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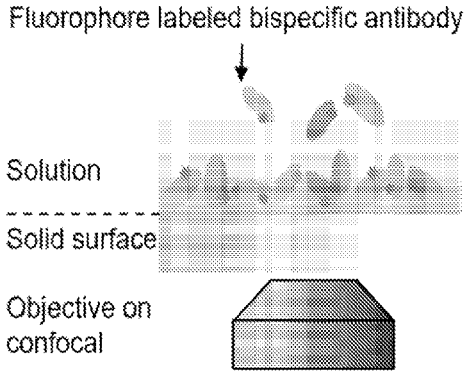
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— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

(54) **Title:** COMPOSITIONS AND METHODS FOR MINIMIZING PROTEIN LOSS AT LOW PROTEIN CONCENTRATIONS

Figure 1

Diagram for the assay for measuring protein binding to a solid surface



(57) **Abstract:** The present invention relates to compositions and methods for minimizing protein loss (e.g., due to adsorption to solid surfaces) at low protein concentrations. Inventions disclosed herein generally relate to the field of compositions comprising proteins, in particular, pharmaceutical compositions comprising therapeutic proteins at low protein concentrations. Inventions disclosed herein also relate to methods of administering the composition to a subject in need thereof.

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COMPOSITIONS AND METHODS FOR MINIMIZING PROTEIN LOSS AT LOW PROTEIN CONCENTRATIONS

CROSS REFERENCE OF RELATED APPLICATION

[0001] This application claims the benefit of U. S. Provisional Application No. 62/926,089 filed October. 25, 2019, which is incorporated in its entirety by reference herein.

SUBMISSION OF SEQUENCE LISTING ON ASCII TEXT FILE

[0002] The content of the following submission on ASCII text file is incorporated herein by reference in its entirety: a computer readable form (CRF) of the Sequence Listing (file name: A-2429-WO-PCT_ST25, date created: October 23, 2020 size: 451,608 bytes).

FIELD OF THE INVENTION

[0001] Inventions disclosed herein generally relate to the field of compositions comprising proteins, in particular, pharmaceutical compositions comprising therapeutic proteins at low protein concentrations. Inventions disclosed herein also relate to methods of administering the composition to a subject in need thereof.

BACKGROUND OF THE INVENTION

[0002] Therapeutic proteins are an important class of therapeutics for treating patients. Protein molecules are surface active and subject to potential adsorption to solid surfaces. Therapeutic proteins in pharmaceutical compositions could be adsorbed to solid surfaces that the proteins come into contact with (e.g., the surfaces of a container containing a pharmaceutical composition), which could lead to protein loss during storage and use. Generally, the concentration of therapeutic proteins in those compositions is high (e.g., 1 mg/mL or higher) such that protein adsorption to solid surfaces does not result in insufficient amount of drug available for administration to patients. However, when the concentration of proteins in compositions is low (e.g., less than 0.1 mg/mL, such as when a composition is diluted before administration to patients), the risk of protein loss can be more pronounced, which could potentially lead to insufficient amount of drug available for patient administration.

[0003] Surfactants are generally used in pharmaceutical compositions comprising therapeutic proteins, e.g., to prevent protein aggregation and stabilize proteins. It is unclear whether surfactants can be used to effectively prevent protein loss due to surface adsorption when proteins are present at low concentrations in pharmaceutical compositions (e.g., 0.1 mg/mL or less).

[0004] There is a need for protein compositions and methods that minimize protein loss due to adsorption to solid surfaces, especially when the compositions comprising protein at low protein concentrations.

SUMMARY OF THE INVENTION

[0005] Disclosed herein are compositions comprising proteins at low protein concentrations as well as methods of administering the compositions to a subject in need thereof. The compositions and methods disclosed herein have the advantage of minimizing or eliminating protein loss due to protein adsorption to solid surfaces and ensure accurate dosing of therapeutic proteins to patients.

[0006] In certain embodiments, disclosed herein is an aqueous composition comprising a protein and a surfactant, wherein the protein is present in the composition at a concentration of between about 0.001 μg/ml and about 100 μg/ml, and the surfactant is present in the composition at a concentration of at least about 0.25 x of the critical micelle concentration (CMC) of the surfactant.

[0007] In certain embodiments, the protein is a bispecific antibody construct comprising a first binding domain that binds to a target cell surface antigen, a second binding domain that binds to human CD3 on the surface of a T cell, and optionally, a third domain comprising, in an amino to carboxyl order, hinge-CH2 domain-CH3 domain-linker-hinge-CH2 domain-CH3 domain. In certain embodiments, the second binding domain comprises a polypeptide having the sequence of SEQ ID NO: 201. In certain embodiments, the bispecific antibody construct is present at a concentration of between about 0.001 μg/ml and about 50 μg/ml, or between about 0.01 μg/ml to about 50 μg/ml, or between 0.1 μg/ml to about 50 μg/ml, or 0.1 μg/ml to about 10 μg/ml, or 1 μg/ml to about 10 μg/ml.

[0008] In certain embodiments, the surfactant is a polysorbate, a poloxamer or triton x-100. In certain embodiments, the surfactant is polysorbate 80, polysorbate 60, polysorbate 40, polysorbate 20, or Triton X-100. In certain embodiments, the surfactant is poloxamer 188 or

poloxamer 407. In certain embodiments, the surfactant is present at a concentration of between about 0.25x and about 20x of the CMC, or between about 0.25x and about 10x of the CMC of the surfactant.

[0009] In certain embodiments, wherein the composition further comprising a salt, an amino acid, a saccharide or saccharide derivative, or combinations thereof. In certain embodiments, the salt is NaCl. In certain embodiments, the saccharide or saccharide derivative is a monosaccharide, a disaccharide, a cyclic polysaccharide or a sugar alcohol. In certain embodiments, the saccharide is sucrose, trehalose, mannitol or sorbitol. In certain embodiments, the amino acid is lysine.

[0010] In certain embodiments, wherein the pH of the composition is between about 3.5 and about 7.5. In certain embodiments, the pH of the composition is between about 4.2 and about 7.0.

[0011] In certain embodiments, the composition further comprises a buffer or a preservative. In certain embodiments, the buffer is an acetate buffer, a glutamate buffer, a citrate buffer, a succinate buffer, a tartrate buffer, a fumarate buffer, a maleate buffer, a histidine buffer, or phosphate buffer.

[0012] In certain embodiments, wherein each of the first and second binding domains of the bispecific antibody construct comprises a VH region and a VL region. In certain embodiments, the bispecific antibody construct is a single chain antibody construct. In certain embodiments, the bispecific antibody construct comprises a polypeptide having the amino acid sequence selected from SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 176, SEQ ID NO: 178, and SEQ ID NO: 192. In certain embodiments, the bispecific antibody construct comprises a polypeptide comprising the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192.

[0013] In certain embodiments, the composition is contained in a plastic container such as an IV bag or IV tube. In certain embodiments, the container is made of a material comprising polyolefin, polyvinyl chloride (PVC), ethyl vinyl acetate (EVA), or polyurethane. In certain

embodiments, the container is made of a material comprising PVC and wherein the PVC is substantially free of di-2-ethylhexyl phthalate(DEHP) or tri-2-ethylhexyltrimellitate (TOTM)

[0014] In certain embodiments, disclosed herein is a pharmaceutical preparation comprising an aqueous pharmaceutical composition contained inside a container, wherein the aqueous pharmaceutical composition comprising: a bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 100 μg/ml, and a surfactant at a concentration of at least about 0.25 x of CMC of the surfactant, wherein the surfactant has an HLB value of at least 20. In certain embodiments, the surfactant is poloxamer 188 or poloxamer 407. In certain embodiments, the aqueous pharmaceutical composition comprises the bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 50 μg/ml. In certain embodiments, the aqueous pharmaceutical composition comprises the surfactant is at a concentration of between about 0.25x and about 20x of the CMC or between about 0.25x and about 10x of the CMC, of the surfactant.

[0015] In certain embodiments, the aqueous pharmaceutical composition further comprising a salt, a buffer, an amino acid, a saccharide or saccharide derivative, or combinations thereof. In certain embodiments, the aqueous pharmaceutical composition has a pH of between about 4.2 and about 7.0.

[0016] In certain embodiments, the container is made of a material comprising polyolefin, PVC, EVA or polyurethane (e.g., polyester and polyether).

[0017] In certain embodiments, the bispecific antibody construct comprises a polypeptide having the amino acid sequences selected from SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 176, SEQ ID NO: 178, and SEQ ID NO: 192. In certain embodiments, the bispecific antibody construct comprises a polypeptide comprising the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192.

[0018] Also disclosed herein is a method of administering a bispecific antibody construct to a patient comprising: preparing an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprises the bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 100 μg/ml and a surfactant at a

concentration of at least about 0.25 x of CMC of the surfactant, and administering the aqueous pharmaceutical composition to the patient, wherein the bispecific antibody construct comprises a polypeptide having the amino acid sequence selected from SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 176, SEQ ID NO: 178, and SEQ ID NO: 192. In certain embodiments, the bispecific antibody construct comprises a polypeptide comprising the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192. In certain embodiments, the aqueous pharmaceutical composition comprises the bispecific antibody construct is at a concentration of between about 0.001 μg/ml and about 50 μg/ml.

[0019] In certain embodiments, the aqueous pharmaceutical composition comprises the surfactant is at a concentration of between about 0.25x and about 20x of the CMC or between about 0.25x and about 10x of the CMC, of the surfactant. In certain embodiments, the surfactant is polysorbate 80, polysorbate 60, polysorbate 40, polysorbate 20, poloxamer 188, poloxamer 407, or Triton X-100.

[0020] In certain embodiments, the aqueous pharmaceutical composition further comprising one or more selected from a salt, a buffer, an amino acid, a saccharide or a saccharide derivative, and a preservative. In certain embodiments, the aqueous pharmaceutical composition has a pH of between about 4.2 and about 7.0.

[0021] In certain embodiments, the container is made of a material comprising polyolefin, PVC, EVA, polyurethane. In certain embodiments, the surfactant is polysorbate 80, polysorbate 60, polysorbate 40, or polysorbate 20, and wherein the container is made of a material comprising PVC that is substantially free of DEHP or TOTM.

[0022] In certain embodiments, the aqueous pharmaceutical composition is prepared by diluting a first composition comprising the bispecific antibody construct with a suitable aqueous solution. In certain embodiments, the first composition is a liquid composition comprising the bispecific antibody construct. In certain embodiments, the first composition is a liquid composition reconstituted from a lyophilized composition comprising the bispecific antibody construct. In certain embodiments, the suitable solution comprises the surfactant at a concentration of at least about 0.25 x of CMC of the surfactant. In certain embodiments, the

aqueous pharmaceutical composition is prepared by adding the suitable aqueous solution into the container followed by adding an appropriate amount of the first composition into the container.

[0023] In certain embodiments, the patient is a cancer patient. In certain embodiments, the administration is IV administration.

BRIEF DESCRIPTION OF THE DRAWINGS

[0024] Figure 1 shows a diagram of the assay for measuring protein binding to a solid surface.

[0025] Figure 2 shows protein binding to a solid surface in the absence of surfactants.

[0026] Figure 3 shows different the addition of various surfactants prevented protein binding to solid surfaces.

[0027] Figure 4 shows that adding surfactants to the solid surface before adding protein prevents protein binding to surfaces more efficiently.

[0028] Figure 5 shows the impacts of different surfactants at the same concentration on the leaching of di-2-ethylhexyl phthalate (DEHP) from DEHP-containing PVC.

[0029] Figure 6 shows the impacts of different surfactants at same folds of CMC on leaching of DEHP from DEHP-containing PVC.

DETAILED DESCRIPTION

[0030] Inventions disclosed herein are based on the surprising finding that surfactants, when used at concentrations lower than their critical micelle concentration, can stabilize proteins at low concentrations in liquid compositions and effectively prevent protein loss due to adsorption to solid surfaces.

[0031] In some embodiments, disclosed herein is an aqueous composition comprising a protein and a surfactant, wherein the protein is present in the composition at a concentration of between about 0.001 μg/ml and about 100 μg/ml, and the surfactant is present in the composition at a concentration of at least about 0.25x of the critical micelle concentration (CMC) of the surfactant.

[0032] Surfactants that can be used in the composition can be any surfactant typically used in pharmaceutical compositions. In some embodiments, the surfactant is a non-ionic surfactant. In some embodiments, the surfactant is a polysorbate such as polysorbate 20, polysorbate 40, polysorbate 60, polysorbate 65, polysorbate 80 or polysorbate 85. In some

embodiments, the surfactant is polysorbate 20, in other embodiments, the surfactant is polysorbate 80. In some embodiments, the surfactant is a poloxamer such as poloxamer 124 poloxamer 188, poloxamer 237, poloxamer 338, and poloxamer 407. In some embodiments, the surfactant is Triton X-100. Various surfactants are available commercially (e.g., Tween 20, Tween 80, Pluronic F68, and Pluronic F127 etc.).

[0033] The surfactant can be present in the composition at a concentration that is at least about 0.25 times (0.25x) the critical micelle concentration (CMC) of that surfactant. In some embodiments, the surfactant is present in the composition at a concentration that is between about 0.25x and about 20x of the CMC of the surfactant. In some embodiments, the surfactant is present in the composition at a concentration that is between about 0.25x and about 15x, or between about 0.25x and about 10x, or between about 0.25x and about 8x, or between about 0.25x and about 6x, or between about 0.25x and about 4, or between about 0.25x and about 2x, or between about 0.25x and about 1x of the CMC of the surfactant.

[0034] In some embodiments, the surfactant is present in the composition at a concentration that is between about 0.5x and about 20x of the CMC of the surfactant. In some embodiments, the surfactant is present in the composition at a concentration that is between about 0.5x and about 15x, or between about 0.5x and about 10x, or between about 0.5x and about 8x, or between about 0.5x and about 6x, or between about 0.5x and about 4x, or between about 0.5x and about 2x, or between about 0.5x and about 1x of the CMC of the surfactant.

[0035] In some embodiments, the surfactant is present in the composition at a concentration of about 0.25x, about 0.5x, about 1x, about 2x, about 3x, about 4x, about 5x, about 6x, about 7x, about 8x, about 9x, about 10x, about 12x, about 14x, about 16x, about 18x, or about 20x of the CMC of the surfactant. In some embodiments, the surfactant is present in the composition at a concentration of about 1.25x, about 2.5x, about 3.5x about 4.5x, about 5.5x, about 6.5x, about 7.5x, about 8.5x or about 9.5x of the CMC of the surfactant.

[0036] As used herein, the term "about," when used to modify a particular value or a range, is understood to mean that there can be variations in a given value or range, including within 20 percent, e.g., within 10 percent, 5 percent, 4 percent, 3 percent, 2 percent, or 1 percent of the stated value or range.

[0037] Critical micelle concentration refers to the concentration of a surfactant above which micelles form, it is a property of a surfactant. The CMC value of a surfactant can be measured by experimental methods well known in the art such as fluorometry, surface tension, conductometry and dynamic light scattering. See e.g., Norman Scholz, Thomas Behnke, Ute

Resch-Genger. Journal of Fluorescence 28:465–476 (2018) and Önder Topel, Burçin Acar Çakır, Leyla Budama, Numan Hoda. Journal of Molecular Liquids 177 40–43 (2013). The CMC value of a surfactant can also be measured automatically using devices such as Attention® Sigma 700 or 701.

[0038] In some embodiments, the CMC value of each of the surfactants is listed in table 1 below.

[0039] Table 1. CMC of commonly used surfactants

Surfactant	CMC* (w/v%)
Polysorbate 20	0.007
Polysorbate 80	0.002
Poloxamer 188	0.4
Poloxamer 407	0.004
Triton X-100	0.014

* For the CMC values listed in the table, see e.g., le Maire M, Champeil P, Moller JV. 2000. Interaction of membrane proteins and lipids with solubilizing detergents. Biochim Biophys Acta 1508:86– 111; Suksiriworapong J, Rungvimolsin T, A-gomol A, Junyaprasert VB, Chantasart D. Development and characterization of lyophilized diazepam-loaded polymeric micelles. 2014. AAPS PharmSciTech. 15(1):52–64; https://www.sigmaaldrich.com/content/dam/sigma-aldrich/docs/Sigma/Product_Information_Sheet/1/t8532pis.pdf

[0040] The protein can be present in the composition at a concentration that is between about 0.001 μg/ml and about 100 μg/ml. In some embodiments, the protein is present in the composition at a concentration that is between about 0.001 μg/ml and about 90 μg/ml, or between about 0.001 μg/ml and about 80 μg/ml, or between about 0.001 μg/ml and about 70 μg/ml, or between about 0.001 μg/ml and about 60 μg/ml, or between about 0.001 μg/ml and about 50 μg/ml, or between about 0.001 μg/ml and about 40 μg/ml, between about 0.001 μg/ml and about 30 μg/ml, or between about 0.001 μg/ml and about 20 μg/ml, or between about 0.001 μg/ml and about 10 μg/ml, or between about 0.001 μg/ml and about 5 μg/ml, or between about 0.001 μg/ml and about 1 μg/ml, or between about 0.001 μg/ml and about 0.01 μg/ml.

[0041] In some embodiments, the protein is present in the composition at a concentration that is between about 0.01 μg/ml and about 100 μg/ml, or between about 0.01 μg/ml and about 80 μg/ml, or between about 0.01 μg/ml and about 70 μg/ml, or between about 0.01 μg/ml and about 60 μg/ml, or between about 0.01 μg/ml and about 50 μg/ml, or between about 0.01 μg/ml

and about 40 μg/ml, between about 0.01 μg/ml and about 30 μg/ml, or between about 0.01 μg/ml and about 20 μg/ml, or between about 0.01 μg/ml and about 10 μg/ml, or between about 0.01 μg/ml and about 5 μg/ml, or between about 0.01 μg/ml and about 1 μg/ml, or between about 0.01 μg/ml and about 0.1 μg/ml, or between about 0.1μg/ml and about 1μg/ml, or between about 0.1μg/ml and about 5 1μg/ml.

[0042] In some embodiments, the protein is present in the composition at a concentration of about 0.001 μg/ml, about 0.005 μg/ml, about 0.01 μg/ml, about 0.05 μg/ml, about 0.1 μg/ml, about 1 μg/ml, about 4 μg/ml, about 8 μg/ml, about 10 μg/ml, about 15 μg/ml, about 20 μg/ml, about 25 μg/ml, about 30 μg/ml, about 35 μg/ml, about 40 μg/ml, about 45 μg/ml, about 50 μg/ml, about 55 μg/ml, about 60 μg/ml, about 65 μg/ml, about 70 μg/ml, about 75 μg/ml, about 80 μg/ml, about 85 μg/ml, about 90 μg/ml, about 95 μg/ml, or about 100 μg/ml.

[0043] In the composition disclosed herein, any of the concentration or concentration range for the protein can be combined with any of the concentration or concentration range for the surfactant.

[0044] Any protein can be the protein in the composition. In some embodiments, the protein in the composition is a therapeutic protein such as an antigen binding protein or a fusion protein.

[0045] As used herein, the term "antigen binding protein" refers to a protein that specifically binds to one or more target antigens. An antigen binding protein includes, but not limited to an antibody (e.g., a monoclonal antibody). An antigen binding protein typically comprises an antigen-binding fragment that specifically binds to an antigen and, optionally, a scaffold or framework portion that allows the antigen-binding fragment to adopt a conformation that promotes binding of the antigen binding protein to the antigen. An "antigen binding fragment" refers to a portion of an antibody that lacks at least some of the amino acids present in a full-length heavy chain and/or light chain, but which is still capable of specifically binding to an antigen. An antigen-binding fragment includes, but is not limited to, a single-chain variable fragment (scFv), a nanobody (e.g. VH domain of camelid heavy chain antibodies; VHH fragment, see Cortez-Retamozo et al., Cancer Research, Vol.64:2853-57, 2004), a Fab fragment, a Fab' fragment, a F(ab')2 fragment, a Fv fragment, a Fd fragment, and a complementarity determining region (CDR) fragment, and can be derived from any mammalian source, such as human, mouse, rat, rabbit, or camelid. Antigen-binding fragments may compete for binding of a target antigen with an intact antibody and the fragments may be produced by the modification of

intact antibodies (e.g. enzymatic or chemical cleavage) or synthesized de novo using recombinant DNA technologies or peptide synthesis known in the art.

[0046] In some embodiments, the protein is an antigen binding protein that is bispecific. As used herein, the term "bispecific" refers to an antigen binding protein capable of specifically binding to two different antigens or targets or epitopes. As used herein, an "epitope" refers to any determinant capable of being specifically bound by an antigen binding protein, such as an antibody or fragment thereof. In some embodiments, the bispecific antigen binding protein comprises a first domain specifically binds to one antigen or target and a second domain specifically binds to another antigen or target. In some embodiments, the first domain of the bispecific antigen binding protein specifically binds to a target cell surface antigen and the second binding domain of the bispecific antigen binding protein specifically binds to the human CD3, a subunit of the T cell receptor complex on T cells. In some preferred embodiments, the bispecific antigen binding protein is a bispecific T cell engager (BiTE®) antibody construct as described in, e.g., WO2008119567 and WO2017134140.

[0047] As used herein, the term "antibody construct" refers to a molecule in which the structure and/or function is/are based on the structure and/or function of an antibody, e.g., of a full-length or whole immunoglobulin molecule and/or is/are drawn from the variable heavy chain (VH) and/or variable light chain (VL) domains of an antibody or fragment thereof. An antibody construct is hence capable of binding to its specific target or antigen. Antibody construct also includes modified fragments of antibodies, such as scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab_2, Fab_3, diabodies, single chain diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, "multibodies" such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable domain, which might be VHH, VH or VL, that specifically bind an antigen or epitope independently of other V regions or domains.

[0048] In some embodiments, the bispecific antibody construct comprises a first binding domain and a second binding domain, wherein the first binding domain specifically binds to a first cell surface antigen and the second binding domain specifically binds to human CD3. In some embodiments, the first and the second domain of the bispecific antibody construct is a "bispecific single chain antibody construct", more preferably a bispecific "single chain Fv" (scFv). In a scFv, VL and VH of an antibody are joined, e.g., by a synthetic linker, as a single protein chain in which the VL and VH regions pair to form a monovalent molecule; see e.g., Huston et al. (1988) Proc. Natl. Acad. Sci USA 85:5879-5883). The linker can be a short peptide

of about ten to about 25 amino acids, preferably about 15 to 20 amino acids. The linker is usually rich in glycine for flexibility, as well as serine or threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa. The scFv retains the specificity of the original immunoglobulin, despite removal of the constant regions and introduction of the linker. The VH and VL regions are arranged in the order VH-VL or VL-VH. It is preferred that the VH-region is positioned N-terminally of a linker sequence, and the VL-region is positioned C-terminally of the linker sequence. In certain embodiments, the first and second domain of the bispecific antibody construct are in a format selected from $(scFv)_2$, scFv-single domain mAb, diabody and oligomers of any of those formats.

[0049] In some embodiments, the bispecific antibody construct further comprises a third domain. In some embodiments, the third domain is a single-chain Fc (scFc) domain. In some embodiments, the scFc domain is a scFc half-life extended (HLE) domain. In some preferred embodiments, the third domain of the bispecific antibody construct is an HLE domain with an amino to carboxyl order: hinge-CH2-CH3-linker-hinge-CH2-CH3.

[0050] In some embodiments, the first binding domain of the bispecific antibody construct binds to a first cell surface antigen. In some embodiment, the first cell surface antigen is CD70. CD70 (also known as CD27L or TNFSF7) is a type II integral membrane protein whose normal expression is restricted to a subset of activated T and B cells, mature dendritic cells and thymic medullar epithelial cells.

[0051] In some embodiments, the first cell surface antigen is a tumor antigen. The term "tumor antigen" as used herein is understood to refer to those antigens that are presented on tumor cells. These antigens can be presented on the cell surface with an extracellular part, which is often combined with a transmembrane and cytoplasmic part of the molecule. These antigens can sometimes be presented only by tumor cells and not by the normal ones. Tumor antigens can be exclusively expressed on tumor cells or might represent a tumor specific mutation compared to normal cells. In this case, they are called tumor-specific antigens. More common are antigens that are presented by tumor cells and normal cells, and they are called tumor-associated antigens. These tumor-associated antigens can be overexpressed compared to normal cells or are accessible for antibody binding in tumor cells due to the less compact structure of the tumor tissue compared to normal tissue. In some embodiments, the first binding domain binds to tumor antigens selected from CD19, CD33, epidermal growth factor receptor variant iii (EGFRvIII), mesothelin (MSLN), cadherin 19 (CDH19), FMS-like tyrosine kinase 3 (FLT3), delta-like ligand 3 (DLL3), Placental-Cadherin (CDH3), B-cell maturation antigen (BCMA), prostate-specific

membrane antigen (PSMA), human mucin 17 (MUC17), and claudin-18 isoform 2 (CLDN18.2). In some embodiments, the tumor antigens are human tumor antigens.

[0052] In some preferred embodiments, the bispecific antibody construct comprises a first domain, a second domain and optionally a third domain, wherein the first domain binds to CD70 and the second domain binds to human CD3, and the third domain (if present) is an HLE domain with an amino to carboxyl order: hinge-CH2-CH3-linker-hinge-CH2-CH3. In other preferred embodiments, the bispecific antibody construct comprises a first domain, a second domain and optionally a third domain, wherein the first domain binds to a tumor antigen selected from CD19, CD33, EGFRvIII, MSLN, CDH19, FLT3, DLL3, CDH3, BCMA, PSMA, MUC17 and C:DN18.2, and the second domain binds to human CD3, and the third domain (if present) is a HLE domain with an amino to carboxyl order: hinge-CH2-CH3-linker-hinge-CH2-CH3. In a preferred embodiment, the first and second domain are linked together via a peptide linker, and are linked to the third domain (if present) via a peptide linker. Preferred peptide linker have been described herein above and are characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly4Ser, or polymers thereof, i.e. (Gly4Ser)x, where x is an integer of 1 or greater (e.g. 2, 3, 4, 5, 6, or 7). In some of the preferred embodiments, the second binding domain comprises a polypeptide having the amino acid sequence of SEQ ID NO: 201.

[0053] In some embodiments, the first binding domain specifically binds to CD33. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 1-15.

[0054] In some embodiments, the first binding domain specifically binds to EGFRvIII. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 16-26.

[0055] In some embodiments, the first binding domain specifically binds to MSLN. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 27-38 and 165.

[0056] In some embodiments, the first binding domain specifically binds to CDH19. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 39-56.

[0057] In some embodiments, the first binding domain specifically binds to DLL3. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of SEQ ID NOs: 68-78.

[0058] In some embodiments, the first binding domain specifically binds to CD19. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 79-88.

[0059] In some embodiments, the first binding domain specifically binds to FLT3. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 57-67.

[0060] In some embodiments, the first binding domain specifically binds to CDH3. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 89-99.

[0061] In some embodiments, the first binding domain specifically binds to BCMA. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 100-110.

[0062] In some embodiments, the first binding domain specifically binds to PSMA. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 111-155, 166 and 167.

[0063] In some embodiments, the first binding domain specifically binds to CD70. In some embodiments, the first binding domain comprises a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 156-164.

[0064] In some embodiments, the second binding domain of the bispecific antibody construct specifically binds to the human CD3 epsilon on the surface of a T cell. In some embodiments, the second domain of the bispecific antibody construct specifically binds to an extracellular epitope of the human CD3ε chain. In some embodiments, the second domain of the bispecific antibody construct that specifically binds to the human CD3 comprises a VL region comprising CDR-L1 having the amino acid sequence of sequence of SEQ ID NO: 193, CDR-L2 having the amino acid of SEQ ID NO: 194, and CDR-L3 having the amino acid sequence of sequence of SEQ ID NO: 195, and a VH region comprising CDR-H1 having the amino acid sequence of sequence of SEQ ID NO: 196, CDR-H2 having the amino acid sequence of sequence of SEQ ID NO: 197, and CDR-H3 having the amino acid sequence of sequence of SEQ ID NO: 198.

[0065] In some embodiments, the second domain of the bispecific antibody construct comprises a VH having the amino acid sequence of SEQ ID NO: 199 and a VL having the amino acid of SEQ ID NO: 200. In some embodiments, the second domain of the bispecific antibody construct comprises a polypeptide having the amino acid sequence of SEQ ID NO: 201.

[0066] In some embodiments, the protein is a CD70xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to CD70 and a second domain that specifically binds to CD3. In one embodiment, the first domain specifically binds to CD70 and comprises the CDRs as depicted in SEQ ID NOs: 156 to 161, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193-198. In some embodiments, the bispecific antibody construct further comprises an HLE domain (third domain). In one embodiment, the bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 162 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 163. In one embodiment, the CD70xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 164.

[0067] In some embodiments, the protein is a BCMAxCD3 bispecific antibody construct, which comprises a first domain that specifically binds to BCMA and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to BCMA and has the CDRs as depicted in SEQ ID NOs: 100 to 105, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193-198. In one embodiment, the BCMAxCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 106 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 107. In one embodiment, the BCMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 108. In one embodiment, the BCMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 109. In another embodiment, the BCMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 110.

[0068] In some embodiments, the bispecific antibody is a CD33xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to CD33 and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody construct further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to CD33 and has the CDRs as depicted in SEQ ID NOs: 3 to 5 and 8 to 10, the second

domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193-198. In one embodiment, the CD33xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 1 or 2 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 6 or 7. In another embodiment, the CD33xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any one of SEQ ID NO: 11 or 12. In another embodiment, the BCMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 13 or 15.

[0069] In some embodiments, the protein is an EGFRvIIIxCD3 bispecific antibody construct, which comprises a first domain that specifically binds to EGFRvIII and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to EGFRvIII and has the CDRs as depicted in SEQ ID NOs: 16 to 21, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193-198. In one embodiments, the EGFRvIIIxCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 22 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 23. In one embodiment, the EGFRvIIIxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 24 or 25. In one embodiment, the EGFRvIIIxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 24 or 26.

[0070] In some embodiments, the protein is a MSLNxCD3 bispecific antibody construct, which comprises a first domain that specifically binds to MSLN and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody construct further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to MSLN and has the CDRs as depicted in SEQ ID NOs: 27 to 32, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193 to 198. In one embodiment, the MSLNxCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 33 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid

sequence of SEQ ID NO: 34. In one embodiment, the MSLNxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any one of SEQ ID NOs: 35-38. In one embodiment, the MSLNxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 165.

[0071] In some embodiments, the protein is a CDH19xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to CDH19 and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to CDH19 and has the CDRs as depicted in SEQ ID NOs: 39 to 44, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193 to 198. In one embodiment, the CDH19xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 45 or 51and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 46 or 52. In one embodiment, the CDH19xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any one of SEQ ID NOs: 47, 48-50, and 53-56, . In one embodiment, the CDH19xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 48.

[0072] In some embodiments, the protein is a DLL3xCD3 bispecific antibody, which comprises a first domain that specifically binds to DLL3 and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to DLL3 and has the CDRs as depicted in SEQ ID NOs: 68 to 73, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193 to 198. In one embodiment, the DLL3xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 74 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 75. In one embodiment, the DLL3xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 76-78. In one embodiment, the DLL3xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 78.

[0073] In some embodiments, the protein is a FLT3xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to FLT3 and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to FLT3 and has the CDRs as depicted in SEQ ID NOs: 57 to 62, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs 193 to 198. In one embodiment, the FLT3xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 63 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 64. In one embodiment, the FTL3xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any of SEQ ID NO: 65-67. In one embodiment, the FTL3xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 67.

[0074] In some embodiments, the protein is a CDH3xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to CDH3 and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody construct further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to CDH3 and has the CDRs as depicted in SEQ ID NOs: 89 to 94, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193 to 198. In one embodiment, the CDH3xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 95 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 96. In one embodiment, the CDH3xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any of SEQ ID NO: 97-99. In one embodiment, the CDH3xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 99.

[0075] In some embodiments, the protein is a PSMAxCD3 bispecific antibody construct, which comprises a first domain that specifically binds to PSMA and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody construct further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to PSMA and has the CDRs as depicted in any of SEQ ID NOs: 111-116, the second domain specifically binds to

CD3 and has the CDRs as depicted in SEQ ID NOs: 193 to 198. In one embodiment, the first domain binds to PSMA and has the CDRs as depicted in any of SEQ ID NOs: 126-131 and 141-146, the second domain binds to CD3 and has the CDRs as depicted in SEQ ID NOs: 193 to 198. In one embodiment, the PSMAxCD3 bispecific antibody comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 117, 132 or 147 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 118, 133, or 148. In one embodiment, the PSMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any one of SEQ ID NOs: 119-125, 134-140, and 149-155. In one embodiment, the PSMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of any of SEQ ID NOs: 121, 122, 124, 125, 136, 137, 139, 140, 151, 152, 154 and 155. In one embodiment, the PSMAxCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 166 or 167.

[0076] In some embodiments, the protein is a Cldn18.2xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to Cldn18.2 and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to Cldn18.2 and has the CDRs as depicted in SEQ ID NOs: 168 to 173, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs 193 to 198. In one embodiment, the Cldn18.2xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 174 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 175. In one embodiment, the Cldn18.2xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 176 or 178. In one embodiment, the Cldn18.2xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 178.

[0077] In some embodiments, the protein is a MUC17xCD3 bispecific antibody construct, which comprises a first domain that specifically binds to MUC17and a second domain that specifically binds to CD3. In some embodiments, the bispecific antibody further comprises an HLE domain (third domain). In one embodiment, the first domain specifically binds to MUC17and has the CDRs

as depicted in SEQ ID NOs: 184 to 189, the second domain specifically binds to CD3 and has the CDRs as depicted in SEQ ID NOs 193 to 198. In one embodiment, the MUC17xCD3 bispecific antibody construct comprises a VH and a VL, wherein the VH comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 190 and the VL comprises a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO: 191. In one embodiment, the MUC17xCD3 bispecific antibody construct comprises a polypeptide that comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 192.

[0078] In certain embodiments, the bispecific antibody construct comprises a polypeptide that comprises, consists essentially or consists of the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192.

[0079] The bispecific antibody disclosed herein can be prepared by methods known in the art. For example, the bispecific antibody can be prepared by methods disclosed in WO2008/119657 and WO2017/134140.

Additional Excipients that May be Used in the Composition

[0080] In some embodiments, the composition further comprises one or more excipients suitable for pharmaceutical compositions. In some embodiments, the composition further comprises a salt, a buffer, a saccharide or a saccharide derivative, an amino acid, or a preservative, or combinations of two or more of the forgoing. In some embodiments, the composition further comprises a salt, a saccharide or a saccharide derivative, an amino acid, and optionally a preservative. In some embodiments, the composition further comprises a salt, a buffer, a saccharide or a saccharide derivative, and an amino acid. In some embodiments, the composition further comprises a salt, a buffer, a saccharide or a saccharide derivative, an amino acid, and a preservative.

[0081] Exemplary salts that may be used in the composition include salts that are suitable to be used in pharmaceutical compositions (e.g., NaCl). Exemplary buffers that may be used in the composition include acetate buffer, glutamate buffer, citrate buffer, succinate buffer, tartrate buffer, fumarate buffer, maleate buffer, histidine buffer, and phosphate buffer. Exemplary saccharides or saccharide derivatives include monosaccharides, disaccharides, cyclic polysaccharides and sugar alcohols, such as sugars (e.g., sucrose and trehalose) and sugar alcohol (e.g., mannitol and sorbitol). Exemplary amino acids include lysine, histidine, arginine,

glycine, methionine, and alanine. Exemplary preservatives include benzoates (e.g., benzyl alcohol and sodium benzoate) and sorbates (e.g., potassium sorbate).

[0082] The pH of the composition can be in the range of from about 3.5 to 7.5. In some embodiments, the composition has a pH of from about 4.0 to about 7.0. In some embodiments, the composition has a pH of from about 4.2 to about 7.0, or from about 5.0 to about 7.0, or from about 5.5 to about 7.0, or from about 6.0 to about 7.0, or from about 6.5 to about 7.0, or from about 4.2 to about 6.5, or from about 4.2 to about 6.0, or from about 4.2 to about 5.5, or from about 4.2 to about 5.0, or from about 5.0 to about 6.0, or from about 5.0 to about 6.5, or from about 5.0 to about 6.0, or from about 5.0 to about 5.5, or from about 5.5 to about 6.0, or from about 5.5 to about 6.5, or from about 5.5 to about 6.0, or from about 6.0 to about 6.5. In some embodiments, the pH of the composition is about 3.5, about 4.0, about 4.5, about 5.0, about 5.5, about 6.0, about 6.5, about 7.0, or about 7.5.

[0083] The pH of the composition may be achieved by using one or more buffers listed above. In some embodiments, the composition comprising a buffer selected from an acetate buffer, a glutamate buffer, a citrate buffer, a succinate buffer, a tartrate buffer, a fumarate buffer, a maleate buffer, a histidine buffer, and a phosphate buffer. In some embodiments, the composition comprising a combination of two buffers selected from the above list of buffers, e.g., a glutamate buffer and a citrate buffer.

[0084] In some embodiments, the composition comprises substantially no additional buffer. As used herein, the phrase "substantially no additional buffer" refers that the composition contains no buffering agent added therein for the purpose of adjusting and/or maintaining the pH of the composition. For example, saline solution (0.9% NaCl solution) contains no additional buffer and has a pH of about 5.5. It is believed that the pH of saline solution is achieved and maintained in part by atmospheric CO_2 dissolved in water. See e.g., Reddi, B. AJ Int. J. Med. Sci. 10: 747-750 (2013). Such a composition may contain residual buffer that does not contribute to the buffering capacity of the composition.

[0085] In some embodiments, the composition comprises a protein at any of the concentration disclosed above, a surfactant at any of the concentration disclosed above, and further comprises a salt (e.g., NaCl), a sugar (e.g., sucrose), an amino acid (e.g., lysine), and optionally a preservative (e.g., benzyl alcohol). In some embodiments, the composition comprises a protein at any of the concentration disclosed above, a surfactant at any of the concentration disclosed above, and further comprises a salt (e.g., NaCl), a sugar (e.g., sucrose), an amino acid (e.g., lysine), a buffer (e.g., a glutamate and/or citrate buffer), and optionally a

preservative (e.g., benzyl alcohol). The pH of the composition can be any of the pH value disclosed above. In some embodiments, the pH of the composition is about 5.5.

[0086] In some embodiments, the composition disclosed herein is a pharmaceutical composition. As used herein, the term "pharmaceutical composition" is understood to refer to a formulation comprising a protein (e.g., a bispecific antibody construct) suitable for injection and/or administration into a patient (e.g., a human) in need thereof. More particularly, a pharmaceutical composition is substantially sterile and does not contain any agents that are unduly toxic or infectious to the recipient.

Containers for the Composition

[0087] In some embodiments, the composition disclosed herein is contained in a container. Containers that may be used herein include those suitable for pharmaceutical use, e.g., containers made of materials that are nontoxic and maintain physical integrity. In some embodiments, the container is a component for intravenous (IV) administration. As used herein, the phrase "component for IV administration" is understood to refer to a container or a part of a system that may contact the composition during IV administration. In some embodiments, the container is an IV bag or IV tubing.

[0088] Materials that may be used for making containers include those typically used for making pharmaceutical containers such as glass and plastic.

[0089] In some embodiments, the container is a plastic container. In some embodiments, the container is made of a material comprising polyolefin (e.g., polypropylene (PP) and polyethylene (PE)), polyvinyl chloride (PVC), ethyl vinyl acetate (EVA), or polyurethane (e.g., polyester and polyether). In some embodiments, the container is made of a material comprising PVC. In some embodiments, the PVC is substantially free of di-2-ethylhexyl phthalate (DEHP) or tri-2-ethylhexyltrimellitate (TOTM). As used herein, the term "substantially free of" is understood to refer to PVC in which DEHP or TOTM is not used and/or detected. DEHP and TOTM are plasticizers that may be used in making PVC softer therefore could be made into different shapes. In some embodiments, the container is made of a material that does not comprise PVC. In some embodiments, the container is made of a material comprising polyolefin, EVA, or polyurethane (e.g., polyester and polyether). In some embodiments, the container is made of a material comprising PP and/or PE.

[0090] Under certain conditions, DEHP or TOTM contained in certain types of PVC plastic can leach from the plastic in the presence of certain concentrations of certain surfactants (e.g., polysorbates, see Example 3). Not wish to be bound by any particular theory, it is believed

that the more lipophilic a surfactant, the easier DEHP or TOTM can leach out in the presence of the surfactant. The hydrophilic-lipophilic balance (HLB) of a surfactant is a measure of the degree to which it is hydrophilic or lipophilic, and can be calculated by methods known in the art. See e.g., Griffin, William C. Calculation of HLB Values of Non-Ionic Surfactants, Journal of the Society of Cosmetic Chemists, 5 (4): 249–56 (1954). The HLB value can be used to predict properties of a surfactant, e.g., HLB > 10 indicates the surfactant is more water-soluble (lipid-insoluble), while HLB< 10 indicates the surfactant is more lipid-soluble (water-insoluble). The HLB value of exemplary surfactants that can be used in the composition disclosed herein include 17 (polysorbate 20), 15 (polysorbate 80) (https://pharmlabs.unc.edu/labs/emulsions/hlb.htm) and 29 (poloxamer 188) (http://www.rumapel.com.ar/cosmetica_miscelaneos/ficha_tecnica/Pluracare%20L-%20F%20Grades.pdf). In embodiments where the container is made of a PVC plastic comprising DEHP or TOTM, the surfactant in the composition preferably have an HLB value of at least 20 (e.g., a poloxamer, see Example 3), more preferably an HLB value of between 20 and 30.

[0091] Containers such as IV components (e.g., IV bags and tubes used for IV administration) that are made of the above listed materials are commercially available. For example, various suitable containers are available from manufactures such as Baxter Healthcare Corporation and B. Braun Medical Inc.

Pharmaceutical Preparation

[0092] Also disclosed herein are pharmaceutical preparations comprising the aqueous composition disclosed above. As used herein, the term "pharmaceutical preparation" is understood to refer to a preparation comprising the aqueous composition disclosed herein in a suitable pharmaceutical container prior to administration to a patient (e.g., a human). In some embodiments, disclosed herein is a pharmaceutical preparation comprising an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprising: a) a protein at a concentration of between about 0.001 μg/ml and about 100 μg/ml, and b) a surfactant at a concentration of at least about 0.25 x of the CMC of the surfactant, and wherein the protein is not blinatumomab.

[0093] In some embodiments, the surfactant comprised in the composition is a polysorbate. In some embodiments, the surfactant is a polysorbate selected from polysorbate 20, polysorbate 40, polysorbate 60, polysorbate 65, polysorbate 80 and polysorbate 85. In some embodiments, the surfactant is polysorbate 20 or polysorbate 80. In some embodiments, the

surfactant is a poloxamer. In some embodiments, the surfactant is poloxamer 188 or poloxamer 407. In some embodiments, the surfactant is Triton X-100.

[0094] In some embodiments, disclosed herein is a pharmaceutical preparation comprising an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprising: a) a bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 100 μg/ml, and b) a surfactant at a concentration of at least about 0.25 x of CMC of the surfactant, wherein the surfactant is a poloxamer. In some embodiments, the poloxamer is poloxamer 188 or poloxamer 407.

[0095] In some embodiments, the surfactant is present in the composition at a concentration that is between about 0.25x and about 20x of the CMC of the surfactant. In some embodiments, the surfactant is present in the composition at a concentration that is between about 0.25x and about 10x of the CMC of the surfactant. In some embodiments, the surfactant is present in the composition at a concentration that is within any of the concentration ranges disclosed above. In some embodiments, the surfactant is present in the composition at a concentration that is any of the concentration disclosed above. The CMC value of a surfactant can be determined by the methods disclosed above. In some embodiments, the CMC value of certain commonly used surfactants are listed in Table 1.

[0096] In some embodiments, the aqueous pharmaceutical composition comprising the protein at a concentration of between about 0.001 μg/ml and about 50 μg/ml. In some embodiments, the composition comprising the protein (e.g., a bispecific antibody construct) at a concentration that is within any of the ranges disclosed above. In some embodiments, the protein (e.g., a bispecific antibody construct) is present in the composition at any of the concentrations disclosed above. Any of the concentration or concentration range for the protein disclosed above can be combined with any of the concentration or concentration range for the surfactant disclosed above.

[0097] As disclosed above, the protein can be a therapeutic protein such as an antigen binding protein and a fusion protein. In some embodiments, the protein is a bispecific antigen binding protein. In some embodiments, the protein is a bispecific antibody construct disclosed above. In some embodiments, the protein is a CD70xCD3 bispecific antibody construct. In some embodiments, the protein is a BCMAxCD3 bispecific antibody construct. In some embodiments, the protein is a CD33xCD3 bispecific antibody construct. In some embodiments, the protein is an EGFRvIIIxCD3 bispecific antibody construct. In some embodiments, the protein is a MSLNxCD3 bispecific antibody construct. In some embodiments, the protein is a CDH19xCD3

bispecific antibody construct. In some embodiments, the protein is a DLL3xCD3 bispecific antibody construct. In some embodiments, the protein is a FLT3xCD3 bispecific antibody construct. In some embodiments, the protein is a CDH3xCD3 bispecific antibody construct. In some embodiments, the protein is a PSMAxCD3 bispecific antibody construct. In some embodiments, the protein is a Cldn18.2xCD3 bispecific antibody construct. In some embodiments, the protein is a MUC17xCD3 bispecific antibody construct. Each of these bispecific antibody constructs is disclosed above. In certain embodiments, the protein comprises, consists essentially or consists of the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192.

[0098] The pH of the composition can be within any of the pH ranges disclosed above. In some embodiments, the pH of the composition can be any pH disclosed above.

[0099] In some embodiments, the aqueous pharmaceutical composition further comprises one or more excipients suitable for use in a pharmaceutical composition. In some embodiments, the aqueous pharmaceutical composition further comprises a salt, a buffer, an amino acid, a saccharide or a saccharide derivative, a preservative or combinations thereof. In some embodiments, the aqueous pharmaceutical composition further comprises a salt, an amino acid, a saccharide or a saccharide derivative, a preservative or combinations thereof. Exemplary salts, buffers, amino acids, saccharides or derivatives thereof, and preservatives that may be used in the composition are disclosed above.

[00100] In some embodiments, the container is a plastic container. In some embodiments, the container is made of a material comprising polyolefin (e.g., PP and PE), PVC, EVA, or polyurethane (e.g., polyester and polyether). In some embodiments, the container is made of a material comprising PVC. In some embodiments, the PVC is substantially free of DEHP or TOTM. In some embodiments, the container is made of a material that does not comprise PVC.

[00101] In some embodiments, the surfactant comprised in the composition is a poloxamer, and the container can be made of a material comprising polyolefin, PVC, EVA, or polyurethane (e.g., polyester and polyether). In some embodiments, the surfactant comprised in the composition is a polysorbate or Triton X-100, and the container can be made of a material comprising polyolefin, PVC that is substantially free of DEHP or TOTM, EVA, or polyurethane (e.g., polyester and polyether).

[00102] In some embodiments, the container is a component for intravenous (IV) administration. In some embodiments, the container is an IV bag or IV tubing.

[00103] In some embodiments, the pharmaceutical preparation comprises an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprising a bispecific antibody construct (e.g., any of the bispecific antibody construct disclosed herein), a surfactant (e.g., any of the surfactant disclosed herein), and further comprises a salt (e.g., NaCl), an amino acid (e.g., lysine), a saccharide or a saccharide derivative (e.g., sucrose or mannitol), optionally a preservative (e.g., and benzyl alcohol), and wherein the container is made of a material comprising polyolefin, PVC, EVA, or polyurethane (e.g., polyester and polyether). In some embodiments, the pharmaceutical preparation comprises an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprising a bispecific antibody construct (e.g., any of the bispecific antibody construct disclosed herein), a surfactant (e.g., any of the surfactant disclosed herein), and further comprises a salt (e.g., NaCl), a buffer (e.g., a glutamate buffer and/or a citrate buffer), an amino acid (e.g., lysine), a saccharide or a saccharide derivative (e.g., sucrose or mannitol), optionally a preservative (e.g., benzyl alcohol), and wherein the container is made of a material comprising polyolefin, PVC, EVA, or polyurethane (e.g., polyester and polyether). The concentration of the bispecific antibody construct can be any of the concentration disclosed above for the protein. The concentration of the surfactant can be any of the concentration disclosed above. The pH of the composition is in the range of between about 3.5 and about 7.0. In some embodiments, the pH of the composition is about 5.5. In some embodiments, the container is an IV bag.

Methods of Administering the Composition

[00104] Also disclosed herein are methods of administering the composition disclosed herein to a patient. In some embodiments, disclosed herein is a method of administering a protein to a patient, the method comprises a) preparing an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprises a protein (e.g., a bispecific antibody construct disclosed herein) at a concentration of between about 0.001 μg/ml and about 100 μg/ml and a surfactant at a concentration of at least about 0.25 x of CMC of the surfactant, and b) administering the aqueous pharmaceutical composition to the patient, wherein the protein is not blinatumomab.

[00105] In some embodiments, the aqueous pharmaceutical composition is prepared by diluting a first composition comprising the protein (e.g., a bispecific antibody construct) with a suitable aqueous solution. In some embodiments, the aqueous pharmaceutical composition is

prepared by adding the suitable solution into the container followed by adding an appropriate amount of a first composition into the container thereby diluting the first composition comprising the protein.

[00106] In some embodiments, the first composition is a liquid composition comprising the protein. In some embodiments, the first composition is a liquid composition reconstituted from a lyophilized composition comprising the protein. In some embodiments, the first composition is a liquid composition reconstituted from a lyophilized composition comprising the protein using sterile water.

[00107] In some embodiments, the suitable aqueous solution that is used for diluting the first composition comprises the surfactant at a concentration of at least about 0.25x of the CMC of the surfactant. In some embodiments, the suitable aqueous solution that is used for diluting the first composition comprises the surfactant at a concentration of between about 0.25x and 20x, or between about 0.25x and about 10x of the CMC of the surfactant. In some embodiments, the suitable aqueous solution that is used for diluting the first composition comprises the surfactant at a concentration of 0.25x, about 0.5 x, about 1x, about 2x, about 3x, about 4x, about 5x, about 6x, about 7x, about 8x, about 9x, about 10x, about 15x or about 20x of the CMC of the surfactant. In some embodiments, the suitable aqueous solution that is used for diluting the first composition further comprises NaCl. In some embodiments, the suitable aqueous solution that is used for diluting the first composition has a pH of between about 3.5 and about 7.0, or between about 4.0 and about 6.5. In some embodiments, the suitable aqueous solution that is used for diluting the first composition has a pH of about 5.5. In some embodiments, the method further comprising rinsing the container with the suitable aqueous solution that is used for diluting the first composition before the preparing step.

[00108] In some embodiments, the surfactant in the aqueous pharmaceutical composition is a polysorbate. In some embodiments, the surfactant is a polysorbate selected from polysorbate 20, polysorbate 40, polysorbate 60, polysorbate 65, polysorbate 80 and polysorbate 85. In some embodiments, the surfactant is polysorbate 20 or polysorbate 80. In some embodiments, the surfactant is a poloxamer. In some embodiments, the surfactant is poloxamer 188 or poloxamer 407. In some embodiments, the surfactant is Triton X-100.

[00109] In some embodiments, the surfactant in the aqueous pharmaceutical composition is present in the composition at a concentration that is between about 0.25x and about 20x of the CMC of the surfactant. In some embodiments, the surfactant is present in the aqueous pharmaceutical composition at a concentration that is between about 0.25x and about 10x of the

CMC of the surfactant. In some embodiments, the surfactant is present in the aqueous pharmaceutical composition at a concentration that is within any of the concentration ranges disclosed above. In some embodiments, the surfactant is present in the aqueous pharmaceutical composition at a concentration that is any of the concentrations disclosed above. The CMC value of a surfactant can be determined by the methods disclosed above. In some embodiments, the CMC value of certain commonly used surfactants are listed in Table 1.

[00110] In some embodiments, the aqueous pharmaceutical composition comprising the protein at a concentration of between about 0.001 μg/ml and about 50 μg/ml. In some embodiments, the aqueous pharmaceutical composition comprising the protein at a concentration that is within any of the ranges disclosed above. In some embodiments, the protein is present in the composition at any of the concentrations disclosed above.

[00111] As disclosed above, the protein can be a therapeutic protein such as an antigen binding protein, a mAb or a fusion protein. In some embodiments, the protein is a bispecific antigen binding protein. In some embodiments, the protein is a bispecific antibody construct disclosed above. In some embodiments, the protein is a CD70xCD3 bispecific antibody construct. In some embodiments, the protein is a BCMAxCD3 bispecific antibody construct. In some embodiments, the protein is a CD33xCD3 bispecific antibody construct. In some embodiments, the protein is an EGFRvIIIxCD3 bispecific antibody construct. In some embodiments, the protein is a MSLNxCD3 bispecific antibody construct. In some embodiments, the protein is a CDH19xCD3 bispecific antibody construct. In some embodiments, the protein is a DLL3xCD3 bispecific antibody construct. In some embodiments, the protein is a FLT3xCD3 bispecific antibody construct. In some embodiments, the protein is a CDH3xCD3 bispecific antibody construct. In some embodiments, the protein is a PSMAxCD3 bispecific antibody construct. In some embodiments, the protein is a Cldn18.2xCD3 bispecific antibody construct. In some embodiments, the protein is a MUC17xCD3 bispecific antibody construct. Each of these bispecific antibody constructs is disclosed above. In certain embodiments, the protein comprises, consists essentially or consists of the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192.

[00112] The pH of the composition can be within any of the pH ranges disclosed above. In some embodiments, the pH of the composition can be any pH disclosed above.

[00113] In some embodiments, the aqueous pharmaceutical composition further comprises one or more excipients suitable for use in a pharmaceutical composition. In some embodiments, the aqueous pharmaceutical composition further comprises a salt, a buffer, an amino acid, a saccharide or a saccharide derivative, optionally a preservative, or combinations of two or more of the forgoing. In some embodiments, the aqueous pharmaceutical composition further comprises a salt, an amino acid, a saccharide or a saccharide derivative, optionally a preservative, or combinations of two or more of the forgoing. Exemplary salts, buffers, amino acids, saccharides or derivatives thereof, and preservatives that may be used in the composition are disclosed above.

[00114] In some embodiments, the container is a plastic container or component. In some embodiments, the container is made of a material comprising polyolefin (e.g., PP and PE), PVC, EVA, or polyurethane (e.g., polyester and polyether). In some embodiments, the container is made of a material comprising PVC. In some embodiments, the PVC is substantially free of DEHP or TOTM. In some embodiments, the container is made of a material that does not comprise PVC. In some embodiments, the container is an IV bag or IV tube.

[00115] In some embodiments, the aqueous pharmaceutical composition is administered to the patient via IV administration. In some embodiments, the patient is a cancer patient. In some embodiments, the patient is a human.

Method for Accessing Binding of Protein to a Solid Surface

[00116] Also disclosed herein is a method for accessing binding of proteins to solid surfaces. In some embodiments, disclosed herein is of accessing binding of a protein to a solid surface, comprising: a) incubating an aqueous solution comprising the protein with the solid surface, wherein the protein is labeled with a fluorophore, b) removing the aqueous solution from the solid surface and rinse the surface, and c) imaging the solid surface using confocal microscopy.

Table 2 below lists the sequences disclosed herein

	Designation			AMINO ACID SEQUENCE
1.	CD33 ccVH E11	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGM NWVKQAPGQCLEWMGWINTYTGEPTYADKFQG RVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWS WSDGYYVYFDYWGQGTSVTVSS

2.	CD33 VH E11	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGM NWVKQAPGQGLEWMGWINTYTGEPTYADKFQG RVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWS WSDGYYVYFDYWGQGTSVTVSS
3.	CD33 HCDR1 E11	artificial	aa	NYGMN
4.	CD33 HCDR2 E11	artificial	aa	WINTYTGEPTYADKFQG
5.	CD33 HCDR3 E11	artificial	aa	WSWSDGYYVYFDY
6.	CD33 CC VL E11	artificial	aa	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNK NSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGS GSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGCG TRLEIK
7.	CD33 VL E11	artificial	aa	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNK NSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGS GSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQG TRLEIK
8.	CD33 LCDR1 E11	artificial	aa	KSSQSVLDSSTNKNSLA
9.	CD33 LCDR2 E11	artificial	aa	WASTRES
10.	CD33 LCDR3 E11	artificial	aa	QQSAHFPIT
11.	CD33 HL CC E11	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGM NWVKQAPGQCLEWMGWINTYTGEPTYADKFQG RVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWS WSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSG GGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDS STNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDR FSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITF GCGTRLEIK
12.	CD33 HL E11	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGM NWVKQAPGQGLEWMGWINTYTGEPTYADKFQG RVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWS WSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSG GGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDS STNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDR FSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITF GQGTRLEIK
13.	CD33 CC E11 HL x I2C HL Bispecific molecule	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGM NWVKQAPGQCLEWMGWINTYTGEPTYADKFQG RVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWS WSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSG

				GGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDS STNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDR FSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKGLEWVARIRS KYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT VSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGG TVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEA EYYCVLWYSNRWVFGGGTKLTVL
14.	CD33 E11 HL x I2C HL	artificial	aa	MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGE SVKVSCKASGYTFTNYGMNWVKQAPGQGLEWM GWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEI RNLGGDDTAVYYCARWSWSDGYYVYFDYWGQG TSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLT VSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPG QPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSP QPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG NYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFG GGTKLTVLHHHHHH
15.	CD33 CC x I2C-scFc Bispecific HLE molecule	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMN WVKQAPGQCLEWMGWINTYTGEPTYADKFQGRVT MTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDG YYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSL AWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGT DFTLTIDSPQPEDSATYYCQQSAHFPITFGCGTRLEIKS GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK

				TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
16.	EGFRvIIIxCD3-scFc VH CDR1	artificial	aa	NYGMH
17.	EGFRvIIIxCD3-scFc VH CDR2	artificial	aa	VIWYDGSDKYYADSVRG
18.	EGFRvIIIxCD3-scFc VH CDR3	artificial	aa	DGYDILTGNPRDFDY
19.	EGFRvIIIxCD3-scFc VL CDR1	artificial	aa	RSSQSLVHSDGNTYLS
20.	EGFRvIIIxCD3-scFc VL CDR2	artificial	aa	RISRRFS
21.	EGFRvIIIxCD3-scFc VL CDR3	artificial	aa	MQSTHVPRT
22.	EGFRvIII_CCxCD3-scFc VH	artificial	aa	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMH WVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTI SRDNSKNTLYLQMNSLRAEDTAVYYCARDGYDILTG NPRDFDYWGQGTLVTVSS
23.	EGFRvIII_CCxCD3-scFc VL	artificial	aa	DTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTY LSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGT DFTLEISRVEAEDVGVYYCMQSTHVPRTFGCGTKVEI K
24.	EGFRvIII_CCxCD3-scFc scFv	artificial	aa	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMH WVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTI SRDNSKNTLYLQMNSLRAEDTAVYYCARDGYDILTG NPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSD TVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYL SWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTD FTLEISRVEAEDVGVYYCMQSTHVPRTFGCGTKVEIK
25.	EGFRvIII_CCxCD3-scFc Bispecific molecule	artificial	aa	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMH WVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTI SRDNSKNTLYLQMNSLRAEDTAVYYCARDGYDILTG NPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSD TVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYL SWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTD FTLEISRVEAEDVGVYYCMQSTHVPRTFGCGTKVEIK SGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR

				HGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVL
26.	EGFRvIII_CCxCD3-scFc Bispecific HLE molecule	artificial	aa	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMH WVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTI SRDNSKNTLYLQMNSLRAEDTAVYYCARDGYDILTG NPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSD TVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYL SWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTD FTLEISRVEAEDVGVYYCMQSTHVPRTFGCGTKVEIK SGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
27.	MSLN_5 VH CDR1	artificial	aa	DYYMT
28.	MSLN_5 VH CDR2	artificial	aa	YISSSGSTIYYADSVKG
29.	MSLN_5 VH CDR3	artificial	aa	DRNSHFDY
30.	MSLN_5 VL CDR1	artificial	aa	RASQGINTWLA
31.	MSLN_5 VL CDR2	artificial	aa	GASGLQS
32.	MSLN_5 VL CDR3	artificial	aa	QQAKSFPRT

33.	MSLN _5 VH	artificial	aa	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMT WIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISR DNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDY WGQGTLVTVSS
34.	MSLN_5 VL	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGINTWLA WYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQAKSFPRTFGQGTKVEI K
35.	MSLN_5 scFv	artificial	aa	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMT WIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISR DNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDY WGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQ SPSSVSASVGDRVTITCRASQGINTWLAWYQQKP GKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQAKSFPRTFGQGTKVEIK
36.	MSLN_5xI2C0 bispecific molecule	artificial	aa	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMT WIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISR DNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDY WGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQ SPSSVSASVGDRVTITCRASQGINTWLAWYQQKP GKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQAKSFPRTFGQGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVL
37.	MSLN_5xCD3-scFc Bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMT WIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISR DNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDY WGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQ SPSSVSASVGDRVTITCRASQGINTWLAWYQQKP GKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQAKSFPRTFGQGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW

				YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSG GGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
38.	MSLN_5_CCxC D3-scFc Bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMS WIRQAPGKCLEWFSYISSSGGIIYYADSVKGRFTISR DNAKNSLYLQMNSLRAEDTAVYYCARDVGSHFDY WGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQ SPSSVSASVGDRVTITCRASQDISRWLAWYQQKPG KAPKLLISAASRLQSGVPSRFSGSGSGTDFTLTISSLQ PEDFAIYYCQQAKSFPRTFGCGTKVEIKSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNW VRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGG GGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
39.	CDR-H1 CDH19 65254.007	artificial	aa	SYGMH

40.	CDR-H2 CDH19 65254.007	artificial	aa	FIWYEGSNKYYAESVKD
41.	CDR-H3 CDH19 65254.007	artificial	aa	RAGIIGTIGYYYGMDV
42.	CDR-L1 CDH19 65254.007	artificial	aa	SGDRLGEKYTS
43.	CDR-L2 CDH19 65254.007	artificial	aa	QDTKRPS
44.	CDR-L3 CDH19 65254.007	artificial	aa	QAWESSTVV
45.	VH CDH19 65254.007	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIG TIGYYYGMDVWGQGTTVTVSS
46.	VL CDH19 65254.007	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQ QRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATL TISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLS
47.	VH-VL CDH19 65254.007	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIG TIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGG GGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTS WYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGN TATLTISGTQAMDEADYYCQAWESSTVVFGGGTKL TVLS
48.	CDH19 65254.007 x I2C	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIG TIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGG GGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTS WYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGN TATLTISGTQAMDEADYYCQAWESSTVVFGGGTKL TVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASG FTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGG GSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTC GSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFL APGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVLHHHHHH
49.	CDH19 65254.007 x I2C -scFc	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY

	Bispecific HLE molecule			YYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSS YELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQR PGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISG TQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
50.	CDH19 65254.007 x I2C - scFc_delGK Bispecific HLE molecule	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY YYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSS YELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQR PGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISG TQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGGGGSGGGGSGGGGSGGGGSG

				GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
51.	CDH19 65254.007_CC x I2C -scFc VH	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY YYGMDVWGQGTTVTVSS
52.	CDH19 65254.007_CC x I2C -scFc VL	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQ RPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTIS GTQAMDEADYYCQAWESSTVVFGCGTKLTVL
53.	CDH19 65254.007_CC x I2C -scFc scFv	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY YYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSS YELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQR PGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISG TQAMDEADYYCQAWESSTVVFGCGTKLTVL
54.	CDH19 65254.007_CC x I2C -scFc Bispecific molecule	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY YYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSS YELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQR PGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISG TQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L
55.	CDH19 65254.007_CC x I2C -scFc Bispecific HLE molecule	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY YYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSS YELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQR PGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISG TQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN

				SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
56.	CDH19 65254.007_CC x I2C - scFc_delGK Bispecific HLE molecule	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMH WVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGY YYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSS YELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQR PGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISG TQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK

57.	FLT3_7 A8xCD3-scFc VH CDR1	artificial	aa	NARMGVS
58.	FLT3_7 A8xCD3-scFc VH CDR2	artificial	aa	HIFSNDEKSYSTSLKN
59.	FLT3_7 A8xCD3-scFc VH CDR3	artificial	aa	IVGYGSGWYGFFDY
60.	FLT3_7 A8xCD3-scFc VL CDR1	artificial	aa	RASQGIRNDLG
61.	FLT3_7 A8xCD3-scFc VL CDR2	artificial	aa	AASTLQS
62.	FLT3_7 A8xCD3-scFc VL CDR3	artificial	aa	LQHNSYPLT
63.	FLT3_7 A8xCD3-scFc VH	artificial	aa	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVS WIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDS SKTQVVLTMTNVDPVDTATYYCARIVGYGSGWYGFF DYWGQGTLVTVSS
64.	FLT3_ A8-scFc VL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWY QQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLT ISSLQPEDFATYYCLQHNSYPLTFGCGTKVEIK
65.	FLT3_7 A8xCD3- scFv	artificial	aa	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVS WIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDS SKTQVVLTMTNVDPVDTATYYCARIVGYGSGWYGFF DYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMT QSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
66.	FLT3_7 A8xCD3 Bispecific molecule	artificial	aa	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVS WIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDS SKTQVVLTMTNVDPVDTATYYCARIVGYGSGWYGFF DYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMT QSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

67.	FLT3_7 A8xCD3-scFc Bispecific HLE molecule	artificial	aa	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVS WIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDS SKTQVVLTMTNVDPVDTATYYCARIVGYGSGWYGFF DYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMT QSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
68	VH CDR1 DLL3_1_CC_del GK	artificial	aa	SYYWS
69	VH CDR2 DLL3_1_CC_del GK	artificial	aa	YVYYSGTTNYNPSLKS
70	VH CDR3 DLL3_1_CC_del GK	artificial	aa	IAVTGFYFDY
71	VL CDR1 DLL3_1_CC_del GK	artificial	aa	RASQRVNNNYLA
72	VL CDR2 DLL3_1_CC_del GK	artificial	aa	GASSRAT

73	VL CDR3 DLL3_1_CC_del GK	artificial	aa	QQYDRSPLT
74.	VH DLL3_1_CC_del GK	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWI RQPPGKCLEWIGYVYYSGTTNYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCASIAVTGFYFDYWGQG TLVTVSS
75.	VL DLL3_1_CC_del GK	artificial	aa	EIVLTQSPGTLSLSPGERVTLSCRASQRVNNNYLAWY QQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTL TISRLEPEDFAVYYCQQYDRSPLTFGCGTKLEIK
76.	DLL3_1_CC_del GK	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWI RQPPGKCLEWIGYVYYSGTTNYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCASIAVTGFYFDYWGQG TLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSP GERVTLSCRASQRVNNNYLAWYQQRPGQAPRLLIY GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQQYDRSPLTFGCGTKLEIK
77.	DLL3_1_CCxCD 3_delGK Bispecific molecule	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWI RQPPGKCLEWIGYVYYSGTTNYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCASIAVTGFYFDYWGQG TLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSP GERVTLSCRASQRVNNNYLAWYQQRPGQAPRLLIY GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQQYDRSPLTFGCGTKLEIKSGGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVL
78.	DLL3_1_CCxCD 3-scFc_delGK Bispecific HLE molecule	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWI RQPPGKCLEWIGYVYYSGTTNYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCASIAVTGFYFDYWGQG TLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSP GERVTLSCRASQRVNNNYLAWYQQRPGQAPRLLIY GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQQYDRSPLTFGCGTKLEIKSGGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV

				DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
79.	VH CDR1 CD19 97-G1RE-C2	artificial	aa	SYGMH
80.	VH CDR2 CD19 97-G1RE-C2	artificial	aa	VISYEGSNKYYAESVKG
81.	VH CDR3 CD19 97-G1RE-C2	artificial	aa	DRGTIFGNYGLEV
82.	VH CD19 97-G1RE-C2 CC	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMH WVRQAPGKCLEWVAVISYEGSNKYYAESVKGRFTIS RDNSKNTLYLQMNSLRDEDTAVYYCARDRGTIFGNY GLEVWGQGTTVTVSS
83.	VL CDR1 CD19 97-G1RE-C2	artificial	aa	RSSQSLLHKNAFNYLD
84.	VL CDR2 CD19 97-G1RE-C2	artificial	aa	LGSNRAS
85.	VL CDR3 CD19 97-G1RE-C2	artificial	aa	MQALQTPFT
86.	VL CD19 97-G1RE-C2 CC	artificial	aa	DIVMTQSPLSLPVISGEPASISCRSSQSLLHKNAFNYL DWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDI K
87.	CD19 97-G1RE-C2 CC x I2C0	artificial	aa	MDMRVPAQLLGLLLLWLRGARCDIVMTQSPLSLPVI SGEPASISCRSSQSLLHKNAFNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCMQALQTPFTFGCGTKVDIKGGGGSGGGGSGG GGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYG MHWVRQAPGKCLEWVAVISYEGSNKYYAESVKGRF TISRDNSKNTLYLQMNSLRDEDTAVYYCARDRGTIFG NYGLEVWGQGTTVTVSSGGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEW VARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL

				IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEA EYYCVLWYSNRWVFGGGTKLTVL
88.	CD19 97-G1RE-C2 CC x I2C0-scFc	artificial	aa	MDMRVPAQLLGLLLLWLRGARCDIVMTQSPLSLPVI SGEPASISCRSSQSLLHKNAFNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCMQALQTPFTFGCGTKVDIKGGGGSGGGGSGG GGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYG MHWVRQAPGKCLEWVAVISYEGSNKYYAESVKGRF TISRDNSKNTLYLQMNSLRDEDTAVYYCARDRGTIFG NYGLEVWGQGTTVTVSSGGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEW VARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEA EYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG KGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
89.	VH CDR1 CDH3 G8A 6-B12	artificial	aa	SYPIN
90.	VH CDR2 CDH3 G8A 6-B12	artificial	aa	VIWTGGGTNYASSVKG
91.	VH CDR3 CDH3 G8A 6-B12	artificial	aa	SRGVYDFDGRGAMDY
92.	VL CDR1 CDH3 G8A 6-B12	artificial	aa	KSSQSLLYSSNQKNYFA
93.	VL CDR2 CDH3 G8A 6-B12	artificial	aa	WASTRES
94.	VL CDR3 CDH3 G8A 6-B12	artificial	aa	QQYYSYPYT
95.	VH CDH3 G8A 6-B12	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWV RQAPGKGLEWVGVIWTGGGTNYASSVKGRFTISRD

				NSKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGR GAMDYWGQGTLVTVSS
96.	VL CDH3 G8A 6-B12	artificial	aa	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKN YFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGS GTDFTLTISSLQAEDVAVYYCQQYYSYPYTFGQGTKL EIK
97.	CDH3 G8A 6-B12 scFv	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWV RQAPGKGLEWVGVIWTGGGTNYASSVKGRFTISRD NSKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGR GAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNYF AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGT DFTLTISSLQAEDVAVYYCQQYYSYPYTFGQGTKLEIK
98.	CDH3 G8A 6-B12 x I2C0 bispecific molecule	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWV RQAPGKGLEWVGVIWTGGGTNYASSVKGRFTISRD NSKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGR GAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNYF AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGT DFTLTISSLQAEDVAVYYCQQYYSYPYTFGQGTKLEIK SGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVL
99.	CDH3 G8A 6-B12 x I2C0 bispecific molecule HLE	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWV RQAPGKGLEWVGVIWTGGGTNYASSVKGRFTISRD NSKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGR GAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNYF AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGT DFTLTISSLQAEDVAVYYCQQYYSYPYTFGQGTKLEIK SGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE

				EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
100.	BCMA A7 27-C4-G7 CDR1 VH	artificial	aa	NHIIH
101.	BCMA A7 27-C4-G7 CDR2 VH	artificial	aa	YINPYPGYHAYNEKFQG
102.	BCMA A7 27-C4-G7 CDR3 VH	artificial	aa	DGYYRDTDVLDY
103.	BCMA A7 27-C4-G7 CDR1 VL	artificial	aa	QASQDISNYLN
104.	BCMA A7 27-C4-G7 CDR2 VL	artificial	aa	YTSRLHT
105.	BCMA A7 27-C4-G7 CDR3 VL	artificial	aa	QQGNTLPWT
106.	BCMA A7 27-C4-G7 CC (44/100) VH	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHW VRQAPGQCLEWMGYINPYPGYHAYNEKFQGRATM TSDTSTSTVYMELSSLRSEDTAVYYCARDGYYRDTDV LDYWGQGTLVTVSS
107.	BCMA A7 27-C4-G7 CC (44/100) VL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWY QQKPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFT ISSLEPEDIATYYCQQGNTLPWTFGCGTKLEIK
108.	BCMA A7 27-C4-G7 CC (44/100) scFv	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHW VRQAPGQCLEWMGYINPYPGYHAYNEKFQGRATM TSDTSTSTVYMELSSLRSEDTAVYYCARDGYYRDTDV LDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMT QSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPG KAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPE DIATYYCQQGNTLPWTFGCGTKLEIK
109.	BCMA A7 27-C4-G7 CC (44/100) x I2C0 bispecific molecule	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHW VRQAPGQCLEWMGYINPYPGYHAYNEKFQGRATM TSDTSTSTVYMELSSLRSEDTAVYYCARDGYYRDTDV LDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMT QSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPG KAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPE DIATYYCQQGNTLPWTFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD

				SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
110.	BCMA A7 27-C4-G7 CC (44/100) x I2C0-scFc bispecific molecule HLE	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNHIIHW VRQAPGQCLEWMGYINPYPGYHAYNEKFQGRATM TSDTSTSTVYMELSSLRSEDTAVYYCARDGYYRDTDV LDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMT QSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPG KAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPE DIATYYCQQGNTLPWTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
111.	PM 76-B10.17 CC VH CDR1	artificial	aa	DYYMY
112.	PM 76-B10.17 CC VH CDR2	artificial	aa	IISDAGYYTYYSDIIKG
113.	PM 76-B10.17 CC VH CDR3	artificial	aa	GFPLLRHGAMDY
114.	PM 76-B10.17 CC VL CDR1	artificial	aa	KASQNVDANVA
145.	PM 76-B10.17 CC VL CDR2	artificial	aa	SASYVYW

116.	PM 76-B10.17 CC VL CDR3	artificial	aa	QQYDQQLIT
117.	PM 76-B10.17 CC VH	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSS
118.	PM 76-B10.17 CC VL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQNVDANVAW YQQKPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFT LTISSVQSEDFATYYCQQYDQQLITFGCGTKLEIK
119.	PM 76-B10.17 CC scFv	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIK
120.	PM 76-B10.17 CC x I2C0 bispecific molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
121.	PM 76-B10.17 CC x I2C0-scFc bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP

				EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
122.	PM 76-B10.17 CC x I2C0-scFc_delGK bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
123.	PM 76-B10.17 CC x I2C0 CC (103/43)-scFc	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ

	bispecific molecule			APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
124.	PM 76-B10.17 CC x I2C0 CC (103/43)-scFc bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
125.	PM 76-B10.17 CC x I2C0 CC (103/43)-scFc_delGK bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDAGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDANVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD

				SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
126.	PM 76-B10.11 CC VH CDR1	artificial	aa	DYYMY
127.	PM 76-B10.11 CC VH CDR2	artificial	aa	IISDGGYYTYYSDIIKG
128.	PM 76-B10.11 CC VH CDR3	artificial	aa	GFPLLRHGAMDY
129.	PM 76-B10.11 CC VL CDR1	artificial	aa	KASQNVDTNVA
130.	PM 76-B10.11 CC VL CDR2	artificial	aa	SASYVYW
131.	PM 76-B10.11 CC VL CDR3	artificial	aa	QQYDQQLIT
132.	PM 76-B10.11 CC VH	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSS
133.	PM 76-B10.11 CC VL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQNVDTNVAWY QQKPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTL TISSVQSEDFATYYCQQYDQQLITFGGGTKLEIK
134.	PM 76-B10.11 CC scFv	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS

				PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIK
135.	PM 76-B10.11 CC x I2C0 bispecific molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
136.	PM 76-B10.11 CC x I2C0-scFc bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK

137.	PM 76-B10.11 CC x I2C0-scFc_delGK bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
138.	PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
139.	PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS

	HLE molecule			PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
140.	PM 76-B10.11 CC x I2C0 CC (103/43)-scFc_delGK bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGGGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI

				SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
141.	PM 76-B10.11 CC x I2C0-scFc VH CDR1	artificial	aa	DYYMY
142.	PM 76-B10.11 CC x I2C0-scFc VH CDR2	artificial	aa	IISDGGYYTYYSDIIKG
143.	PM 76-B10.11 CC x I2C0-scFc VH CDR3	artificial	aa	GFPLLRHGAMDY
144.	PM 76-B10.11 CC x I2C0-scFc VL CDR1	artificial	aa	KASQNVDTNVA
145.	PM 76-B10.11 CC x I2C0-scFc VL CDR2	artificial	aa	SASYVYW
146.	PM 76-B10.11 CC x I2C0-scFc VL CDR3	artificial	aa	QQYDQQLIT
147.	PM 76-B10.11 CC x I2C0-scFc VH	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSS
148.	PM 76-B10.11 CC x I2C0-scFc VL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQNVDTNVAWY QQKPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTL TISSVQSEDFATYYCQQYDQQLITFGCGTKLEIK
149.	PM 76-B10.11 CC x I2C0-scFc scFv	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIK
150.	PM 76-B10.11 CC x I2C0-scFc bispecific molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL

				VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
151.	PM 76-B10.11 CC x I2C0-scFc bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
152.	PM 76-B10.11 CC x I2C0-scFc_delGK bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV

				TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
153.	PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
154.	PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE

				VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
155.	PM 76-B10.11 CC x I2C0 CC (103/43)-scFc_delGK bispecific HLE molecule	artificial	aa	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYCGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQCPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
156.	CD70_21D_CC VH CDR1	artificial	aa	TYAMS
157.	CD70_21D_CC VH CDR2	artificial	aa	AISGSGGRTFYAESVEG

158.	CD70_21D_CC VH CDR3	artificial	aa	HDYSNYPYFDY
1659.	CD70_21D_CC VL CDR1	artificial	aa	RASQSVRSTYLA
160.	CD70_21D_CC VL CDR2	artificial	aa	GASSRAT
161.	CD70_21D_CC VL CDR3	artificial	aa	QQYGDLPFT
162.	CD70_21D_CC VH	artificial	aa	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMS WVRQAPGKCLEWVSAISGSGGRTFYAESVEGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYF DYWGQGTLVTVSS
163.	CD70_21D_CC VL	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQ QK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL E PEDFAVYSCQQYGDLPFTFGCGTKLEIK
164.	CD70_21D_CCx 12C scFc	artificial	aa	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMS WVRQAPGKCLEWVSAISGSGGRTFYAESVEGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYF DYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQS PGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE DFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK

165	MSLN_5_CCxCD3-scFc Bispecific HLE molecule			MGWSCIILFLVATATGVHSQVQLVESGGGLVKPGGS LRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSS GSTIYYADSVKGRFTISRDNAKNSLFLQMNSLRAEDT AVYYCARDRNSHFDYWGQGTLVTVSSGGGGSGGG GSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGI NTWLAWYQQKPGKAPKLLIYGASGLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAKSFPRTFGQGT KVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR WVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGG SGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
166	Anti-PSMA xI2C0 with cys-clamp, scFc Bispecific molecule HLE PM76-B10.11			QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKCLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQS EDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT

				CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
167	Anti-PSMA IC20 bispecific molecule PM76-B10.17			QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCKASQNVDTNVAWYQQKPGQ APKSLIYSASYRYSDVPSRFSGSASGTDFTLTISSVQSE DFATYYCQQYDSYPYTFGGGTKLEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
168	Anti-Cldn 18.2 VH CDR1 **CL-1 and CL-2**	artificial	aa	GYYMH
169	Anti-Cldn18.2 VH CDR2	artificial	aa	WINPNSGGTKYAQKFQG
170	Anti-Cldn18.2 VH CDR3	artificial	aa	DRITVAGTYYYYGMDV
171	Anti-Cldn18.2 VL CDR1	artificial	aa	RASQGVNNWLA
172	Anti-Cldn18.2 VL CDR2	artificial	aa	TASSLQS
173	Anti-Cldn18.2 VL CDR3	artificial	aa	QQANSFPIT
174	Anti-Cldn18.2 VH anti- **CL-1**	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVR QAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRDT SISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMDV WGQGTTVTVSS
175	Anti-Cldn18.2 VL **CL-1**	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGVNNWLAWYQQ KPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQP EDFATYYCQQANSFPITFGCGTRLEIK
176	Anti-Cldn18.2 scFv	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVR QAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRDT

	CL-1			SISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMDV WGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSV SASVGDRVTITCRASQGVNNWLAWYQQKPGKAPKLLIYT ASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQA NSFPITFGCGTRLEIK
177	Anti-Cldn 18.2xCD3 bispecific molecule **CL-1 xI2C**	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVR QAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRDT SISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMDV WGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSV SASVGDRVTITCRASQGVNNWLAWYQQKPGKAPKLLIYT ASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQA NSFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
178	Anti-Cldn 18.2xCD3 Bispecific scFc molecule **CL-1 xI2C-scFc**	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVR QAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRDT SISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMDV WGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSV SASVGDRVTITCRASQGVNNWLAWYQQKPGKAPKLLIYT ASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQA NSFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGG SGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK
179	Anti-Cldn18.2 VH **CL-2**	artificial	aa	QVQMVQSGAEVKKHGASVKVSCKASGYTFTGYYMHWV RQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRD TSISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMD VWGQGTTVTVSS

180	Anti-Cldn18.2 VL **CL-2**	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGVNNWLAWYQQ KPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQP EDFATYYCQQANSFPITFGCGTRLEIK
181	Anti-Cldn18.2 scFv **CL-2**	artificial	aa	QVQMVQSGAEVKKHGASVKVSCKASGYTFTGYYMHWV RQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRD TSISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMD VWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSS VSASVGDRVTITCRASQGVNNWLAWYQQKPGKAPKLLIY TASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQ ANSFPITFGCGTRLEIK
182	Anti-Cldn18.2xCD3 bispecific molecule **CL-2xI2C**	artificial	aa	QVQMVQSGAEVKKHGASVKVSCKASGYTFTGYYMHWV RQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRD TSISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMD VWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSS VSASVGDRVTITCRASQGVNNWLAWYQQKPGKAPKLLIY TASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQ ANSFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
183	Anti-Cldn18.2xCD3 Bispecific scFc molecule **CL-2xI2C-scFc**	artificial	aa	QVQMVQSGAEVKKHGASVKVSCKASGYTFTGYYMHWV RQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTRD TSISTAYMELSRLRSDDTAVYYCARDRITVAGTYYYYGMD VWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSS VSASVGDRVTITCRASQGVNNWLAWYQQKPGKAPKLLIY TASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQ ANSFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGS GGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
184	Anti-MUC17	artificial	aa	GYYWS

	VH CDR1 **MU 8-B7**			
185	Anti-MUC17 VH CDR2 **MU 8-B7**	artificial	aa	DIDASGSTKYNPSLKS
186	Anti-MUC17 VH CDR3 **MU 8-B7**	artificial	aa	KKYSTVWSYFDN
187	Anti-MUC17 VL CDR1 **MU 8-B7**	artificial	aa	SGDKLGDKYAS
188	Anti-MUC17 VL CDR2 **MU 8-B7**	artificial	aa	QDRKRPS
189	Anti-MUC17 VL CDR3 **MU 8-B7**	artificial	aa	QAWGSSTAV
190	Anti-MUC17 VH **MU 8-B7**	artificial	aa	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPG KCLEWIGDIDASGSTKYNPSLKSRVTISLDTSKNQFSLKLNSVTAA DTAVYFCARKKYSTVWSYFDNWGQGTLVTVSS
191	Anti-MUC17 VL **MU 8-B7**	artificial	aa	SYELTQPSSVSVPPGQTASITCSGDKLGDKYASWYQQKPG QSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAM DEADYYCQAWGSSTAVFGCGTKLTVL
192	bispecific molecule **MU 8-B7 x I2C0scFc**	artificial	aa	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIR QPPGKCLEWIGDIDASGSTKYNPSLKSRVTISLDTSKNQFS LKLNSVTAADTAVYFCARKKYSTVWSYFDNWGQGTLVTV SSGGGGSGGGGSGGGGSSYELTQPSSVSVPPGQTASITCS GDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFS GSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCG TKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFT FNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGS GGGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG

				SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
193	CDR-L1 of I2C	artificial	aa	GSSTGAVTSGNYPN
194	CDR-L2 of I2C	artificial	aa	GTKFLAP
195	CDR-L3 of I2C	artificial	aa	VLWYSNRWV
196	CDR-H1 of I2C	artificial	aa	KYAMN
197	CDR-H2 of I2C	artificial	aa	RIRSKYNNYATYYADSVKD
198	CDR-H3 of I2C	artificial	aa	HGNFGNSYISYWAY
199	VH of I2C	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
200	VL of I2C	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
201	VH-VL of I2C	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL

[00117] The invention will be more fully understood by reference to the following examples. The examples should not, however, be construed as limiting the scope of the invention.

EXAMPLES

EXAMPLE 1. METHOD OF MEASURING PROTEIN BINDING TO SOLID SURFACES

[00118] Bispecific antibody constructs were internally sourced. They were labeled with a fluorophore and purified after the labeling procedure.

[00119] Each measurement chamber contains a plastic coverslip. To measure the protein binding to solid surfaces, the measurement chambers with plastic coverslips on the bottom were incubated with a solution containing a fluorophore-protein (e.g., a fluorophore labeled antibody construct) first. Then the sample solution was aspirated out, the from the coverslips were rinsed and filled with buffer for imaging on a confocal microscope later. Fluorescence intensity as measured by the confocal microscope shows the binding of the bispecific antibody constructs to the coverslips. **Figure 1** shows the diagram of the experimental set-up.

[00120] **Figure** 2 shows titrations of two fluorophore-labeled antibody constructs binding to the solid surfaces (e.g., coverslips), separately, in the absence of surfactant. The fluorescence intensities of bound fluorophore-labeled antibody constructs were measured by the confocal xy scans of the surface.

EXAMPLE 2. TREATMENT OF SOLID SURFACES WITH SURFACTANTS PREVENTING PROTEIN BINDING TO THE SURFACES

[00121] Several surfactants were used at different folds of their respective CMC to determine the effectiveness of each surfactant at preventing bispecific antibody construct binding to solid surface. In this study, a solution containing surfactants was incubated with the surface first, then the fluorophore labeled antibody constructs were added and incubated. After that, the solution was aspirated out, the surface was rinsed and filled with buffer for imaging on a confocal microscope. The results are shown in **Figure 3**. In the figure, the first group of bars are the bispecific antibody binding to the surface without any surfactants. These were served as benchmark and all the following groups of data were compared to those. From the 2nd to the last group are the relative percentages of protein bound to the surfaces pre-treated with different surfactants at different folds of their distinguish CMCs. The insert is a zoom-in for the lower region of the graph. PS 80, PS 20, P188, P407 and Triton X-100 were investigated.

[00122] The order of adding the surfactants and the antibodies to the surface was tested. For bispecific antibodies 1 & 2, two orders were tested: in the first one, a surfactant-containing solution was added to the surface before adding the antibodies to the surface; while the other one was vice versa. The results were shown in **Figure 4** (left is antibody 1 and right is antibody 2). For both graphs, the first group of bars are the bispecific antibody binding to the surface without any surfactants. These were served as benchmark and all the following groups of data were compared to those. From the 2nd to the last group are the relative percentages of the antibodies bound to the surfaces pre-treated with PS 80 at different folds of its CMC. The surfactants effectively prevented the proteins binding to the surfaces.

EXAMPLE 3. INCOMPATIBILITY OF CERTAIN SURFACTANTS AND THE PLASTICIZERS USED IN PLASTIC IV COMPONENTS

[00123] Baxter Viaflex PVC-DEHP IV bags pre-filled with saline diluent were used for the study. Surfactants polysorbate 80 (PS80), polysorbate 20 (PS20), poloxamer 188 (P188), poloxamer 407 (P407) and Triton X-100 were used in the study. Different amounts of different

surfactants were incubated with the bags at 25 °C for 24 hrs or 48 hrs. Then the bags were sampled and analyzed by reversed-phase ultra-high pressure liquid chromatography (RP-UHPLC) and detected by an UV detector. The mobile phase A & B are 0.1% trifluoroacetic acid (TFA) in DI-water and 0.1% TFA in acetonitrile. The gradient is listed in the Table 3 below. Flow rate is 0.6 ml/min. For quantification, a standard curve of DEHP was established under the same conditions.

Table 3. RP-UPLC gradient

Time (min)	Flow (mL/min)	%A	%B
0.0	0.6	95	5
1.5	0.6	5	95
3.1	0.6	5	95
3.2	0.6	95	5
4.0	0.6	95	5

[00124] PS 80, PS 20 and P188 were compared at 0.3 wt% in saline in PVC-DEHP IV bags for 24 hrs and 48 hrs at 25 °C. The results are shown in **Figure 5**. PS80 & PS20 caused significant leaching of DEHP from PVC-DEHP IV bags, while P188 didn't cause any leaching (Figure 5). Saline only was used as a control.

[00125] PS 80, PS 20, P188, P407 and Triton X-100 were compared at different folds of their respective CMC by incubating in saline in PVC-DEHP IV bags for 24 hrs at 25 °C. The amount of leached DEHP was plotted as a function of the folds of CMC in **Figure 6**. Clearly, polysorbates extract certain amounts of DEHP while poloxamers don't. And the amounts of DEHP leached are correlated with the amounts of surfactants used.

CLAIMS

What is claimed:

1. An aqueous composition comprising a bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 100 μg/ml and a surfactant at a concentration of at least about 0.25 x of the critical micelle concentration (CMC) of the surfactant, wherein the bispecific antibody construct comprises a first binding domain that binds to a target cell surface antigen, a second binding domain that binds to human CD3 on the surface of a T cell, and optionally, a third domain comprising, in an amino to carboxyl order, hinge-CH2 domain-CH3 domain-linker-hinge-CH2 domain-CH3 domain, wherein the second binding domain comprises a polypeptide having the sequence of SEQ ID NO: 201.

2. The composition of claim 1, wherein the bispecific antibody construct is present at a concentration of between about 0.001 μg/ml and about 50 μg/ml.

3. The composition of claim 1 or 2, wherein the bispecific antibody construct is present at a concentration of between about 0.01 μg/ml to about 50 μg/ml, or between 0.1 μg/ml to about 50 μg/ml, or 0.1 μg/ml to about 10 μg/ml, or 1 μg/ml to about 10 μg/ml.

4. The composition of any one of claims 1-3, wherein the surfactant is a polysorbate, a poloxamer or triton x-100.

5. The composition of any one of claims 1-4, wherein the surfactant is polysorbate 80, polysorbate 60, polysorbate 40, polysorbate 20, or Triton X-100.

6. The composition of any one of claims 1-4, wherein the surfactant is poloxamer 188 or poloxamer 407.

7. The composition of any one of claims 1-6, wherein the surfactant is present at a concentration of between about 0.25x and about 20x of the CMC, or between about 0.25x and about 10x of the CMC of the surfactant.

8. The composition of any one of claims 1-7, wherein the composition further comprising a salt, an amino acid, a saccharide or saccharide derivative, or combinations thereof.

9. The composition of claim 8, wherein the composition further comprises a buffer or a preservative.

10. The composition of claim 8 or 9, wherein the pH of the composition is between about 3.5 and about 7.5.

11. The composition of claim 10, wherein the pH of the composition is between about 4.2 and about 7.0.

12. The composition of any one of claims 8-11, wherein the salt is NaCl.

13. The composition of any one of claims 8-12, wherein the saccharide or saccharide derivative is a monosaccharide, a disaccharide, a cyclic polysaccharide or a sugar alcohol.

14. The composition of claim 8-13, wherein the saccharide is sucrose, trehalose, mannitol or sorbitol.

15. The composition of any one of claims 8-14, wherein the amino acid is lysine.

16. The composition of any one of claims 9-15, wherein the buffer is an acetate buffer, a glutamate buffer, a citrate buffer, a succinate buffer, a tartrate buffer, a fumarate buffer, a maleate buffer, a histidine buffer, or phosphate buffer.

17. The composition of any one of claims 1-16, wherein each of the first and second binding domains of the bispecific antibody construct comprises a VH region and a VL region.

18. The composition of any one of claims 1-17, wherein the bispecific antibody construct is a single chain antibody construct.

19. The composition of any one of claims 1-18, wherein the bispecific antibody construct comprises a polypeptide having the amino acid sequence selected from SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 176, SEQ ID NO: 178, and SEQ ID NO: 192.

20. The composition of any one of claims 1-19, wherein the composition is a pharmaceutical composition.

21. The composition of any one of claims 1-20, wherein the composition is contained in a plastic container.

22. The composition of claim 21, wherein the container is made of a material comprising polyolefin, PVC, EVA, or polyurethane.

23. The composition of claim 22, wherein the container is made of a material comprising PVC and wherein the PVC is substantially free of DEHP or TOTM.

24. The composition of any one of claims 21-23, wherein the container is an IV bag or IV tube.

25. A pharmaceutical preparation comprising an aqueous pharmaceutical composition contained inside a container, wherein the aqueous pharmaceutical composition comprising:

a) a bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 100 μg/ml, and
b) a surfactant at a concentration of at least about 0.25 x of CMC of the surfactant, wherein the surfactant has an HLB value of at least 20.

26. The pharmaceutical preparation of claim 25, wherein the aqueous pharmaceutical composition comprises the bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 50 μg/ml.

27. The pharmaceutical preparation of claim 25 or 26, wherein the aqueous pharmaceutical composition comprises the surfactant is at a concentration of between about 0.25x and about 20x of the CMC or between about 0.25x and about 10x of the CMC, of the surfactant.

28. The pharmaceutical preparation of any one of claims 25-27, wherein the aqueous pharmaceutical composition further comprising a salt, a buffer, an amino acid, a saccharide or saccharide derivative, or combinations thereof.

29. The pharmaceutical preparation of any one of claims 25-28, wherein the aqueous pharmaceutical composition has a pH of between about 4.2 and about 7.0.

30. The pharmaceutical preparation of any one of claims 25-29, wherein the container is made of a material comprising polyolefin, PVC, EVA or polyurethane.

31. The pharmaceutical preparation of any one of claims 25-30, wherein the bispecific antibody construct comprises a polypeptide having the amino acid sequences selected from SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 176, SEQ ID NO: 178, and SEQ ID NO: 192.

32. A method of administering a bispecific antibody construct to a patient comprising:

a) preparing an aqueous pharmaceutical composition in a container, wherein the aqueous pharmaceutical composition comprises the bispecific antibody construct at a concentration of between about 0.001 μg/ml and about 100 μg/ml and a surfactant at a concentration of at least about 0.25 x of CMC of the surfactant, and

b) administering the aqueous pharmaceutical composition to the patient.

wherein the bispecific antibody construct comprises a polypeptide having the amino acid sequence selected from SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 176, SEQ ID NO: 178, and SEQ ID NO: 192.

33. The method of claim 32, wherein the aqueous pharmaceutical composition comprises the bispecific antibody construct is at a concentration of between about 0.001 μg/ml and about 50 μg/ml.

34. The method of claim 32 or 33, wherein the aqueous pharmaceutical composition comprises the surfactant is at a concentration of between about 0.25x and about 20x of the CMC or between about 0.25x and about 10x of the CMC, of the surfactant.

35. The method of any one of claims 32-34, wherein the surfactant is polysorbate 80, polysorbate 60, polysorbate 40, polysorbate 20, poloxamer 188, poloxamer 407, or Triton X-100.

36. The method of any one of claims 32-35, wherein the aqueous pharmaceutical composition further comprising one or more selected from a salt, a buffer, an amino acid, a saccharide, and a preservative.

37. The method of any one of claims 32-36, wherein the aqueous pharmaceutical composition has a pH of between about 4.2 and about 7.0.

38. The method of any one of claims 32-37, wherein the container is made of a material comprising polyolefin, PVC, EVA, or polyurethane.

39. The method of any one of claims 32-38, wherein the surfactant is polysorbate 80, polysorbate 60, polysorbate 40, or polysorbate 20, and wherein the container is made of a material comprising PVC that is substantially free of DEHP or TOTM.

40. The method of any one of claims 32-39, wherein the aqueous pharmaceutical composition is prepared by diluting a first composition comprising the bispecific antibody construct with a suitable aqueous solution.

41. The method of claim 40, wherein the first composition is a liquid composition comprising the bispecific antibody construct.

42. The method of claim 40, wherein the first composition is a liquid composition reconstituted from a lyophilized composition comprising the bispecific antibody construct.

43. The method of any one of claims 41-42, wherein the suitable solution comprises the surfactant at a concentration of at least about 0.25 x of CMC of the surfactant.

44. The method of any one of claims 40-43, wherein the aqueous pharmaceutical composition is prepared by adding the suitable aqueous solution into the container followed by adding an appropriate amount of the first composition into the container.

45. The method of any one of claims 32-44, wherein the patient is a cancer patient.

46. The method of any one of claims 32-45, wherein the administration is IV administration.

47. The pharmaceutical preparation of any one of claims 25-31, wherein the surfactant is poloxamer 188 or poloxamer 407.

48. The composition of claim 19, the pharmaceutical preparation of claim 31 or the method of claim 32, wherein the bispecific antibody construct comprises a polypeptide having the amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 25, SEQ ID NO: 48, SEQ ID NO: 67, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 178 or SEQ ID NO: 192.

Figure 1

Diagram for the assay for measuring protein binding to a solid surface

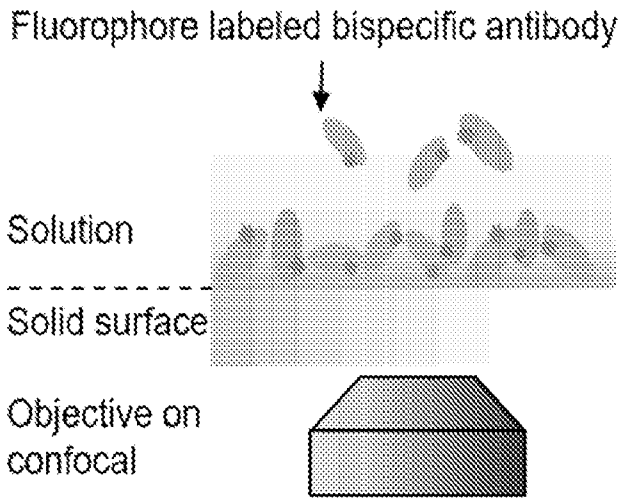


Figure 2

Proteins bind to solid surface in the absence of surfactant

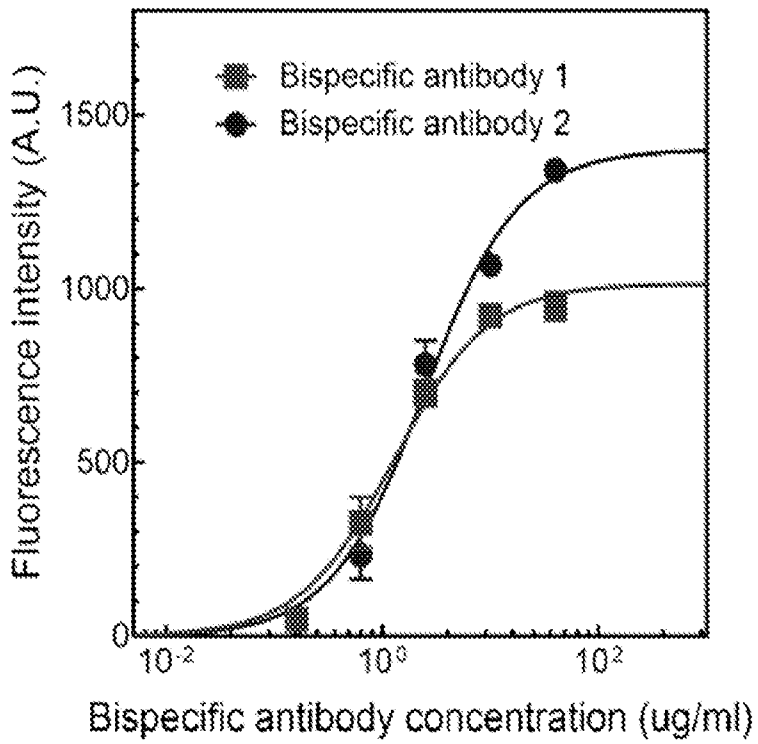


Figure 3

Screening of different surfactant

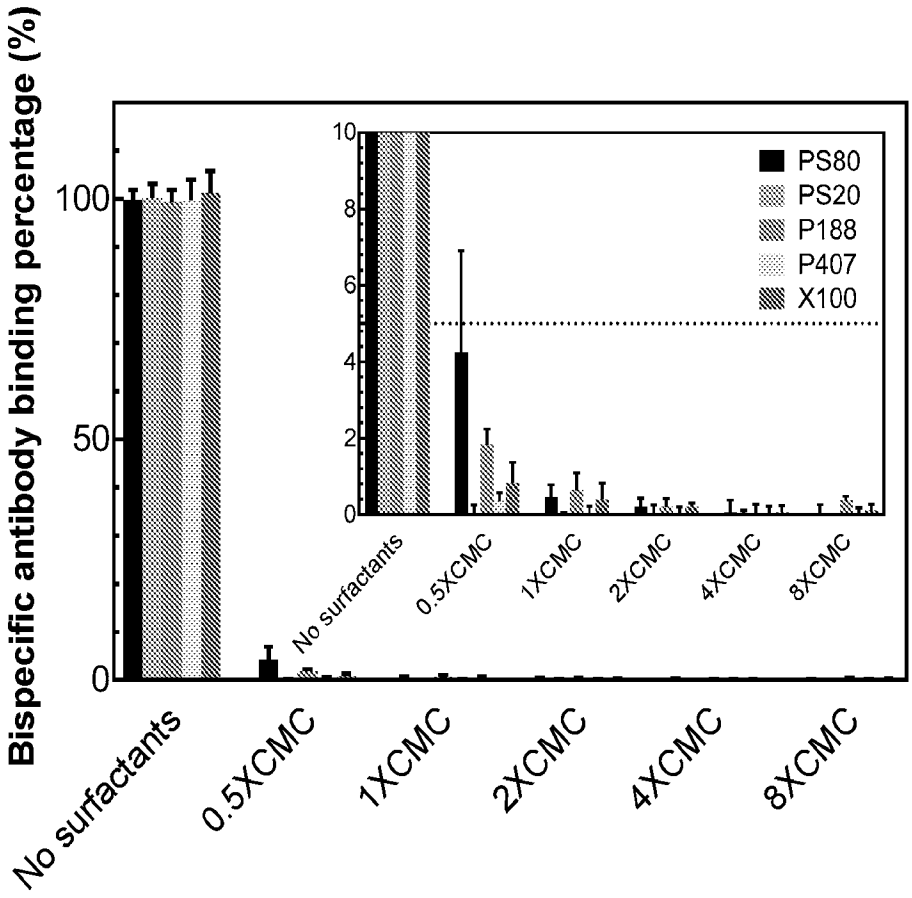


Figure 4

Adding surfactant to solid surface before adding protein prevents protein binding more efficiently

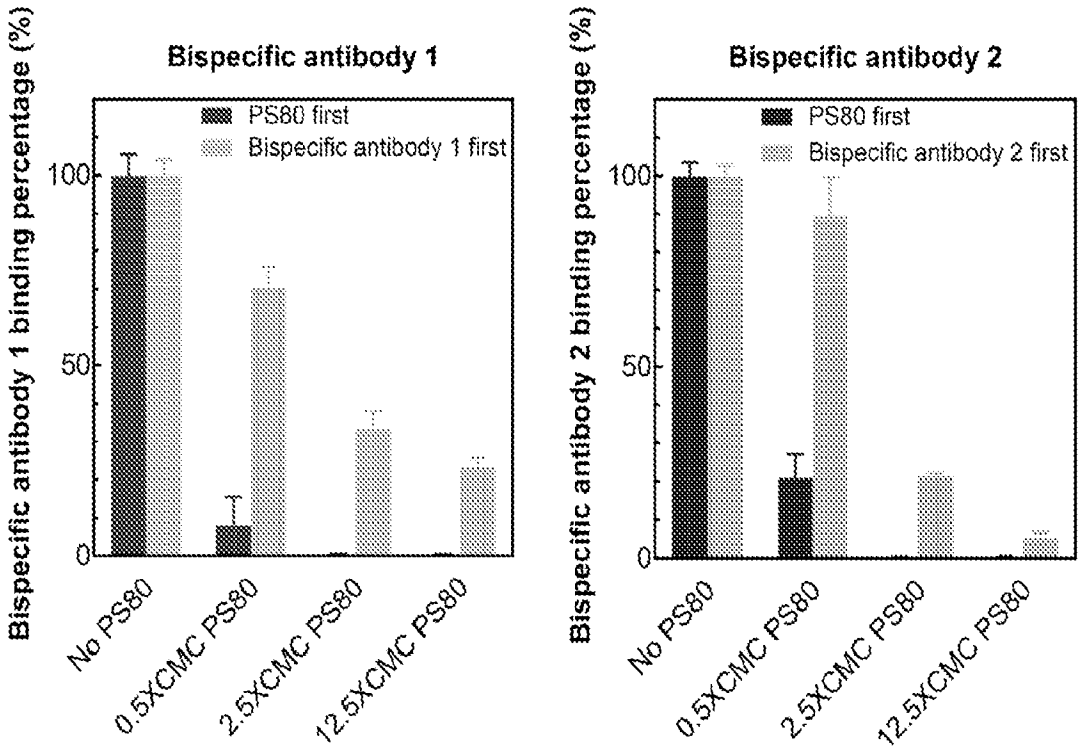


Figure 5

The impacts of different surfactants at the same concentration on leaching of DEHP

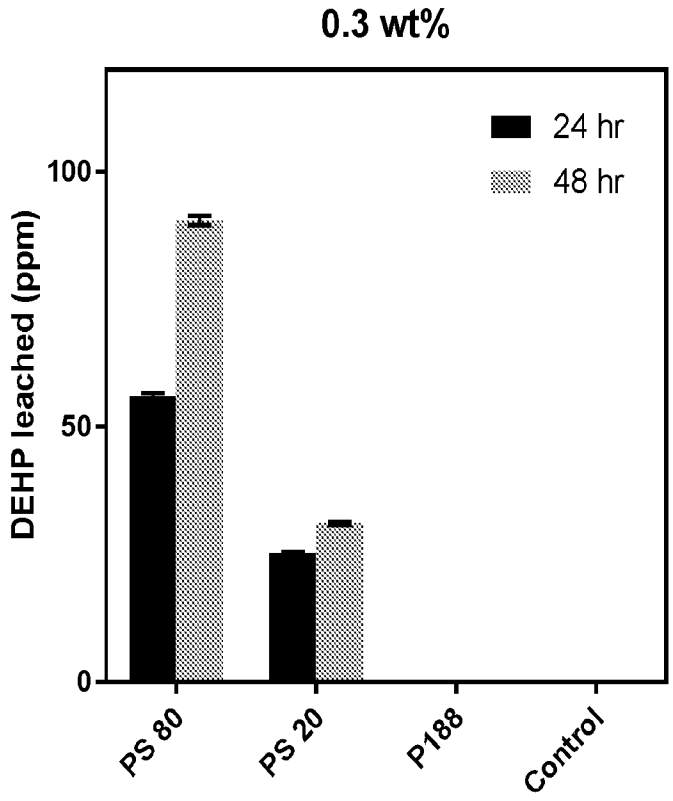
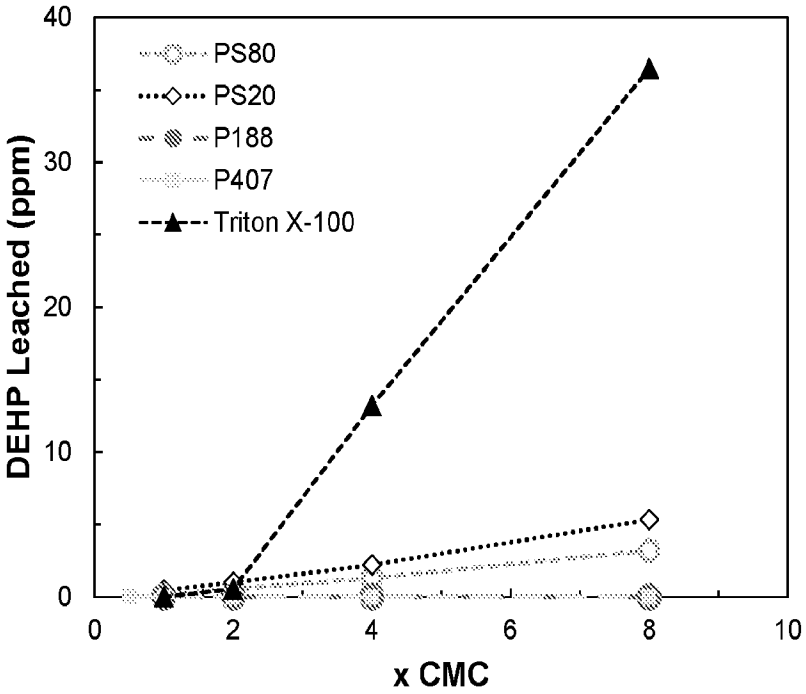


Figure 6

Compare the impacts of different surfactants at same folds of CMC on leaching of DEHP in 24 hrs



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<120> Compositions and Methods for Minimizing Protein Loss at Low Protein Concentrations

<130> A-2429-WO-PCT

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Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Lys Phe
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Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
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Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80


Ile Asp Ser Pro Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln
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            100                 105                 110

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Lys Ser Ser Gln Ser Val Leu Asp Ser Ser Thr Asn Lys Asn Ser Leu
                165                 170                 175

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

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

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

Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Ala His Phe Pro Ile Thr
225                 230                 235                 240

Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
                245                 250                 255

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

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

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

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

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
                325                 330                 335

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

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

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

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

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

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

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
        435                 440                 445

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

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

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

Gly Gly Gly Thr Lys Leu Thr Val Leu
            500                 505


<210>  14
<211>  530
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD33 E11 HL x I2C HL

<400>  14

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                   10                  15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Glu Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
```

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

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65                  70                  75                  80

Asp Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Ile Arg Asn Leu Gly Gly Asp Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Trp Ser Trp Ser Asp Gly Tyr Tyr Val Tyr Phe
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
145                 150                 155                 160

Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly Glu Arg Thr Thr
                165                 170                 175

Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Ser Ser Thr Asn Lys
            180                 185                 190

Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        195                 200                 205

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

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

Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Ala His Phe
                245                 250                 255

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly
            260                 265                 270

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
        275                 280                 285

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    290                 295                 300

Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
```

305 310 315 320

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
325 330 335

Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
340 345 350

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
355 360 365

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
370 375 380

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
385 390 395 400

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
405 410 415

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
420 425 430

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
435 440 445

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
450 455 460

Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser
465 470 475 480

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
485 490 495

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg
500 505 510

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu His His His His
515 520 525

His His
530

<210> 15
<211> 993
<212> PRT
<213> Artificial Sequence

<220>

<223> CD33 CC x I2C-scFc Bispecific HLE molecule

<400> 15

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


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


Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45


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


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


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


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


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


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


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


Lys Ser Ser Gln Ser Val Leu Asp Ser Ser Thr Asn Lys Asn Ser Leu
                165                 170                 175


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


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


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


Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Ala His Phe Pro Ile Thr
225                 230                 235                 240


Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
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                245                 250                 255

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

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

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

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

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
                325                 330                 335

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

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

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

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

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

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

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
        435                 440                 445

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

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

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

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr
            500                 505                 510
```

```
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
        515                 520                 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
    530                 535                 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545                 550                 555                 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
                565                 570                 575

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
            580                 585                 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
        595                 600                 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
    610                 615                 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625                 630                 635                 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
                645                 650                 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
            660                 665                 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
        675                 680                 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
    690                 695                 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705                 710                 715                 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                725                 730                 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            740                 745                 750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys
        755                 760                 765
```

```
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
    770                 775                 780

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
785                 790                 795                 800

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
                805                 810                 815

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
            820                 825                 830

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
        835                 840                 845

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
    850                 855                 860

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
865                 870                 875                 880

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                885                 890                 895

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
            900                 905                 910

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
        915                 920                 925

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
    930                 935                 940

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
945                 950                 955                 960

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                965                 970                 975

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            980                 985                 990

Lys
```

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIIIxCD3-scFc VH CDR1

<400> 16

Asn Tyr Gly Met His
1 5

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

<220>
<223> EGFRvIIIxCD3-scFc VH CDR2

<400> 17

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

Gly

<210> 18
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIIIxCD3-scFc VH CDR3

<400> 18

Asp Gly Tyr Asp Ile Leu Thr Gly Asn Pro Arg Asp Phe Asp Tyr
1 5 10 15

<210> 19
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIIIxCD3-scFc VL CDR1

<400> 19

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

<210> 20
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIIIxCD3-scFc VL CDR2

<400> 20

Arg Ile Ser Arg Arg Phe Ser
1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIIIxCD3-scFc VL CDR3

<400> 21

Met Gln Ser Thr His Val Pro Arg Thr
1 5

<210> 22
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII_CCxCD3-scFc VH

<400> 22

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
1 5 10 15

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

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

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

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

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

Ala Arg Asp Gly Tyr Asp Ile Leu Thr Gly Asn Pro Arg Asp Phe Asp
100 105 110

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

<210> 23
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII_CCxCD3-scFc VL

<400> 23

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45

Pro Arg Leu Leu Ile Tyr Arg Ile Ser Arg Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Glu Ile
65 70 75 80

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

Thr His Val Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 24
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII_CCxCD3-scFc scFv

<400> 24

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
1 5 10 15

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

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

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Gly Tyr Asp Ile Leu Thr Gly Asn Pro Arg Asp Phe Asp
100 105 110

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

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

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

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
165 170 175

Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro Pro Arg Leu Leu Ile
180 185 190

Tyr Arg Ile Ser Arg Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

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

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser Thr His Val Pro Arg
225 230 235 240

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 25
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII_CCxCD3-scFc Bispecific molecule

<400> 25

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
1 5 10 15

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

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

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

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

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

Ala Arg Asp Gly Tyr Asp Ile Leu Thr Gly Asn Pro Arg Asp Phe Asp
            100                 105                 110

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

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

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

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
                165                 170                 175

Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro Pro Arg Leu Leu Ile
            180                 185                 190

Tyr Arg Ile Ser Arg Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

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

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser Thr His Val Pro Arg
225                 230                 235                 240

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
                245                 250                 255

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

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

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

Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala
```

305 310 315 320

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

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

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

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

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

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

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

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

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

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 26
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII_CCxCD3-scFc Bispecific HLE molecule

<400> 26

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
1 5 10 15

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

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

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

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

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

Ala Arg Asp Gly Tyr Asp Ile Leu Thr Gly Asn Pro Arg Asp Phe Asp
            100                 105                 110

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

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

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

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
                165                 170                 175

Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro Pro Arg Leu Leu Ile
            180                 185                 190

Tyr Arg Ile Ser Arg Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
        195                 200                 205

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

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser Thr His Val Pro Arg
225                 230                 235                 240

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly
                245                 250                 255

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

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
```

275 280 285

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

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

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

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

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

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

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

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

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

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

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

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545                 550                 555                 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                565                 570                 575

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
            580                 585                 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        595                 600                 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    610                 615                 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625                 630                 635                 640

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
                645                 650                 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            660                 665                 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        675                 680                 685

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    690                 695                 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705                 710                 715                 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                725                 730                 735

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
        755                 760                 765

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
    770                 775                 780

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
785                 790                 795                 800
```

```
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
                805                 810                 815

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
            820                 825                 830

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
        835                 840                 845

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
    850                 855                 860

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
865                 870                 875                 880

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
                885                 890                 895

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
            900                 905                 910

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
        915                 920                 925

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
    930                 935                 940

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
945                 950                 955                 960

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                965                 970                 975

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
            980                 985                 990

Gly Lys
```

<210> 27
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5 VH CDR1

<400> 27

```
Asp Tyr Tyr Met Thr
1               5
```

<210> 28
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5 VH CDR2

<400> 28

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

Gly

<210> 29
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5 VH CDR3

<400> 29

Asp Arg Asn Ser His Phe Asp Tyr Asp Arg Asn Ser His Phe Asp Tyr
1 5 10 15

<210> 30
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5 VL CDR1

<400> 30

Arg Ala Ser Gln Gly Ile Asn Thr Trp Leu Ala
1 5 10

<210> 31
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5 VL CDR2

<400> 31

Gly Ala Ser Gly Leu Gln Ser
1 5

<210> 32
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> MSLN_5 VL CDR3

<400> 32

Gln Gln Ala Lys Ser Phe Pro Arg Thr
1 5

<210> 33
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN _5 VH

<400> 33

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

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

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

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

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

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

Ala Arg Asp Arg Asn Ser His Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 34
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5 VL

<400> 34

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

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


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


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


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


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


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


<210>  35
<211>  239
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN_5 scFv

<400>  35

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


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


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


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


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


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


Ala Arg Asp Arg Asn Ser His Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
```

```
         115                 120                 125

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

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

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

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

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

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

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


<210>  36
<211>  494
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN_5xI2C0 bispecific molecule

<400>  36

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

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

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

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

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

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

```
Ala Arg Asp Arg Asn Ser His Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
```

```
         355                 360                 365

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380

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

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

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

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

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

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

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                485                 490


<210>  37
<211>  982
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN_5xCD3-scFc Bispecific HLE molecule

<400>  37

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

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

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

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

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

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

Ala Arg Asp Arg Asn Ser His Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
```

340 345 350

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

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

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

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

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

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

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

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

Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
500 505 510

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
515 520 525

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
530 535 540

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
545 550 555 560

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser
565 570 575

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
580 585 590

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
595 600 605

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    610                 615                 620

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
625                 630                 635                 640

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                645                 650                 655

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            660                 665                 670

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        675                 680                 685

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    690                 695                 700

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
705                 710                 715                 720

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                725                 730                 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            740                 745                 750

Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        755                 760                 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    770                 775                 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785                 790                 795                 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                805                 810                 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
            820                 825                 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        835                 840                 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    850                 855                 860
```

```
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
865                 870                 875                 880


Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
                885                 890                 895


Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            900                 905                 910


Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        915                 920                 925


Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    930                 935                 940


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
945                 950                 955                 960


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                965                 970                 975


Ser Leu Ser Pro Gly Lys
            980


<210>  38
<211>  982
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN_5_CCxCD3-scFc Bispecific HLE molecule

<400>  38

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


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


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Phe
        35                  40                  45


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


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380

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

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

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

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

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

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

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

Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            500                 505                 510

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        515                 520                 525

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    530                 535                 540

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
545                 550                 555                 560

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser
                565                 570                 575

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            580                 585                 590

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        595                 600                 605
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    610                 615                 620

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
625                 630                 635                 640

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                645                 650                 655

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            660                 665                 670

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        675                 680                 685

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    690                 695                 700

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
705                 710                 715                 720

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                725                 730                 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            740                 745                 750

Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        755                 760                 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    770                 775                 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785                 790                 795                 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                805                 810                 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
            820                 825                 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        835                 840                 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    850                 855                 860

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
```

865 870 875 880

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
885 890 895

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
900 905 910

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
915 920 925

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
930 935 940

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
945 950 955 960

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
965 970 975

Ser Leu Ser Pro Gly Lys
980

<210> 39
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1 CDH19 65254.007

<400> 39

Ser Tyr Gly Met His
1 5

<210> 40
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2 CDH19 65254.007

<400> 40

Phe Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val Lys
1 5 10 15

Asp

<210> 41
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3 CDH19 65254.007

<400> 41

Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 42
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1 CDH19 65254.007

<400> 42

Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser
1 5 10

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2 CDH19 65254.007

<400> 43

Gln Asp Thr Lys Arg Pro Ser
1 5

<210> 44
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3 CDH19 65254.007

<400> 44

Gln Ala Trp Glu Ser Ser Thr Val Val
1 5

<210> 45
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDH19 65254.007

<400> 45

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

1 5 10 15

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

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

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

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

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

Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
100 105 110

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

<210> 46
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDH19 65254.007

<400> 46

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

Thr Ala Ser Ile Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr
20 25 30

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

Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val
85 90 95

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


<210>  47
<211>  247
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VH-VL  CDH19 65254.007

<400>  47

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


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


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


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


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


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


Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110


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


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140


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


Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175


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


Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205
```

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


Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Gly Gly
225                 230                 235                 240


Thr Lys Leu Thr Val Leu Ser
                245


<210>  48
<211>  507
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CDH19 65254.007 x I2C

<400>  48

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


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


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


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


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


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


Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110


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


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140


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


Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175
```

```
Gln Arg Pro Gly Gln Ser Pro Leu Leu Val Ile Tyr Gln Asp Thr Lys
            180                 185                 190

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205

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

Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Gly Gly
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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


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


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


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


Lys Leu Thr Val Leu His His His His His His
            500                 505


<210>  49
<211>  989
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CDH19 65254.007 x I2C -scFc Bispecific HLE molecule

<400>  49

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


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


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


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


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


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


Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110


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


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140
```

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

Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175

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

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205

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

Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Gly Gly
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
            500                 505                 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        515                 520                 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    530                 535                 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545                 550                 555                 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                565                 570                 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
            580                 585                 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        595                 600                 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    610                 615                 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625                 630                 635                 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                645                 650                 655
```

```
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            660                 665                 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        675                 680                 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    690                 695                 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705                 710                 715                 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
                725                 730                 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
        755                 760                 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    770                 775                 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785                 790                 795                 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                805                 810                 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            820                 825                 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
        835                 840                 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    850                 855                 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865                 870                 875                 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                885                 890                 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            900                 905                 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
```

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 50
<211> 987
<212> PRT
<213> Artificial Sequence

<220>
<223> CDH19 65254.007 x I2C -scFc_delGK Bispecific HLE molecule

<400> 50

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

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

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

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

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

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

Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
130 135 140

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


Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175


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


Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205


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


Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Gly Gly
225                 230                 235                 240


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


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


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


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


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


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


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


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


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


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


Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
```

405 410 415

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

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

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

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

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

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

```
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        675                 680                 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    690                 695                 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705                 710                 715                 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
                725                 730                 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            740                 745                 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
        755                 760                 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    770                 775                 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785                 790                 795                 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                805                 810                 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
            820                 825                 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
        835                 840                 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    850                 855                 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865                 870                 875                 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
                885                 890                 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            900                 905                 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        915                 920                 925
```

```
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    930                 935                 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945                 950                 955                 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                965                 970                 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985
```

<210> 51
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CDH19 65254.007_CC x I2C -scFc VH

<400> 51

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

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

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

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

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

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

Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110

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

<210> 52
<211> 106
<212> PRT
<213> Artificial Sequence

<220>

<223> CDH19 65254.007_CC x I2C -scFc VL

<400> 52

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


Thr Ala Ser Ile Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr
            20                  25                  30


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


Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val
                85                  90                  95


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

<210> 53
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> CDH19 65254.007_CC x I2C -scFc scFv

<400> 53

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


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


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


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


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


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

```
Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110


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


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140


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


Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175


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


Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205


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


Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Cys Gly
225                 230                 235                 240


Thr Lys Leu Thr Val Leu
                245


<210>  54
<211>  501
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CDH19 65254.007_CC x I2C -scFc Bispecific molecule

<400>  54

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


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


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


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

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

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

Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140

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

Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175

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

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205

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

Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Cys Gly
225                 230                 235                 240

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

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

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

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

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

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


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


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


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


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


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


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


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


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


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


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


Lys Leu Thr Val Leu
            500


<210>  55
<211>  989
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CDH19 65254.007_CC x I2C -scFc Bispecific HLE molecule

<400>  55

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


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

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

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

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

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

Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140

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

Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175

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

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205

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

Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Cys Gly
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
            500                 505                 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        515                 520                 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    530                 535                 540
```

```
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545                 550                 555                 560


Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                565                 570                 575


Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
            580                 585                 590


Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        595                 600                 605


Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    610                 615                 620


Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625                 630                 635                 640


Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                645                 650                 655


Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            660                 665                 670


Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        675                 680                 685


Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    690                 695                 700


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705                 710                 715                 720


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
                725                 730                 735


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
        755                 760                 765


Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    770                 775                 780


Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785                 790                 795                 800


Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
```

805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 56
<211> 987
<212> PRT
<213> Artificial Sequence

<220>
<223> CDH19 65254.007_CC x I2C -scFc_delGK Bispecific HLE molecule

<400> 56

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

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

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

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

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

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

Ala Arg Arg Ala Gly Ile Ile Gly Thr Ile Gly Tyr Tyr Tyr Gly Met
            100                 105                 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu
    130                 135                 140

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

Thr Cys Ser Gly Asp Arg Leu Gly Glu Lys Tyr Thr Ser Trp Tyr Gln
                165                 170                 175

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

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn
        195                 200                 205

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

Tyr Tyr Cys Gln Ala Trp Glu Ser Ser Thr Val Val Phe Gly Cys Gly
225                 230                 235                 240

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

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

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

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
```

```
    290                 295                 300

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

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

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
            500                 505                 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        515                 520                 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    530                 535                 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545                 550                 555                 560
```

```
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                565                 570                 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
            580                 585                 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        595                 600                 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    610                 615                 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625                 630                 635                 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                645                 650                 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            660                 665                 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        675                 680                 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    690                 695                 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705                 710                 715                 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
                725                 730                 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            740                 745                 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
        755                 760                 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    770                 775                 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785                 790                 795                 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                805                 810                 815
```

```
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
            820                 825                 830


Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
        835                 840                 845


Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    850                 855                 860


Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865                 870                 875                 880


Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
                885                 890                 895


Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            900                 905                 910


Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        915                 920                 925


Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    930                 935                 940


Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945                 950                 955                 960


Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                965                 970                 975


Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


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

<220>
<223>  FLT3_7 A8xCD3-scFc VH CDR1

<400>  57

Asn Ala Arg Met Gly Val Ser
1               5


<210>  58
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> FLT3_7 A8xCD3-scFc VH CDR2

<400> 58

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

His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Asn
20 25 30

<210> 59
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_7 A8xCD3-scFc VH CDR3

<400> 59

Ile Val Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp Tyr Ile Val
1 5 10 15

Gly Tyr Gly Ser Gly Trp Tyr Gly Phe Phe Asp Tyr
20 25

<210> 60
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_7 A8xCD3-scFc VL CDR1

<400> 60

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

<210> 61
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_7 A8xCD3-scFc VL CDR2

<400> 61

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 62
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_7 A8xCD3-scFc VL CDR3

<400> 62

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 63
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_7 A8xCD3-scFc VH

<400> 63

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

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

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

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

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

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

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

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

<210> 64
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_ A8-scFc VL

<400> 64

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

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

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

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

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

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

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


<210>  65
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  FLT3_7 A8xCD3- scFv

<400>  65

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

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

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

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
```

```
    130                 135                 140

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

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

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

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

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

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

Thr Lys Val Glu Ile Lys
                245
```

<210> 66
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> FLT3_7 A8xCD3 Bispecific molecule

<400> 66

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
```

```
         355                 360                 365

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu
            500


<210>  67
<211>  989
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  FLT3_7 A8xCD3-scFc Bispecific HLE molecule

<400>  67

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

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

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

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

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


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


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


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


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


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


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


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


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


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


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


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


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


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


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


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


Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
```

325 330 335

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

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

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

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

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

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

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

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

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

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

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

```
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        595                 600                 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    610                 615                 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625                 630                 635                 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                645                 650                 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            660                 665                 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        675                 680                 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    690                 695                 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705                 710                 715                 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
                725                 730                 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
        755                 760                 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    770                 775                 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785                 790                 795                 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                805                 810                 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            820                 825                 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
        835                 840                 845
```

```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    850                 855                 860


Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865                 870                 875                 880


Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                885                 890                 895


Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            900                 905                 910


Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        915                 920                 925


Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    930                 935                 940


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945                 950                 955                 960


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                965                 970                 975


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


<210>  68
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VH CDR1 DLL3_1_CC_delGK

<400>  68

Ser Tyr Tyr Trp Ser
1               5


<210>  69
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VH CDR2 DLL3_1_CC_delGK

<400>  69

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

<210> 70
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR3 DLL3_1_CC_delGK

<400> 70

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

<210> 71
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR1 DLL3_1_CC_delGK

<400> 71

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

<210> 72
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR2 DLL3_1_CC_delGK

<400> 72

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 73
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR3 DLL3_1_CC_delGK

<400> 73

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 74
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> VH DLL3_1_CC_delGK

<400> 74

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


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


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


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


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


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


Leu Val Thr Val Ser Ser
        115


<210>  75
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VL DLL3_1_CC_delGK

<400>  75

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


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


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


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


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


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Arg Ser Pro
                85                  90                  95
```

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


<210>  76
<211>  241
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DLL3_1_CC_delGK

<400>  76

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


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


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


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


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


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


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


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


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


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


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


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
```

195 200 205

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

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

Lys

<210> 77
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL3_1_CCxCD3_delGK Bispecific molecule

<400> 77

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
```

```
            420                 425                 430

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

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

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

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


<210>  78
<211>  982
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DLL3_1_CCxCD3-scFc_delGK  Bispecific HLE molecule

<400>  78

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

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

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

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

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


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


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


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


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


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


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


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


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


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


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


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


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


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


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


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


Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
```

405 410 415

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

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

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

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

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

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

```
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        675                 680                 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    690                 695                 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705                 710                 715                 720

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                725                 730                 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            740                 745                 750

Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        755                 760                 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    770                 775                 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785                 790                 795                 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                805                 810                 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
            820                 825                 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        835                 840                 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    850                 855                 860

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
865                 870                 875                 880

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
                885                 890                 895

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            900                 905                 910

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        915                 920                 925
```

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
930 935 940

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
945 950 955 960

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
965 970 975

Ser Leu Ser Pro Gly Lys
980

<210> 79
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR1 CD19 97-G1RE-C2

<400> 79

Ser Tyr Gly Met His
1 5

<210> 80
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR2 CD19 97-G1RE-C2

<400> 80

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

Gly

<210> 81
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR3 CD19 97-G1RE-C2

<400> 81

Asp Arg Gly Thr Ile Phe Gly Asn Tyr Gly Leu Glu Val
1 5 10

<210> 82
<211> 122

<212> PRT
<213> Artificial Sequence

<220>
<223> VH CD19 97-G1RE-C2 CC

<400> 82

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

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

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

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

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

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

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

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

<210> 83
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR1 CD19 97-G1RE-C2

<400> 83

Arg Ser Ser Gln Ser Leu Leu His Lys Asn Ala Phe Asn Tyr Leu Asp
1 5 10 15

<210> 84
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR2 CD19 97-G1RE-C2

<400> 84

Leu Gly Ser Asn Arg Ala Ser

1 5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR3 CD19 97-G1RE-C2

<400> 85

Met Gln Ala Leu Gln Thr Pro Phe Thr
1 5

<210> 86
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CD19 97-G1RE-C2 CC

<400> 86

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

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

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

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

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

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

<210> 87
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 97-G1RE-C2 CC x I2C0

<400> 87

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

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

Leu Pro Val Ile Ser Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
        35                  40                  45

Gln Ser Leu Leu His Lys Asn Ala Phe Asn Tyr Leu Asp Trp Tyr Leu
    50                  55                  60

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn
65                  70                  75                  80

Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
                85                  90                  95

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
            100                 105                 110

Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Cys Gly
        115                 120                 125

Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
145                 150                 155                 160

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                165                 170                 175

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
            180                 185                 190

Cys Leu Glu Trp Val Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr
        195                 200                 205

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

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Thr Ile Phe Gly Asn Tyr
                245                 250                 255

Gly Leu Glu Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
```

260 265 270

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
275 280 285

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
290 295 300

Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
305 310 315 320

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
325 330 335

Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
340 345 350

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
355 360 365

Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
370 375 380

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
385 390 395 400

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
405 410 415

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
420 425 430

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
435 440 445

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
450 455 460

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe
465 470 475 480

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
485 490 495

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
500 505 510

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
515 520 525

<210> 88
<211> 1013
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 97-G1RE-C2 CC x I2C0-scFc

<400> 88

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


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


Leu Pro Val Ile Ser Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
        35                  40                  45


Gln Ser Leu Leu His Lys Asn Ala Phe Asn Tyr Leu Asp Trp Tyr Leu
    50                  55                  60


Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn
65                  70                  75                  80


Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
                85                  90                  95


Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
            100                 105                 110


Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Cys Gly
        115                 120                 125


Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140


Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
145                 150                 155                 160


Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                165                 170                 175


Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
            180                 185                 190


Cys Leu Glu Trp Val Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr
        195                 200                 205


Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
```

```
    210                 215                 220

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Thr Ile Phe Gly Asn Tyr
                245                 250                 255

Gly Leu Glu Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
            260                 265                 270

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
        275                 280                 285

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
    290                 295                 300

Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
305                 310                 315                 320

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
                325                 330                 335

Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
            340                 345                 350

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
        355                 360                 365

Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
    370                 375                 380

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
385                 390                 395                 400

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                405                 410                 415

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
            420                 425                 430

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
        435                 440                 445

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
    450                 455                 460

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe
465                 470                 475                 480
```

```
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
                485                 490                 495

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
            500                 505                 510

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
        515                 520                 525

Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
    530                 535                 540

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
545                 550                 555                 560

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                565                 570                 575

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
            580                 585                 590

Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr
        595                 600                 605

Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
    610                 615                 620

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
625                 630                 635                 640

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                645                 650                 655

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
            660                 665                 670

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
        675                 680                 685

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    690                 695                 700

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
705                 710                 715                 720

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                725                 730                 735
```

```
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            740                 745                 750

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    770                 775                 780

Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
785                 790                 795                 800

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                805                 810                 815

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            820                 825                 830

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        835                 840                 845

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser
    850                 855                 860

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
865                 870                 875                 880

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                885                 890                 895

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            900                 905                 910

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        915                 920                 925

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    930                 935                 940

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
945                 950                 955                 960

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                965                 970                 975

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            980                 985                 990
```

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        995   1000   1005

Leu Ser Pro Gly Lys
    1010

<210> 89
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR1 CDH3 G8A 6-B12

<400> 89

Ser Tyr Pro Ile Asn
1   5

<210> 90
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR2 CDH3 G8A 6-B12

<400> 90

Val Ile Trp Thr Gly Gly Gly Thr Asn Tyr Ala Ser Ser Val Lys Gly
1   5   10   15

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR3 CDH3 G8A 6-B12

<400> 91

Ser Arg Gly Val Tyr Asp Phe Asp Gly Arg Gly Ala Met Asp Tyr
1   5   10   15

<210> 92
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR1 CDH3 G8A 6-B12

<400> 92

Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Phe
1   5   10   15

Ala

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

<220>
<223> VL CDR2 CDH3 G8A 6-B12

<400> 93

Trp Ala Ser Thr Arg Glu Ser
1 5

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

<220>
<223> VL CDR3 CDH3 G8A 6-B12

<400> 94

Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr
1 5

<210> 95
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDH3 G8A 6-B12

<400> 95

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

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

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

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

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

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

Lys Ser Arg Gly Val Tyr Asp Phe Asp Gly Arg Gly Ala Met Asp Tyr
100 105 110

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

<210> 96
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDH3 G8A 6-B12

<400> 96

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

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

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

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

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

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

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

Lys

<210> 97
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> CDH3 G8A 6-B12 scFv

<400> 97

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr

```
            20                  25                  30

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

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

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

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

Lys Ser Arg Gly Val Tyr Asp Phe Asp Gly Arg Gly Ala Met Asp Tyr
            100                 105                 110

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

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

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

Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
                165                 170                 175

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
                245                 250


<210>  98
<211>  506
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> CDH3 G8A 6-B12 x I2C0 bispecific molecule

<400> 98

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


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


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


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


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


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


Lys Ser Arg Gly Val Tyr Asp Phe Asp Gly Arg Gly Ala Met Asp Tyr
            100                 105                 110


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


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


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


Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
                165                 170                 175


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


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


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


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


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly
```

```
                245                 250                 255

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

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

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

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

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
                325                 330                 335

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

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

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

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

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

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
            420                 425                 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
        435                 440                 445

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

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

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
                485                 490                 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            500                 505
```

<210> 99
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> CDH3 G8A 6-B12 x I2C0 bispecific molecule HLE

<400> 99

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


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


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


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


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


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


Lys Ser Arg Gly Val Tyr Asp Phe Asp Gly Arg Gly Ala Met Asp Tyr
            100                 105                 110


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


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


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


Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
                165                 170                 175


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


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


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
```

210 215 220

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly
245 250 255

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

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

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

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

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
325 330 335

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

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

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

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

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

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
435 440 445

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

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

```
Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
                485                 490                 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys
            500                 505                 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
        515                 520                 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    530                 535                 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545                 550                 555                 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                565                 570                 575

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
            580                 585                 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        595                 600                 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    610                 615                 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625                 630                 635                 640

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
                645                 650                 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            660                 665                 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        675                 680                 685

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    690                 695                 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705                 710                 715                 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                725                 730                 735
```

```
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
        755                 760                 765

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
    770                 775                 780

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
785                 790                 795                 800

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
                805                 810                 815

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
            820                 825                 830

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
        835                 840                 845

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
    850                 855                 860

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
865                 870                 875                 880

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
                885                 890                 895

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
            900                 905                 910

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
        915                 920                 925

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
    930                 935                 940

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
945                 950                 955                 960

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                965                 970                 975

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
            980                 985                 990
```

Gly Lys

<210> 100
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CDR1 VH

<400> 100

Asn His Ile Ile His
1 5

<210> 101
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CDR2 VH

<400> 101

Tyr Ile Asn Pro Tyr Pro Gly Tyr His Ala Tyr Asn Glu Lys Phe Gln
1 5 10 15

Gly

<210> 102
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CDR3 VH

<400> 102

Asp Gly Tyr Tyr Arg Asp Thr Asp Val Leu Asp Tyr
1 5 10

<210> 103
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CDR1 VL

<400> 103

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

<210> 104

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

<220>
<223> BCMA A7 27-C4-G7 CDR2 VL

<400> 104

Tyr Thr Ser Arg Leu His Thr
1 5

<210> 105
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CDR3 VL

<400> 105

Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 106
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CC (44/100) VH

<400> 106

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

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

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

Gly Tyr Ile Asn Pro Tyr Pro Gly Tyr His Ala Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Asp Gly Tyr Tyr Arg Asp Thr Asp Val Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

<220>
<223> BCMA A7 27-C4-G7 CC (44/100) VL

<400> 107

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

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

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

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

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

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

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

<210> 108
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CC (44/100) scFv

<400> 108

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

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

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

Gly Tyr Ile Asn Pro Tyr Pro Gly Tyr His Ala Tyr Asn Glu Lys Phe

```
     50                  55                  60

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

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

Ala Arg Asp Gly Tyr Tyr Arg Asp Thr Asp Val Leu Asp Tyr Trp Gly
            100                 105                 110

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

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

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

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

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

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

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

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

Glu Ile Lys
```

<210> 109
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA A7 27-C4-G7 CC (44/100) x I2C0 bispecific molecule

<400> 109

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

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

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

Gly Tyr Ile Asn Pro Tyr Pro Gly Tyr His Ala Tyr Asn Glu Lys Phe
    50                  55                  60

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

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

Ala Arg Asp Gly Tyr Tyr Arg Asp Thr Asp Val Leu Asp Tyr Trp Gly
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
```

```
         275                 280                 285

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Leu
```

<210> 110
<211> 986
<212> PRT
<213> Artificial Sequence

<220>

<223> BCMA A7 27-C4-G7 CC (44/100) x I2C0-scFc bispecific molecule HLE

<400> 110

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


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


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


Gly Tyr Ile Asn Pro Tyr Pro Gly Tyr His Ala Tyr Asn Glu Lys Phe
    50                  55                  60


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


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


Ala Arg Asp Gly Tyr Tyr Arg Asp Thr Asp Val Leu Asp Tyr Trp Gly
            100                 105                 110


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


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


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


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


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


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


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


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


Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
```

245 250 255

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

```
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765
```

```
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


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

<220>
<223>  PM 76-B10.17 CC VH CDR1
```

<400> 111

Asp Tyr Tyr Met Tyr
1 5

<210> 112
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC VH CDR2

<400> 112

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

Gly

<210> 113
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC VH CDR3

<400> 113

Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr
1 5 10

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

<220>
<223> PM 76-B10.17 CC VL CDR1

<400> 114

Lys Ala Ser Gln Asn Val Asp Ala Asn Val Ala
1 5 10

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

<220>
<223> PM 76-B10.17 CC VL CDR2

<400> 115

Ser Ala Ser Tyr Val Tyr Trp
1 5

<210> 116
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC VL CDR3

<400> 116

Gln Gln Tyr Asp Gln Gln Leu Ile Thr
1 5

<210> 117
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC VH

<400> 117

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

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

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

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

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

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

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 118
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC VL

<400> 118

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

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

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

Tyr Ser Ala Ser Tyr Val Tyr Trp Asp Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 119
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC scFv

<400> 119

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

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

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

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

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

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

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly

```
            100                 105                 110

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

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

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

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

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

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

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

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys



<210>  120
<211>  498
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.17 CC x I2C0 bispecific molecule

<400>  120

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

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

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

Ala Ile Ile Ser Asp Ala Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60
```

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


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


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110


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


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


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


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


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


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


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


Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240


Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255


Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270


Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285


Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300


Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320


Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
```

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 121
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC x I2C0-scFc bispecific HLE molecule

<400> 121

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

```
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Ser Asp Ala Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Ala Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
```

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815
```

```
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


<210>  122
<211>  984
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.17 CC x I2C0-scFc_delGK bispecific HLE molecule

<400>  122

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45
```

```
Ala Ile Ile Ser Asp Ala Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Ala Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300
```

```
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560
```

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575


Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605


Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620


Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655


Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670


Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720


Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
                725                 730                 735


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750


Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        755                 760                 765


Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
```

```
            820                 825                 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys
            980


<210>  123
<211>  498
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.17 CC x I2C0 CC (103/43)-scFc bispecific molecule

<400>  123

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45
```

```
Ala Ile Ile Ser Asp Ala Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Ala Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
```

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 124
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.17 CC x I2C0 CC (103/43)-scFc bispecific HLE molecule

<400> 124

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Ser Asp Ala Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Ala Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
```

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

```
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800
```

```
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830


Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895


Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940


Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


<210>  125
<211>  984
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.17 CC x I2C0 CC (103/43)-scFc_delGK bispecific HLE
       molecule

<400>  125

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
```

20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Ala Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145 150 155 160

Ala Ser Gln Asn Val Asp Ala Asn Val Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
180 185 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

```
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540
```

```
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
                725                 730                 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        755                 760                 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800
```

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
            820                 825                 830


Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                885                 890                 895


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975


Ser Leu Ser Leu Ser Pro Gly Lys
            980


<210>  126
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC VH CDR1

<400>  126

Asp Tyr Tyr Met Tyr
1               5


<210>  127
<211>  17
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VH CDR2

<400> 127

Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile Lys
1 5 10 15

Gly

<210> 128
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VH CDR3

<400> 128

Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr
1 5 10

<210> 129
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VL CDR1

<400> 129

Lys Ala Ser Gln Asn Val Asp Thr Asn Val Ala
1 5 10

<210> 130
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VL CDR2

<400> 130

Ser Ala Ser Tyr Val Tyr Trp
1 5

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VL CDR3

<400> 131

Gln Gln Tyr Asp Gln Gln Leu Ile Thr
1 5

<210> 132
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VH

<400> 132

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 133
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC VL

<400> 133

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn
20 25 30

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Ser Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Tyr Val Tyr Trp Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Ala Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ser
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Gln Gln Leu Ile
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  134
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC scFv

<400>  134

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140
```

```
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160


Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190


Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240


Glu Ile Lys



<210>  135
<211>  498
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0 bispecific molecule

<400>  135

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
```

```
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365
```

```
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu
```

<210> 136
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc bispecific HLE molecule

<400> 136

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
```

```
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335
```

```
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590
```

```
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845
```

```
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895


Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940


Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


<210>  137
<211>  984
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0-scFc_delGK bispecific HLE molecule

<400>  137

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335
```

```
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
```

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

```
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys
            980


<210>  138
<211>  498
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific molecule

<400>  138

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350
```

```
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu
```

<210> 139
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific HLE molecule

<400> 139

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
```

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145 150 155 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
180 185 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

```
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575
```

```
Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830
```

```
Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895


Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940


Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985


<210>  140
<211>  984
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0 CC (103/43)-scFc_delGK bispecific HLE
       molecule

<400>  140

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320
```

```
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575
```

```
Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
                725                 730                 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        755                 760                 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
            820                 825                 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
```

```
         835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys
            980


<210>  141
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0-scFc VH CDR1

<400>  141

Asp Tyr Tyr Met Tyr
1               5


<210>  142
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0-scFc VH CDR2

<400>  142

Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile Lys
1               5                   10                  15
```

Gly

<210> 143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc VH CDR3

<400> 143

Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr
1 5 10

<210> 144
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc VL CDR1

<400> 144

Lys Ala Ser Gln Asn Val Asp Thr Asn Val Ala
1 5 10

<210> 145
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc VL CDR2

<400> 145

Ser Ala Ser Tyr Val Tyr Trp
1 5

<210> 146
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc VL CDR3

<400> 146

Gln Gln Tyr Asp Gln Gln Leu Ile Thr
1 5

<210> 147
<211> 121
<212> PRT

<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc VH

<400> 147

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 148
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc VL

<400> 148

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn
            20                  25                  30


Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Ser Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Tyr Val Tyr Trp Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Ala Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ser
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Gln Gln Leu Ile
85 90 95

Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 149
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc scFv

<400> 149

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145 150 155 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
165 170 175

```
Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190


Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240


Glu Ile Lys



<210>  150
<211>  498
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0-scFc bispecific molecule

<400>  150

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140
```

```
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400
```

```
Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415


Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430


Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445


Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460


Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480


Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495


Val Leu
```

<210> 151
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc bispecific HLE molecule

<400> 151

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110
```

```
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365
```

```
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620
```

```
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655


Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670


Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720


Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750


Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765


Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800


Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830


Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
```

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 152
<211> 984
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0-scFc_delGK bispecific HLE molecule

<400> 152

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

```
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
```

```
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640
```

```
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
                725                 730                 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        755                 760                 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
            820                 825                 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                885                 890                 895
```

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975


Ser Leu Ser Leu Ser Pro Gly Lys
            980


<210>  153
<211>  498
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific molecule

<400>  153

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380
```

```
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400


Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415


Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430


Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445


Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460


Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480


Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495


Val Leu
```

<210> 154
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0 CC (103/43)-scFc bispecific HLE molecule

<400> 154

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350
```

```
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605
```

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
```

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 155
<211> 984
<212> PRT
<213> Artificial Sequence

<220>
<223> PM 76-B10.11 CC x I2C0 CC (103/43)-scFc_delGK bispecific HLE molecule

<400> 155

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
            180                 185                 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350
```

```
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Cys Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Cys Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
```

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 156
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VH CDR1

<400> 156

Thr Tyr Ala Met Ser
1 5

<210> 157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VH CDR2

<400> 157

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu
1 5 10 15

Gly

<210> 158
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> CD70_21D_CC VH CDR3

<400> 158

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr
1 5 10

<210> 159
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VL CDR1

<400> 159

Arg Ala Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala
1 5 10

<210> 160
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VL CDR2

<400> 160

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 161
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VL CDR3

<400> 161

Gln Gln Tyr Gly Asp Leu Pro Phe Thr
1 5

<210> 162
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VH

<400> 162

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 163
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CC VL

<400> 163

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro
85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 164
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> CD70_21D_CCx12C scFc

<400> 164

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

```
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys
    210                 215                 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
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465                 470                 475                 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
                725                 730                 735
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985
```

<210> 165
<211> 1001
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_5_CCxCD3-scFc Bispecific HLE molecule

<400> 165

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asp Tyr Tyr Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Leu Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Ser Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Arg Asn Ser His Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
145 150 155 160

Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
165 170 175

Ser Gln Gly Ile Asn Thr Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
180 185 190

Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser Gly Leu Gln Ser Gly
195 200 205

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
210 215 220

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
225                 230                 235                 240

Gln Ala Lys Ser Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu
                245                 250                 255

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
            260                 265                 270

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
        275                 280                 285

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
    290                 295                 300

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
305                 310                 315                 320

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
                325                 330                 335

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
            340                 345                 350

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
        355                 360                 365

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
    370                 375                 380

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385                 390                 395                 400

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
                405                 410                 415

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
            420                 425                 430

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
        435                 440                 445

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
    450                 455                 460

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
465                 470                 475                 480
```

```
Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
                485                 490                 495

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
            500                 505                 510

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        515                 520                 525

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    530                 535                 540

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
545                 550                 555                 560

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                565                 570                 575

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
            580                 585                 590

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
        595                 600                 605

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    610                 615                 620

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
625                 630                 635                 640

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                645                 650                 655

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            660                 665                 670

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        675                 680                 685

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    690                 695                 700

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
705                 710                 715                 720

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                725                 730                 735
```

```
Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        755                 760                 765

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
    770                 775                 780

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
785                 790                 795                 800

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                805                 810                 815

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
            820                 825                 830

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
        835                 840                 845

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
    850                 855                 860

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
865                 870                 875                 880

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                885                 890                 895

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
            900                 905                 910

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        915                 920                 925

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    930                 935                 940

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
945                 950                 955                 960

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
                965                 970                 975

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            980                 985                 990

Lys Ser Leu Ser Leu Ser Pro Gly  Lys
```

995 1000

<210> 166
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-PSMA xI2C0 with cys-clamp, scFc Bispecific molecule HLE PM76-B10.11

<400> 166

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145 150 155 160

Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Val Tyr Trp
180 185 190

Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
195 200 205

```
Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Tyr Asp Gln Gln Leu Ile Thr Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385                 390                 395                 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
                405                 410                 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
            420                 425                 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
        435                 440                 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
    450                 455                 460
```

```
Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465                 470                 475                 480


Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
                485                 490                 495


Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            500                 505                 510


Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540


Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545                 550                 555                 560


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
                565                 570                 575


Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
            580                 585                 590


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605


Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620


Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625                 630                 635                 640


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655


Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670


Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    690                 695                 700


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720


Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
```

```
                725                 730                 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
        755                 760                 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
    770                 775                 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785                 790                 795                 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                805                 810                 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
            820                 825                 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
        835                 840                 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    850                 855                 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865                 870                 875                 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                885                 890                 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
            900                 905                 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
        915                 920                 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
    930                 935                 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945                 950                 955                 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
                965                 970                 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985
```

<210> 167
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-PSMA IC20 bispecific molecule PM76-B10.17

<400> 167

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ile Ile Ser Asp Gly Gly Tyr Tyr Thr Tyr Tyr Ser Asp Ile Ile
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Phe Pro Leu Leu Arg His Gly Ala Met Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145                 150                 155                 160


Ala Ser Gln Asn Val Asp Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Gln Ala Pro Lys Ser Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser
            180                 185                 190


Asp Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Val Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys
```

210 215 220

Gln Gln Tyr Asp Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 168
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn 18.2 VH CDR1 CL-1 and CL-2

<400> 168

Gly Tyr Tyr Met His
1 5

<210> 169
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 VH CDR2

<400> 169

Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 170
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 VH CDR3

<400> 170

Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 171
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 VL CDR1

<400> 171

```
Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala
1               5                   10


<210>  172
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-Cldn18.2 VL CDR2

<400>  172

Thr Ala Ser Ser Leu Gln Ser
1               5


<210>  173
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-Cldn18.2 VL CDR3

<400>  173

Gln Gln Ala Asn Ser Phe Pro Ile Thr
1               5


<210>  174
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-Cldn18.2 VH anti-CL-1

<400>  174

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 175
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 VL CL-1

<400> 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile
85 90 95

Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 176
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 scFv CL-1

<400> 176

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

```
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile Thr Phe Gly Cys
225                 230                 235                 240

Gly Thr Arg Leu Glu Ile Lys
                245
```

<210> 177
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn 18.2xCD3 bispecific molecule CL-1 xI2C

<400> 177

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile Thr Phe Gly Cys
225                 230                 235                 240

Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln
                245                 250                 255
```

```
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
            260                 265                 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
        275                 280                 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
    290                 295                 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
305                 310                 315                 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
                325                 330                 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
            340                 345                 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
        355                 360                 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385                 390                 395                 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
                405                 410                 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
            420                 425                 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
        435                 440                 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
    450                 455                 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465                 470                 475                 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
                485                 490                 495

Thr Lys Leu Thr Val Leu
            500
```

<210> 178
<211> 990
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn 18.2xCD3 Bispecific scFc molecule CL-1 xI2C-scFc

<400> 178

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
180 185 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

```
Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile Thr Phe Gly Cys
225                 230                 235                 240

Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln
                245                 250                 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
            260                 265                 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
        275                 280                 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
    290                 295                 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
305                 310                 315                 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
                325                 330                 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
            340                 345                 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
        355                 360                 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385                 390                 395                 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
                405                 410                 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
            420                 425                 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
        435                 440                 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
    450                 455                 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465                 470                 475                 480
```

```
Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
                485                 490                 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys
            500                 505                 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        515                 520                 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    530                 535                 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
545                 550                 555                 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                565                 570                 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
            580                 585                 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        595                 600                 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    610                 615                 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625                 630                 635                 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                645                 650                 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            660                 665                 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        675                 680                 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    690                 695                 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705                 710                 715                 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
                725                 730                 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
```

740 745 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
755 760 765

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
770 775 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
785 790 795 800

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
805 810 815

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
820 825 830

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val
835 840 845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
850 855 860

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
865 870 875 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
885 890 895

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
900 905 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
915 920 925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
930 935 940

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
945 950 955 960

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
965 970 975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985 990

<210> 179
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 VH CL-2

<400> 179

Gln Val Gln Met Val Gln Ser Gly Ala Glu Val Lys Lys His Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 180
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2 VL CL-2

<400> 180

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile
                85                  90                  95


Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210>  181
<211>  247
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-Cldn18.2 scFv CL-2

<400>  181

Gln Val Gln Met Val Gln Ser Gly Ala Glu Val Lys Lys His Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110


Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
    130                 135                 140


Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160


Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala Trp Tyr
                165                 170                 175
```

```
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
            180                 185                 190


Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205


Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220


Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile Thr Phe Gly Cys
225                 230                 235                 240


Gly Thr Arg Leu Glu Ile Lys
                245


<210>  182
<211>  502
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-Cldn18.2xCD3 bispecific molecule CL-2xI2C

<400>  182

Gln Val Gln Met Val Gln Ser Gly Ala Glu Val Lys Lys His Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110


Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
```

```
    130                 135                 140

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile Thr Phe Gly Cys
225                 230                 235                 240

Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln
                245                 250                 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
            260                 265                 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
        275                 280                 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
    290                 295                 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
305                 310                 315                 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
                325                 330                 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
            340                 345                 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
        355                 360                 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385                 390                 395                 400
```

```
Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
                405                 410                 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
            420                 425                 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
        435                 440                 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
    450                 455                 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465                 470                 475                 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
                485                 490                 495

Thr Lys Leu Thr Val Leu
            500
```

<210> 183
<211> 990
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Cldn18.2xCD3 Bispecific scFc molecule CL-2xI2C-scFc

<400> 183

```
Gln Val Gln Met Val Gln Ser Gly Ala Glu Val Lys Lys His Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Ile Thr Val Ala Gly Thr Tyr Tyr Tyr Tyr Gly Met
```

```
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Gly Val Asn Asn Trp Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Ile Thr Phe Gly Cys
225                 230                 235                 240

Gly Thr Arg Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln
                245                 250                 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
            260                 265                 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
        275                 280                 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
    290                 295                 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
305                 310                 315                 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
                325                 330                 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
            340                 345                 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
        355                 360                 365
```

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385                 390                 395                 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
                405                 410                 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
            420                 425                 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
        435                 440                 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
    450                 455                 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465                 470                 475                 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
                485                 490                 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys
            500                 505                 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        515                 520                 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    530                 535                 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
545                 550                 555                 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                565                 570                 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
            580                 585                 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        595                 600                 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    610                 615                 620
```

```
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625                 630                 635                 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                645                 650                 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            660                 665                 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        675                 680                 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    690                 695                 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705                 710                 715                 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
                725                 730                 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            740                 745                 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
        755                 760                 765

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
    770                 775                 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
785                 790                 795                 800

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
                805                 810                 815

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            820                 825                 830

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val
        835                 840                 845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    850                 855                 860

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
865                 870                 875                 880
```

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Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                885                 890                 895


Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            900                 905                 910


Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        915                 920                 925


Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    930                 935                 940


Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
945                 950                 955                 960


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                965                 970                 975


Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985                 990


<210>  184
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-MUC17 VH CDR1 MU 8-B7

<400>  184

Gly Tyr Tyr Trp Ser
1               5


<210>  185
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-MUC17 VH CDR2 MU 8-B7

<400>  185

Asp Ile Asp Ala Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu Lys Ser
1               5                   10                  15


<210>  186
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-MUC17 VH CDR3 MU 8-B7

<400>  186
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Lys Lys Tyr Ser Thr Val Trp Ser Tyr Phe Asp Asn
1 5 10

<210> 187
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-MUC17 VL CDR1 MU 8-B7

<400> 187

Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala Ser
1 5 10

<210> 188
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-MUC17 VL CDR2 MU 8-B7

<400> 188

Gln Asp Arg Lys Arg Pro Ser
1 5

<210> 189
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-MUC17 VL CDR3 MU 8-B7

<400> 189

Gln Ala Trp Gly Ser Ser Thr Ala Val
1 5

<210> 190
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-MUC17 VH MU 8-B7

<400> 190

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

```
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
        35                  40                  45


Gly Asp Ile Asp Ala Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu Lys
    50                  55                  60


Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80


Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
                85                  90                  95


Arg Lys Lys Tyr Ser Thr Val Trp Ser Tyr Phe Asp Asn Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  191
<211>  106
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Anti-MUC17 VL MU 8-B7

<400>  191

Ser Tyr Glu Leu Thr Gln Pro Ser Ser Val Ser Val Pro Pro Gly Gln
1               5                   10                  15


Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45


Gln Asp Arg Lys Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Gly Ser Ser Thr Ala Val
                85                  90                  95


Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  192
<211>  984
<212>  PRT
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<213> Artificial Sequence

<220>
<223> bispecific molecule MU 8-B7 x I2C0scFc

<400> 192

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Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30


Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
        35                  40                  45


Gly Asp Ile Asp Ala Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu Lys
    50                  55                  60


Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80


Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
                85                  90                  95


Arg Lys Lys Tyr Ser Thr Val Trp Ser Tyr Phe Asp Asn Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu Thr Gln Pro Ser Ser
    130                 135                 140


Val Ser Val Pro Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp
145                 150                 155                 160


Lys Leu Gly Asp Lys Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln
                165                 170                 175


Ser Pro Val Leu Val Ile Tyr Gln Asp Arg Lys Arg Pro Ser Gly Val
            180                 185                 190


Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr
        195                 200                 205


Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
    210                 215                 220


Trp Gly Ser Ser Thr Ala Val Phe Gly Cys Gly Thr Lys Leu Thr Val
225                 230                 235                 240
```

```
Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
                245                 250                 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
            260                 265                 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
        275                 280                 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
    290                 295                 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305                 310                 315                 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                325                 330                 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            340                 345                 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        355                 360                 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    370                 375                 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385                 390                 395                 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
                405                 410                 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
            420                 425                 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
        435                 440                 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
    450                 455                 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465                 470                 475                 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                485                 490                 495
```

```
Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            500                 505                 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        515                 520                 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    530                 535                 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545                 550                 555                 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
                565                 570                 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
            580                 585                 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        595                 600                 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    610                 615                 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625                 630                 635                 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                645                 650                 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            660                 665                 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        675                 680                 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    690                 695                 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705                 710                 715                 720

Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
                725                 730                 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750
```

```
Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        755                 760                 765


Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
            820                 825                 830


Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                885                 890                 895


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975


Ser Leu Ser Leu Ser Pro Gly Lys
            980


<210>  193
<211>  14
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> CDR-L1 of I2C

<400> 193

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 194
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2 of I2C

<400> 194

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3 of I2C

<400> 195

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 196
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1 of I2C

<400> 196

Lys Tyr Ala Met Asn
1 5

<210> 197
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2 of I2C

<400> 197

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 198
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3 of I2C

<400> 198

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 199
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of I2C

<400> 199

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 200
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of I2C

<400> 200

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
20 25 30

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 201
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-VL of I2C

<400> 201

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

```
Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
            100                 105                 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
    130                 135                 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
145                 150                 155                 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
                165                 170                 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
            180                 185                 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
        195                 200                 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
    210                 215                 220

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Leu Thr Val Leu
                245
```