ser Phe Cys Val Thr Tyr Ile Gly Thr Trp Glu Thr Val Cys
1 5 10 15

Lys Arg Ser Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 225
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 225

Gly Asp Asn Asp Gly Cys Thr Asp Thr Asn Trp Ser Trp Met Phe Asp
1 5 10 15

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Cys Pro Pro Leu Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 226
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 226

Gly Asp Ser Pro Tyr Cys Lys Ile Ala Leu Phe Gln His Phe Glu Val
1 5 10 15

Cys Ala Ala Asp Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 227
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 227

Gly Asp Pro Arg Ser Cys Val Glu Lys Tyr Tyr Trp Asp Val Leu Ile
1 5 10 15

Cys Gly Phe Phe Asp Pro Gly Gly Gly Lys
20 25

<210> SEQ ID NO 228
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 228

Gly Ser Arg Ser Phe Cys Met Asp Trp Pro Asn His Arg Asp Cys Asp
1 5 10 15

Tyr Ser Ala Pro Gly Gly Gly Lys
20

<210> SEQ ID NO 229
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 229

Ala Gly Lys Trp Tyr Cys Ala Trp Asp Pro Leu Val Cys Glu Ile Phe
1 5 10 15

Gly Thr Gly Gly Gly Lys
20

<210> SEQ ID NO 230
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 230

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Ala Gly Trp Thr Thr Cys His Ile Tyr Asp Trp Phe Cys Ser Ser Ser
1 5 10 15

Gly Thr Gly Gly Gly Lys
20

<210> SEQ ID NO 231
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 231

Ala Gly Leu Glu Tyr Cys Phe Tyr Gln Trp Trp Gly Cys Pro His Ala
1 5 10 15

Gly Thr Gly Gly Gly Lys
20

<210> SEQ ID NO 232
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 232

Ala Gly Tyr Gln Phe Cys Thr Trp Asp Pro Ile Phe Cys Gly Trp His
1 5 10 15

Gly Thr Gly Gly Gly Lys
20

<210> SEQ ID NO 233
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin-binding agent

<400> SEQUENCE: 233

Gly Ser Leu Trp Asp Cys Trp Leu Tyr Asp Cys Glu Gly Asn Ala Pro
1 5 10 15

Gly Gly Gly Lys
20

<210> SEQ ID NO 234
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: exemplary motif
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Z1 = 6 amino acid with at least one
cysteine residue
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Gly, His, Asn, Arg, or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Ala, Asp, Glu, Phe, Ile, Met, or Ser
<220> FEATURE:

-continued

<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Ala, Ile, Leu, Met, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Ile, Met, Thr, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(0)
<223> OTHER INFORMATION: Xaa = Z2 =one amino acid or absent

<400> SEQUENCE: 234

Xaa Xaa Xaa Xaa Xaa Trp Cys Xaa
1 5

<210> SEQ ID NO 235
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: exemplary motif
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Z1 = one amino acid or is absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Phe or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Z2 = Ala, Cys, Phe, Lys, Pro, Arg, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Z2 = Cys, Asp, Glu, Gly, His, Lys, Met,Asn,Gln, Arg, Ser, Thr, Val, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa = Z2 = Ala,Glu, Phe, His, Ile, Lys, Leu, Gln, Arg, Ser, Thr, Val, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(0)
<223> OTHER INFORMATION: Xaa = Z3 =at least one amino acid

<400> SEQUENCE: 235

Xaa Xaa Trp Xaa Xaa Xaa Trp Xaa
1 5

<210> SEQ ID NO 236
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: exemplary motif
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Z1 = polypeptide of at least one amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Z2 = tripeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6

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<223> OTHER INFORMATION: Xaa = Z3 = polypeptide of at least one amino acid

<400> SEQUENCE: 236

Xaa Trp Xaa Trp Trp Xaa
1 5

<210> SEQ ID NO 237
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: exemplary motif
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Z1 = polypeptide of at least one amino acid and includes a cysteine residue
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Ala, Glu, Arg, Ser, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Phe, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 7
<223> OTHER INFORMATION: Xaa = Asp,Glu, Leu, Met, or Gln
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 8
<223> OTHER INFORMATION: Xaa = His, Trp, or Tyr;
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(0)
<223> OTHER INFORMATION: Xaa = Phe or Tyr

<400> SEQUENCE: 237

Xaa Pro Xaa Trp Xaa Cys Xaa Xaa Xaa
1 5

<210> SEQ ID NO 238
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 238

Arg Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
1 5 10 15

Gly His

<210> SEQ ID NO 239
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 239

Trp Gly Glu Cys Thr Val Thr Ser Tyr Gly Glu Leu Ile Trp Cys Gly
1 5 10 15

Gly Leu

-continued

<210> SEQ ID NO 240
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 240

Ser Ser Ala Cys Ala Phe Asp Pro Met Gly Ala Val Ile Trp Cys Thr
1 5 10 15

Tyr Asp

<210> SEQ ID NO 241
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 241

Leu Leu Glu Cys Ala Tyr Asn Thr Ser Gly Glu Leu Ile Trp Cys Asn
1 5 10 15

Gly Ser

<210> SEQ ID NO 242
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 242

Pro Asp Asp Cys Ser Ile His Phe Ser Gly Glu Leu Ile Trp Cys Glu
1 5 10 15

Pro Leu

<210> SEQ ID NO 243
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 243

Leu Gly Glu Cys Thr Val Thr Ser Tyr Gly Glu Leu Ile Trp Cys Gly
1 5 10 15

Gly Leu

<210> SEQ ID NO 244
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 244

Trp Gly Glu Cys Thr Val Thr Ser Tyr Gly Glu Leu Ile Trp Cys Gly
1 5 10 15

Gly His

-continued

<210> SEQ ID NO 245
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 245

Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp
1 5 10 15

Asp His

<210> SEQ ID NO 246
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 246

Trp Gly Glu Cys Thr Val Thr Ser Tyr Gly Glu Leu Ile Trp Cys Gly
1 5 10 15

Gly Leu

<210> SEQ ID NO 247
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 247

Cys Arg Ala Cys Ser Arg Asp Trp Pro Gly Ala Leu Val Trp Cys Ala
1 5 10 15

Gly His

<210> SEQ ID NO 248
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 248

Arg Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
1 5 10 15

Gly His

<210> SEQ ID NO 249
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 249

Leu His Ala Cys Ala Phe Asp Pro Met Gly Ala Val Ile Trp Cys Thr
1 5 10 15

Tyr Asp

<210> SEQ ID NO 250

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<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 250

Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Met Trp Cys Asp
1 5 10 15

Asn His

<210> SEQ ID NO 251
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 251

Pro Pro Thr Cys Thr Trp Asp Trp Gln Gly Ile Leu Val Trp Cys Ser
1 5 10 15

Gly His

<210> SEQ ID NO 252
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 252

Ser Asn Lys Cys Ser Asn Thr Trp Asp Gly Ser Leu Ile Trp Cys Ser
1 5 10 15

Ala Asn

<210> SEQ ID NO 253
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 253

Phe Pro Glu Cys Thr Phe Asp Met Glu Gly Phe Leu Ile Trp Cys Ser
1 5 10 15

Ser Phe

<210> SEQ ID NO 254
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 254

His Asp Leu Cys Ala Gln Ala Pro Phe Gly Asp Ala Thr Trp Cys Asp
1 5 10 15

Leu Arg

<210> SEQ ID NO 255
<211> LENGTH: 18

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 255

Pro Asn His Cys Ser Tyr Asn Leu Lys Ser Glu Leu Ile Trp Cys Gln
1 5 10 15

Asp Leu

<210> SEQ ID NO 256
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 256

Pro Leu Asp Cys Ala Arg Asp Ile His Asn Ser Leu Ile Trp Cys Ser
1 5 10 15

Leu Gly

<210> SEQ ID NO 257
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 257

Gly Ser Glu Cys Ser Trp Thr Ser Leu Asn Glu Leu Ile Trp Cys Ala
1 5 10 15

His Trp

<210> SEQ ID NO 258
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 258

Trp Pro Asp Cys Ser Phe Thr Val Gln Arg Asp Leu Ile Trp Cys Glu
1 5 10 15

Ala Leu

<210> SEQ ID NO 259
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 259

Ser His Ser Cys Ala Tyr Asp Tyr Ala His Met Leu Val Trp Cys Thr
1 5 10 15

His Phe

<210> SEQ ID NO 260
<211> LENGTH: 18
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 260

Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp
1 5 10 15

Asn His

<210> SEQ ID NO 261
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 261

Arg Pro Asn Cys Thr Phe Ala Ala Ser Gly Glu Leu Ile Trp Cys Met
1 5 10 15

His Tyr

<210> SEQ ID NO 262
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 262

Trp Trp Gly Cys Gln Phe Asp Trp Arg Gly Glu Leu Val Trp Cys Pro
1 5 10 15

Tyr Leu

<210> SEQ ID NO 263
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 263

Gly Gly Val Cys Ser Tyr Ser Gly Met Gly Glu Ile Val Trp Cys Arg
1 5 10 15

Trp Phe

<210> SEQ ID NO 264
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 264

Ala Leu Met Cys Ser His Asp Met Trp Gly Ser Leu Ile Trp Cys Lys
1 5 10 15

His Phe

<210> SEQ ID NO 265
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 265

Trp Trp Asn Cys His Asn Gly Trp Thr Trp Thr Gly Gly Trp Cys Trp
1 5 10 15

Trp Phe

<210> SEQ ID NO 266
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 266

Tyr His Val Cys Ala Arg Asp Ser Trp Asp Gln Leu Ile Trp Cys Glu
1 5 10 15

Ala Phe

<210> SEQ ID NO 267
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 267

Asn Tyr Trp Cys Asn Phe Trp Gln Leu Pro Thr Cys Asp Asn Leu
1 5 10 15

<210> SEQ ID NO 268
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 268

Tyr Trp Tyr Cys Lys Trp Phe Ser Glu Ser Ala Ser Cys Ser Ser Arg
1 5 10 15

<210> SEQ ID NO 269
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 269

Tyr Trp Tyr Cys Lys Trp Phe Glu Asp Lys His Pro Cys Asp Ser Ser
1 5 10 15

<210> SEQ ID NO 270
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 270

Tyr Trp Tyr Cys Ser Trp Phe Pro Asp Arg Pro Asp Cys Pro Leu Tyr
1 5 10 15

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<210> SEQ ID NO 271
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 271

Asn Tyr Trp Cys Asn Val Trp Leu Leu Gly Asp Val Cys Arg Ser His
1 5 10 15

<210> SEQ ID NO 272
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 272

Leu Tyr Trp Cys His Val Trp Phe Gly Gln His Ala Trp Gln Cys Lys
1 5 10 15

Tyr Pro

<210> SEQ ID NO 273
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 273

Tyr Trp Lys Cys Lys Trp Met Pro Trp Met Cys Gly Phe Asp
1 5 10

<210> SEQ ID NO 274
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 274

Asp Asp His Cys Tyr Trp Phe Arg Glu Trp Phe Asn Ser Glu Cys Pro
1 5 10 15

His Gly

<210> SEQ ID NO 275
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 275

Asn Tyr Trp Cys Asn Ile Trp Gly Leu His Gly Cys Asn Ser His
1 5 10 15

<210> SEQ ID NO 276
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 276

Tyr Trp Phe Cys Gln Trp Phe Ser Gln Asn His Thr Cys Phe Arg Asp
1 5 10 15

<210> SEQ ID NO 277
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 277

His Tyr Trp Cys Asp Ile Trp Phe Gly Ala Pro Ala Cys Gln Phe Arg
1 5 10 15

<210> SEQ ID NO 278
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 278

Ser Gly Asp Cys Gly Phe Trp Pro Arg Ile Trp Gly Leu Cys Met Asp
1 5 10 15

Asn

<210> SEQ ID NO 279
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 279

Phe Trp Tyr Cys Lys Trp Phe Tyr Glu Asp Ala Gln Cys Ser His Asp
1 5 10 15

<210> SEQ ID NO 280
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 280

Tyr Tyr Trp Cys Asn Tyr Trp Gly Leu Cys Pro Asp Gln
1 5 10

<210> SEQ ID NO 281
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 281

Ser Tyr Trp Cys Lys Ile Trp Asp Val Cys Pro Gln Ser
1 5 10

<210> SEQ ID NO 282

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 282

Lys Tyr Trp Cys Asn Leu Trp Gly Val Cys Pro Ala Asn
1 5 10

<210> SEQ ID NO 283
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 283

Gln Tyr Trp Cys Tyr Gln Trp Gly Leu Cys Gly Ala Asn
1 5 10

<210> SEQ ID NO 284
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 284

Lys Tyr Trp Cys Gln Gln Trp Gly Val Cys Asn Gly Ser
1 5 10

<210> SEQ ID NO 285
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 285

Lys Tyr Trp Cys Val Gln Trp Gly Val Cys Pro Glu Ser
1 5 10

<210> SEQ ID NO 286
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 286

Lys Tyr Trp Cys Met Gln Trp Gly Leu Cys Gly Trp Glu
1 5 10

<210> SEQ ID NO 287
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 287

His Phe Trp Cys Glu Val Trp Gly Leu Cys Pro Ser Ile
1 5 10

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<210> SEQ ID NO 288
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 288

Gln Tyr Trp Cys Thr Lys Trp Gly Leu Cys Thr Asn Val
1 5 10

<210> SEQ ID NO 289
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 289

Ala Tyr Trp Cys Lys Val Trp Gly Leu Cys Gln Gly Glu
1 5 10

<210> SEQ ID NO 290
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 290

Lys Tyr Trp Cys Asn Leu Trp Gly Val Cys Pro Ala Asn
1 5 10

<210> SEQ ID NO 291
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 291

Gln Tyr Trp Cys Asn Val Trp Gly Val Cys Leu Pro Ser
1 5 10

<210> SEQ ID NO 292
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 292

His Tyr Trp Cys Gln Gln Trp Gly Ile Cys Glu Arg Pro
1 5 10

<210> SEQ ID NO 293
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 293

Arg Tyr Trp Cys Asn Ile Trp Asp Val Cys Pro Glu Gln

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1 5 10

<210> SEQ ID NO 294
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 294

Gln Tyr Trp Cys Thr His Trp Gly Leu Cys Gly Lys Tyr
1 5 10

<210> SEQ ID NO 295
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 295

Thr Tyr Trp Cys Thr Lys Trp Gly Leu Cys Pro His Asn
1 5 10

<210> SEQ ID NO 296
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 296

Phe Tyr Trp Cys Gly Gln Trp Gly Leu Cys Ala Pro Pro
1 5 10

<210> SEQ ID NO 297
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 297

Gly Tyr Trp Cys Asn Val Trp Gly Leu Cys Ser Thr Glu
1 5 10

<210> SEQ ID NO 298
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 298

Arg Tyr Trp Cys Gly Val Trp Gly Val Cys Glu Ile Asp
1 5 10

<210> SEQ ID NO 299
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 299

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Lys Phe Trp Cys Thr Ile Trp Gly Val Cys His Met Pro
1 5 10

<210> SEQ ID NO 300
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 300

His Tyr Trp Cys Gln Gln Trp Gly Ile Cys Glu Arg Pro
1 5 10

<210> SEQ ID NO 301
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 301

Arg Tyr Trp Cys Asn Ile Trp Asp Val Cys Pro Glu Gln
1 5 10

<210> SEQ ID NO 302
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 302

Phe Tyr Trp Cys Ser Gln Trp Gly Leu Cys Lys Tyr Asp
1 5 10

<210> SEQ ID NO 303
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 303

His Tyr Trp Cys Glu Lys Trp Gly Leu Cys Leu Met Ser
1 5 10

<210> SEQ ID NO 304
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 304

His Tyr Trp Cys Gln Lys Trp Gly Val Cys Pro Thr Asp
1 5 10

<210> SEQ ID NO 305
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

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<400> SEQUENCE: 305

His Tyr Trp Cys Ser Leu Trp Gly Val Cys Asp Ile Asn
1 5 10

<210> SEQ ID NO 306
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 306

Arg Phe Trp Cys Ser Ala Trp Gly Val Cys Pro Ala
1 5 10

<210> SEQ ID NO 307
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 307

Ser Tyr Trp Cys Lys Ile Trp Asp Val Cys Pro Gln Ser
1 5 10

<210> SEQ ID NO 308
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 308

Gln Tyr Trp Cys Ser Ile Trp Lys Val Cys Pro Gly Arg
1 5 10

<210> SEQ ID NO 309
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 309

Tyr Trp Tyr Cys Glu Trp Phe Gly Ala Cys Ile Asn Asp
1 5 10

<210> SEQ ID NO 310
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 310

Glu Tyr Trp Cys Lys Tyr Trp Gly Leu Glu Cys Val His Arg
1 5 10

<210> SEQ ID NO 311
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 311

Lys Tyr Trp Cys Thr Gln Trp Gly Leu Lys Cys Asp Lys Gln
1 5 10

<210> SEQ ID NO 312
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 312

Lys Tyr Trp Cys Ser Phe Trp Gly Leu Gln Cys Lys Thr
1 5 10

<210> SEQ ID NO 313
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 313

Arg Tyr Trp Cys Asn Phe Trp Gly Val Asn Cys Asp Ala Asn
1 5 10

<210> SEQ ID NO 314
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 314

Asn Tyr Trp Cys Thr His Trp Gly Val Met Cys Leu Asp His
1 5 10

<210> SEQ ID NO 315
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 315

Tyr Trp Phe Cys Lys Trp Phe Pro Ser Gln Cys Gln Phe Met
1 5 10

<210> SEQ ID NO 316
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 316

Ala Tyr Trp Cys Lys Gln Trp Gly Leu Lys Cys Gln Leu Gly
1 5 10

<210> SEQ ID NO 317
<211> LENGTH: 14

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 317

Lys Tyr Trp Cys Lys Phe Trp Gly Leu Glu Cys Lys Val Gly
1 5 10

<210> SEQ ID NO 318
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 318

Asn Tyr Trp Cys Thr Glu Trp Gly Leu Asn Cys Asn Asn Lys
1 5 10

<210> SEQ ID NO 319
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 319

Ser Tyr Trp Cys Glu Lys Trp Gly Leu Thr Cys Glu Thr His
1 5 10

<210> SEQ ID NO 320
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 320

Glu Tyr Trp Cys Arg Ile Trp Gly Leu Gln Cys Asn Met Val
1 5 10

<210> SEQ ID NO 321
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 321

Lys Tyr Trp Cys Lys Lys Trp Gly Val Asn Cys Asp Phe Asn
1 5 10

<210> SEQ ID NO 322
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 322

Lys Tyr Trp Cys Ser Val Trp Gly Val Gln Cys Pro His Ser
1 5 10

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<210> SEQ ID NO 323
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 323

Phe Tyr Trp Cys Thr Lys Trp Gly Leu Glu Cys Ile His Ser
1 5 10

<210> SEQ ID NO 324
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 324

His Tyr Trp Cys Gln Gln Trp Gly Leu Met Cys Phe Glu Thr
1 5 10

<210> SEQ ID NO 325
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 325

Lys Tyr Trp Cys Lys Arg Trp Gly Leu Met Cys Asn Gly Gly
1 5 10

<210> SEQ ID NO 326
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 326

Ala Tyr Trp Cys Met Thr Trp Gly Val Pro Cys Ile Ser Trp
1 5 10

<210> SEQ ID NO 327
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 327

Lys Tyr Trp Cys Lys Lys Trp Gly Val Asn Cys Asp Phe Asn
1 5 10

<210> SEQ ID NO 328
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 328

Lys Tyr Trp Cys Ser Val Trp Gly Val Gln Cys Pro Asp Ser
1 5 10

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<210> SEQ ID NO 329
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 329

Lys Tyr Trp Cys Ser Val Trp Gly Val Gln Cys Pro His Ser
1 5 10

<210> SEQ ID NO 330
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 330

Leu Tyr Trp Cys Thr Lys Trp Gly Val Thr Cys Gln Lys Asp
1 5 10

<210> SEQ ID NO 331
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 331

Thr Tyr Trp Cys His Lys Trp Gly Val Lys Cys Ala Thr Thr
1 5 10

<210> SEQ ID NO 332
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 332

Thr Tyr Trp Cys Thr Phe Trp Glu Leu Pro Cys Asp Pro Ala
1 5 10

<210> SEQ ID NO 333
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 333

Lys Tyr Trp Cys Thr Lys Trp Gln Leu Asn Cys Glu Glu Val
1 5 10

<210> SEQ ID NO 334
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 334

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Asn Tyr Trp Cys His Phe Trp Gln Val Pro Cys Leu Glu Gln
1 5 10

<210> SEQ ID NO 335
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 335

Thr Tyr Trp Cys Val Val Trp Asn Val Pro Cys Ser Thr Asp
1 5 10

<210> SEQ ID NO 336
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 336

Asn Phe Trp Cys His Thr Trp Gly Leu Gln Cys Asn Asp Leu
1 5 10

<210> SEQ ID NO 337
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 337

Phe Trp Tyr Cys Tyr Trp Phe Asn Glu Lys Cys Lys Thr Pro
1 5 10

<210> SEQ ID NO 338
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 338

Gly Phe Trp Cys Thr Phe Trp Gly Val Thr Cys Glu Ala Gly
1 5 10

<210> SEQ ID NO 339
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 339

Pro His Asn Cys Asp Asp His Tyr Trp Tyr Cys Lys Trp Phe
1 5 10

<210> SEQ ID NO 340
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

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<400> SEQUENCE: 340

Glu Met Thr Cys Ser Ser His Tyr Trp Tyr Cys Thr Trp Met
1 5 10

<210> SEQ ID NO 341
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 341

His Ile Asp Cys Lys Thr Asn Tyr Trp Trp Cys Arg Trp Thr
1 5 10

<210> SEQ ID NO 342
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 342

Glu Met Arg Cys Gly Gln His Phe Trp Tyr Cys Glu Trp Phe
1 5 10

<210> SEQ ID NO 343
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 343

Asn Tyr Trp Cys Asn Phe Trp Gln Leu Pro Thr Cys Asp Asn Leu
1 5 10 15

<210> SEQ ID NO 344
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 344

Tyr Trp Tyr Cys Gln Trp Phe Gln Glu Val Asn Lys Cys Phe Asn Ser
1 5 10 15

<210> SEQ ID NO 345
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 345

Tyr Tyr Trp Cys Arg His Trp Phe Pro Asp Phe Asp Cys Val His Ser
1 5 10 15

<210> SEQ ID NO 346
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 346

Tyr Trp Tyr Cys Ser Trp Phe Pro Asp Arg Pro Asp Cys Pro Leu Tyr
1 5 10 15

<210> SEQ ID NO 347
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 347

Tyr Trp Tyr Cys Val Trp Phe Asp Asn Ala Asp Gln Cys Val His His
1 5 10 15

<210> SEQ ID NO 348
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 348

Ala Ala Thr Cys Ser Thr Ser Tyr Trp Tyr Tyr Gln Trp Phe Cys Thr
1 5 10 15

Asp Ser

<210> SEQ ID NO 349
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 349

Tyr Trp Ala Cys Val Trp Gly Leu Lys Ser Cys Val Asp Arg
1 5 10

<210> SEQ ID NO 350
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 350

Tyr Trp Arg Cys Val Trp Phe Pro Ala Ser Cys Pro Thr
1 5 10

<210> SEQ ID NO 351
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 351

Asp Trp Gln Cys Leu Trp Trp Gly Asn Ser Phe Trp Pro Tyr Cys Ala
1 5 10 15

Asn Leu

-continued

<210> SEQ ID NO 352
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 352

Phe Trp Arg Cys His Trp Trp Pro Glu Arg Cys Pro Val Asp
1 5 10

<210> SEQ ID NO 353
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 353

Asn Pro Met Cys Trp Lys Lys Ser Trp Trp Glu Asp Ala Tyr Cys Ile
1 5 10 15

Asn His

<210> SEQ ID NO 354
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 354

Ser Trp Val Cys Trp Lys Ala Lys Trp Trp Glu Asp Lys Arg Cys Ala
1 5 10 15

Pro Phe

<210> SEQ ID NO 355
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 355

Ser Arg Gln Cys Trp Lys Glu Leu Trp Trp Thr Asp Gln Met Cys Leu
1 5 10 15

Asp Leu

<210> SEQ ID NO 356
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 356

Ser Phe Arg Cys Gln Ser Ser Phe Pro Ser Trp Tyr Cys Asp Tyr Tyr
1 5 10 15

<210> SEQ ID NO 357
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 357

Ser Trp His Cys Gln Asn Thr Tyr Pro Glu Trp Tyr Cys Gln Trp Tyr
1 5 10 15

<210> SEQ ID NO 358
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 358

Gly Ser Lys Cys Lys Gln Thr Gly Phe Pro Arg Trp Trp Cys Glu His
1 5 10 15

Tyr

<210> SEQ ID NO 359
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 359

Asp Gly Val Cys Gly Pro Arg Gly Phe Gly Pro Ala Trp Phe Cys Met
1 5 10 15

His Tyr

<210> SEQ ID NO 360
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 360

Tyr Ser His Cys Ala Thr His Tyr Pro Thr Trp Tyr Cys Leu His Phe
1 5 10 15

<210> SEQ ID NO 361
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 361

Phe Cys Asn Cys Trp Gly Ser His Glu Phe Thr Phe Cys Val Asp Asp
1 5 10 15

<210> SEQ ID NO 362
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 362

Pro Gly Trp Cys Tyr Ser Asp Ile Trp Gly Phe Lys His Phe Cys Asn
1 5 10 15

-continued

Leu Asp

<210> SEQ ID NO 363
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 363

Asp Ser Ser Cys Ile Lys His His Asn Lys Val Thr Cys Phe Phe Pro
1 5 10 15

<210> SEQ ID NO 364
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 364

Arg Trp Ser Cys Trp Gly Val Trp Gly Cys Val Trp Val
1 5 10

<210> SEQ ID NO 365
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 365

Pro Val Asp Cys Lys His His Phe Trp Trp Cys Tyr Trp Asn
1 5 10

<210> SEQ ID NO 366
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 366

Ser Trp Asn Cys Ala Phe His His Asn Glu Met Val Trp Cys Asp Asp
1 5 10 15

Gly

<210> SEQ ID NO 367
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 367

Tyr Trp Tyr Cys Trp Phe Pro Asp Arg Pro Glu Cys Pro Leu Tyr
1 5 10 15

<210> SEQ ID NO 368
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 368

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 369
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 369

Gly Asp Arg Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp
1 5 10 15

Cys Ala Gly His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 370
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 370

Ala Gly Lys Tyr Trp Cys Ser Phe Trp Gly Leu Gln Cys Lys Thr Gly
1 5 10 15

Thr Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 371
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 371

Ala Gly Ser Tyr Trp Cys Lys Ile Trp Asp Val Cys Pro Gln Ser Pro
1 5 10 15

Gly Pro Glu Gly Gly Gly Lys
20

<210> SEQ ID NO 372
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 372

Ala Gly Lys Tyr Trp Cys Asn Leu Trp Gly Val Cys Pro Ala Asn Pro
1 5 10 15

Gly Pro Glu Gly Gly Gly Lys
20

<210> SEQ ID NO 373

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<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 373

Ala Gly Thr Tyr Trp Cys Thr Phe Trp Glu Leu Pro Cys Asp Pro Ala
1 5 10 15

Pro Gly Pro Glu Gly Gly Gly Lys
20

<210> SEQ ID NO 374
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 374

Ala Gly Pro His Asn Cys Asp Asp His Tyr Trp Tyr Cys Lys Trp Phe
1 5 10 15

Pro Gly Pro Glu Gly Gly Gly Lys
20

<210> SEQ ID NO 375
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 375

Ala Gly Ala Ala Thr Cys Ser Thr Ser Tyr Trp Tyr Tyr Gln Trp Phe
1 5 10 15

Cys Thr Asp Ser Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 376
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 376

Ala Gly Tyr Trp Tyr Cys Trp Phe Pro Asp Arg Pro Glu Cys Pro Leu
1 5 10 15

Tyr Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 377
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 377

Ala Gly Pro Val Asp Cys Lys His His Phe Trp Trp Cys Tyr Trp Asn
1 5 10 15

Gly Thr Pro Gly Pro Glu Gly Gly Gly Lys

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20 25

<210> SEQ ID NO 378
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 378

Gly Asp Asp Asp His Cys Tyr Trp Phe Arg Glu Trp Phe Asn Ser Glu
1 5 10 15

Cys Pro His Gly Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 379
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 379

Ala Gly Tyr Tyr Trp Cys Asn Tyr Trp Gly Leu Cys Pro Asp Gln Gly
1 5 10 15

Thr Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 380
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 380

Gly Asp Ser Trp Val Cys Trp Lys Ala Lys Trp Trp Glu Asp Lys Arg
1 5 10 15

Cys Ala Pro Phe Gly Thr Pro Gly Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 381
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 381

Gly Asp Asn Pro Met Cys Trp Lys Lys Ser Trp Trp Glu Asp Ala Tyr
1 5 10 15

Cys Ile Asn His Gly Thr Pro Gly Pro Glu Gly Gly Gly Lys
20 25 30

<210> SEQ ID NO 382
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 382

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Gly Asp Ser Trp Asn Cys Ala Phe His His Asn Glu Met Val Trp Cys
1 5 10 15

Asp Asp Gly Gly Thr Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 383
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 383

Gly Asp Trp Gly Glu Cys Thr Val Thr Ser Tyr Gly Glu Leu Ile Trp
1 5 10 15

Cys Gly Gly Leu Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 384
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 384

Gly Asp Asn Pro Met Cys Trp Arg Ala Ser Trp Trp Glu Asp Ala Tyr
1 5 10 15

Cys Ile Asn His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 385
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 385

Gly Asp Asn Pro Met Cys Trp Arg Ala His Trp Trp Glu Asp Ala Tyr
1 5 10 15

Cys Ile Asn His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 386
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 27
<223> OTHER INFORMATION: Xaa = J-NH2 = C- terminal group
-NH-(CH2CH2O)2-CH2CH2-NH2

<400> SEQUENCE: 386

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Glu Pro Gly Pro Glu Gly Xaa
20 25

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<210> SEQ ID NO 387
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 24
<223> OTHER INFORMATION: Xaa = J-Su-J-NH2 = C-terminal group
-NH-(CH2CH2O)2-CH2CH2-NH-C:O-CH2CH2-C:O-NH-(CH2CH2
O)2-CH2CH2-NH2

<400> SEQUENCE: 387

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Glu Pro Gly Xaa
20

<210> SEQ ID NO 388
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 24
<223> OTHER INFORMATION: Xaa = J-Z-J-NH2 = C-terminal group
-NH-(CH2CH2O)2-CH2CH2-NH-C:O-CH2-O-(CH2CH2O)2-CH2-
C:O-NH-(CH2CH2O)2-CH2CH2-NH2

<400> SEQUENCE: 388

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Glu Pro Gly Xaa
20

<210> SEQ ID NO 389
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 21
<223> OTHER INFORMATION: Xaa = C-terminal group -NH-(CH2CH2O)2-CH2CH2-
NH2,-J-Su-J-NH2

<400> SEQUENCE: 389

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Xaa
20

<210> SEQ ID NO 390
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 21
<223> OTHER INFORMATION: Xaa = J-Su-J-NH2 = C-terminal group
-NH-(CH2CH2O)2-CH2CH2-NH-C:O-CH2CH2-C:O-NH-(CH2CH2

-continued

O)2-CH2CH2-NH2

<400> SEQUENCE: 390

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Xaa
20

<210> SEQ ID NO 391
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 21
<223> OTHER INFORMATION: Xaa = J-Z-J -NH2 = C-terminal group
-NH-(CH2CH2O)2-CH2CH2-NH-C:O-CH2-O-(CH2CH2O)2-CH2-
C:O-NH-(CH2CH2O)2-CH2CH2-NH2

<400> SEQUENCE: 391

Gly Asp Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp
1 5 10 15

Cys Asp Asn His Xaa
20

<210> SEQ ID NO 392
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 392

Asp His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp
1 5 10 15

Asn His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 393
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 393

Glu His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp
1 5 10 15

Asn His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 394
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 394

Ala Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
1 5 10 15

-continued

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 395
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 395

Thr Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 396
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 396

Glu Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 397
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 397

Val Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 398
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: ACETYLATION
<222> LOCATION: 1
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa =[Nle] = norleucine

<400> SEQUENCE: 398

Xaa Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

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<210> SEQ ID NO 399
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 399

Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His Glu
1 5 10 15

Pro Gly Pro Glu Gly Gly Gly Lys
20

<210> SEQ ID NO 400
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 400

Ser Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
1 5 10 15

Gly His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 401
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 401

Arg Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
1 5 10 15

Gly His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 402
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 402

Glu Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
1 5 10 15

Gly His Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 403
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 403

Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

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Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 404
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 404

Thr Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 405
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 405

Glu Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 406
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 406

Val Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 407
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 407

Gly Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

Glu Pro Gly Pro Glu Gly Gly Gly Lys
20 25

<210> SEQ ID NO 408
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 408

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Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His Glu
1 5 10 15

Pro Gly Pro Glu Gly Gly Gly Lys
20

<210> SEQ ID NO 409
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 409

Asn Pro Met Cys Trp Arg Ala Ser Trp Trp Glu Asp Ala Tyr Cys Ile
1 5 10 15

Asn His

<210> SEQ ID NO 410
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 410

Asn Pro Met Cys Trp Arg Ala His Trp Trp Glu Asp Ala Tyr Cys Ile
1 5 10 15

Asn His

<210> SEQ ID NO 411
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 411

Glu His Met Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp
1 5 10 15

Asn His

<210> SEQ ID NO 412
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 412

Ala Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
1 5 10 15

<210> SEQ ID NO 413
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 413

Thr Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His

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 1               5                  10                  15


<210> SEQ ID NO 414
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 414

Glu Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
 1               5                  10                  15


<210> SEQ ID NO 415
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 415

Val Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
 1               5                  10                  15


<210> SEQ ID NO 416
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = [Nle] = norleucine

<400> SEQUENCE: 416

Xaa Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys Asp Asn His
 1               5                  10                  15


<210> SEQ ID NO 417
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 417

Ser Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
 1               5                  10                  15

Gly His


<210> SEQ ID NO 418
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 418

Glu Arg Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala
 1               5                  10                  15

Gly His
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<210> SEQ ID NO 419
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 419

Ala Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

<210> SEQ ID NO 420
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 420

Thr Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

<210> SEQ ID NO 421
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 421

Glu Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

<210> SEQ ID NO 422
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 422

Val Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

<210> SEQ ID NO 423
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin binding polypeptide

<400> SEQUENCE: 423

Gly Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys Ala Gly His
1 5 10 15

<210> SEQ ID NO 424
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: template sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 13, 14 15
<223> OTHER INFORMATION: Xaa = any amino acid except cysteine (Cys)

-continued

<400> SEQUENCE: 424

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
1 5 10 15

<210> SEQ ID NO 425
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Exemplary motif
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Asn, Leu, or Phe, preferably Leu
<220> FEATURE:
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<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Met,Phe, Ser, Thr, Trp, Tyr, or Val
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<221> NAME/KEY: VARIANT
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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 7
<223> OTHER INFORMATION: Xaa = Ala, Arg, Asp, Gln, Glu, Gly, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 8
<223> OTHER INFORMATION: Xaa = Phe, Trp, or Tyr, preferably Trp
<220> FEATURE:
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<222> LOCATION: (10)...(0)
<223> OTHER INFORMATION: Xaa = His or Phe, preferably Phe
<220> FEATURE:
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<222> LOCATION: (11)...(0)
<223> OTHER INFORMATION: Xaa = Asp, Glu, or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val
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<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr, or Val
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<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(0)
<223> OTHER INFORMATION: Xaa = Pro or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (17)...(18)
<223> OTHER INFORMATION: Xaa = Asn or Pro

<400> SEQUENCE: 425

Xaa Arg Xaa Cys Xaa Thr Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

<210> SEQ ID NO 426

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<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: examplary motif
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Ala, Arg, Asp, Asn, Gly, His, Phe, Pro, Ser, or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Glu, Leu, or Met, preferably Met
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 7
<223> OTHER INFORMATION: Xaa = Trp or Tyr, preferably Trp
<220> FEATURE:
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<222> LOCATION: 10
<223> OTHER INFORMATION: Xaa = Gln, Glu, or Lys
<220> FEATURE:
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<222> LOCATION: (11)...(0)
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<223> OTHER INFORMATION: Xaa = Met, Pro, or Ser, preferably Pro
<220> FEATURE:
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<222> LOCATION: (13)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Arg, Asp, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(0)
<223> OTHER INFORMATION: Xaa = His or Pro, preferably Pro
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Arg, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (18)...(0)
<223> OTHER INFORMATION: Xaa = Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, or Tyr

<400> SEQUENCE: 426

Xaa Xaa Xaa Cys Ile Thr Xaa Pro Phe Xaa Xaa Xaa Xaa Xaa Cys Xaa
 1   5   10   15

Asn Xaa

<210> SEQ ID NO 427
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin segment

<400> SEQUENCE: 427

Cys Val Tyr Thr Thr Trp Gly Glu Leu Ile Trp Cys
 1   5   10

-continued

<210> SEQ ID NO 428
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin segment

<400> SEQUENCE: 428

Cys Ser Arg Asp Trp Ser Gly Ala Leu Val Trp Cys
1 5 10

<210> SEQ ID NO 429
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: immunoglobulin segment

<400> SEQUENCE: 429

Cys Ser Thr Ser Tyr Trp Tyr Tyr Gln Trp Phe Cys
1 5 10

<210> SEQ ID NO 430
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: serum albumin - binding agent

<400> SEQUENCE: 430

Arg Asn Met Cys Lys Phe Ser Trp Ile Arg Ser Pro Ala Phe Cys Ala
1 5 10 15

Arg Ala

What is claimed:

1. A method of evaluating a sample, the method comprising:

providing a sample that comprises (i) a serum albumin, (ii) one or more compounds physically associated with the serum albumin and (iii) a serum albumin-binding agent that is free of an antigen-binding immunoglobulin variable domain;

allowing the serum albumin-binding agent to bind to the serum albumin to form a complex;

separating the complex from one or more components of the sample; and

evaluating one or more of the physically associated compounds.

2. A method of evaluating a sample, the method comprising:

providing a sample that comprises (i) a serum albumin, (ii) one or more compounds physically associated with the serum albumin and (iii) a serum albumin-binding agent that comprises a peptide that independently binds to serum albumin;

allowing the serum albumin-binding agent to bind to the serum albumin to form a complex;

separating the complex from one or more components of the sample; and

evaluating one or more of the physically associated compounds.

3. The method of claim 1 or **2** wherein the serum albumin-binding agent binds serum albumin with an affinity of less than 5 μM.

4. The method of claim 2 wherein the peptide is less than 30 amino acids in length.

5. The method of claim 2 wherein the peptide comprises an intra-molecular disulfide bond.

6. The method of claim 4 wherein the peptide comprises DX-236 or DX-321 or an amino acid sequence that differs from DX-236 or DX-321 by fewer than four amino acid substitutions.

7. The method of claim 1 wherein the serum albumin-binding agent is coupled to an insoluble support.

8. The method of claim 1 wherein the serum albumin-binding agent binds to serum albumin from a plurality of species.

9. The method of claim 1 wherein at least one of the evaluated physically associated compounds is non-covalently associated with the serum albumin.

10. The method of claim 9 further comprising separating one or more of the physically associated compounds from the serum albumin.

11. The method of claim 10 wherein the separating of one or more of the physically associated compounds from the serum albumin is prior to the evaluating.

12. The method of claim 1 or **2** further comprising separating the at least one non-covalently associated compounds from the serum albumin prior to the evaluating.

13. The method of claim 12 wherein the separating from the serum albumin comprises covalently attaching the serum albumin to an insoluble support.

14. The method of claim 13 wherein the covalent attachment is to a free cysteine of the serum albumin.

15. A method of evaluating a sample, the method comprising:

providing a sample that comprises (i) a serum albumin, (ii) one or more compounds physically associated with the serum albumin and (iii) a serum albumin-binding agent;

allowing the serum albumin-binding agent to bind to the serum albumin to form a complex;

separating the complex from one or more components of the sample;

covalently attaching the serum albumin to an insoluble matrix; and

separating at least one of the one or more compounds physically associated with the serum albumin from the serum albumin.

16. The method of claim 15 wherein the covalent attachment is to a free cysteine of the serum albumin.

17. The method of claim 15 further comprising evaluating one or more of the physically associated compounds that becomes separated from the serum albumin.

18. The method of claim 15 wherein the covalent attachment is formed using a thiol reactive group.

19. The method of claim 18 wherein the thiol reactive group comprises a halogen derivative.

20. The method of claim 19 wherein the thiol reactive group comprises iodoacetamide.

21. The method of claim 18 wherein the thiol reactive group comprises a maleimide.

22. The method of claim 18 wherein the thiol reactive group comprises a thiol exchange reagent.

23. The method of claim 22 wherein the thiol exchange reagent is a pyridyl disulfide.

24. The method of claim 15 wherein the separating comprises denaturing the serum albumin.

25. The method of claim 1 wherein at least one of the evaluated covalently associated compounds is non-proteinaceous.

26. The method of claim 1 wherein the evaluating comprises one or more of: gel electrophoresis, mass spectroscopy, chromatography, and protein sequencing.

27. The method of claim 1 wherein the evaluating comprises detecting a given compound using an affinity reagent specific for the given compound.

28. The method of claim 27 wherein the affinity reagent is an antibody.

29. The method of claim 1 wherein the evaluating comprises detecting a compound other than a fatty acid, hematin, and bilirubin.

30. The method of claim 1 wherein the evaluating comprises detecting a polypeptide.

31. The method of claim 1 wherein the evaluating comprises eluting an associated compound from the serum albumin by contacting the complex with a synthetic affinity ligand specific for an epitope on the serum albumin.

32. The method of claim 1 wherein the evaluating comprises eluting an associated compound by contacting the complex with a natural compound that binds to the serum albumin.

33. The method of claim 32 wherein the natural compound comprises a component selected from the group consisting of: a fatty acid, hematin, and bilirubin.

34. The method of claim 32 wherein the natural compound comprises a negatively charged aromatic group having a molecular weight of less than 500 Daltons.

35. The method of claim 1 wherein the serum albumin is a human serum albumin.

36. The method of claim 1 wherein the serum albumin is an artificial mutant of a naturally-occurring serum albumin.

37. The method of claim 1 further comprising digitally recording information that (i) indicates the presences or absence of a given compound among the evaluated one or more physically associated compounds, or (ii) describes the one or more physically associated compounds.

38. The method of claim 1 further comprising providing a second sample, and evaluating one or more of the physically associated compounds in the second sample.

39. The method of claim 38 further comprising comparing the results of evaluating the one or more of the physically associated compounds for the first sample to the second sample.

40. The method of claim 39 wherein the first sample is from a first subject, and the second sample is from a second subject.

41. The method of claim 40 wherein the first subject is treated with an agent, and the second subject is not treated with the agent.

42. The method of claim 40 wherein the first subject and second subject are subjected to different environmental conditions.

43. The method of claim 1 or **2** wherein the serum albumin-binding agent and the serum albumin preferentially dissociate in solutions above pH 8.

44. The method of claim 1 wherein the sample is obtained from a subject.

45. The method of claim 44 wherein the subject is a human.

46. The method of claim 45 wherein the sample comprises blood or serum.

47. The method of claim 45 wherein the sample is obtained from a biopsy.

48. The method of claim 45 wherein the sample is obtained from a tumor or a region within 5 mm of a tumor.

49. The method of claim 45 wherein the subject is treated with a therapeutic composition prior to obtaining the sample.

50. The method of claim 49 wherein one or more of the evaluated physically associated compounds is an endogenous compound.

51. The method of claim 49 wherein one or more of the evaluated physically associated compounds is a component of the therapeutic composition.

52. A method of evaluating a sample, the method comprising:

providing a sample that comprises (i) a soluble immunoglobulin protein that includes at least one immunoglobulin domain, (ii) one or more compounds physically associated with the immunoglobulin protein and (iii) immunoglobulin-binding agent that comprises a peptide that specifically binds to the immunoglobulin protein at a site other than an antigen binding site;

allowing the immunoglobulin-binding agent to bind to the soluble immunoglobulin protein to form a complex that includes one or more compounds physically associated with the soluble immunoglobulin protein;

separating the complex from one or more components of the sample; and

evaluating one or more of the physically associated compounds.

53. The method of claim 52 wherein the soluble immunoglobulin protein is a naturally-occurring protein.

54. The method of claim 52 wherein the soluble immunoglobulin protein is an IgG.

55. The method of claim 52 wherein the one or more physically associated compounds comprises an antigen.

56. The method of claim 52 wherein the sample is obtained from a subject having an infection.

57. The method of claim 52 wherein the sample is obtained from a subject having immunological disorder.

58. The method of claim 57 wherein the immunological disorder is an auto-immune disorder.

59. The method of claim 52 wherein the peptide is less than 30 amino acids in length.

60. The method of claim 52 wherein the peptide comprises an intra-molecular disulfide bond.

61. A method of evaluating a sample, the method comprising:

providing a sample that comprises (i) a soluble serum protein, (ii) one or more compounds physically associated with the soluble serum protein, and (iii) serum protein-binding agent that comprises a peptide that specifically binds to the serum protein;

allowing the serum protein-binding agent to bind to the soluble serum protein to form a complex that includes one or more compounds physically associated with the soluble serum protein;

separating the complex from one or more components of the sample; and

evaluating one or more of the physically associated compounds.

62. The method of claim 61 wherein the serum protein is serum albumin.

63. The method of claim 61 wherein the serum protein is at least 0.01% of the protein fraction in blood serum.

64. The method of claim 61 wherein the serum protein is selected from the group consisting of: transferrin, a macroglobulins, ferritin, apolipoproteins, transthyretin, a protease inhibitor found in serum, retinol binding protein, thiostatin, a-fetoprotein, vitamin-D binding protein, or afamin.

65. A method of mapping a physical interaction between serum albumin and an associated compound, the method comprising:

providing a complex comprising a serum albumin and an associated compound;

evaluating binding of a ligand (e.g., a peptide ligand described herein) to the complex, wherein the ligand binds to serum albumin with an affinity of less than 5 μM, the ligand is free of an immunoglobulin variable domain, and binding of the non-antibody ligand to the complex indicates that the associated compound does not bind an epitope that overlaps the epitope bound by the non-antibody ligand.

66. The method of claim 65 further comprising: evaluating binding of a ligand to the complex, wherein the second ligand binds to serum albumin with an affinity of less than 5 μM.

67. The method of claim 65 wherein one of the first and second non-antibody ligand binds is prevented from binding to the complex.

* * * * *

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[标]申请(专利权)人(译)	戴埃克斯有限公司		
申请(专利权)人(译)	DYAX CORPORATION		
当前申请(专利权)人(译)	DYAX CORP.		
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IPC分类号	G01N33/53 G01N33/564 G01N33/68		
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摘要(译)

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FIG. 1