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(54) Title: AFFINITY ENHANCEMENT AGENTS

(57) **Abstract:** This invention relates to a kit containing a multivalent, multi-specific binding protein and a carrier molecule. The binding protein has two or more binding sites where at least one binding site binds with a hapten moiety and at least one site binds with a target antigen. The carrier molecule contains a linking molecule that bears a diagnostic agent and/or a therapeutic agent and two or more haptens. The present invention further relates to bispecific diabodies that bind with hapten moieties and target antigens and to recombinant vectors useful for the expression of these functional diabodies in a microbial host.

AFFINITY ENHANCEMENT AGENTS

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

Part of the work performed during development of this invention utilized U.S. Government funds. The U.S. Government has certain rights in this invention. Part of the work described in this invention was supported by a DOE grant (DE-FG01-00NE22941) awarded to Dr. Robert Sharkey of the GSRC.

RELATED APPLICATION INFORMATION

This application claims the benefit of priority under 35 U.S.C. § 119 to U.S. Provisional patent applications No. 60/328,835 filed on Oct. 15, 2001 and No. 60/341,881 filed on Dec. 21, 2001, both entitled Affinity Enhancement Agents. The entire contents of these provisional patent applications are hereby incorporated by reference.

FIELD OF THE INVENTION

This invention relates to a kit containing a multivalent, multi-specific binding protein and a carrier molecule. The binding protein has two or more binding sites where at least one site binds with a hapten moiety and at least one site binds with a target antigen. The carrier molecule contains a linking molecule that bears a diagnostic agent and/or a therapeutic agent and two or more haptens. The present invention further relates to bispecific diabodies that bind with hapten moieties and target antigens and to recombinant vectors useful for the expression of these functional diabodies in a microbial host.

BACKGROUND OF THE INVENTION

Man-made binding proteins, in particular monoclonal antibodies and engineered antibodies or antibody fragments, have been tested widely and shown to be of value in detection and treatment of various human disorders, including cancers, autoimmune diseases, infectious diseases, inflammatory diseases, and cardiovascular diseases [Filpula and McGuire, *Exp. Opin. Ther. Patents* (1999) 9: 231-245]. For example, antibodies labeled with radioactive isotopes have been tested to visualize tumors after injection to a patient using detectors available in the art. The clinical utility of an antibody or an antibody-derived agent is primarily dependent on its ability to bind to a specific targeted antigen. Selectivity is essential for delivering a diagnostic or therapeutic agent, such as isotopes, drugs, enzymes, toxins, cytokines, hormones, growth factors, or conjugated derivatives thereof, to a target location during the detection and treatment phases of a human disorder, particularly if the diagnostic or therapeutic agent is toxic to normal tissue in the body.

The major limitations of antibody systems are discussed in Goldenberg, *The American Journal of Medicine* (1993) 94: 298-299. The essential parameters in the detection and treatment techniques are the amount of the injected dose specifically localized at the site(s) where target cells are present and the uptake ratio, *i.e.*, the ratio of the concentration of specifically bound antibody to that of the radioactivity present in surrounding normal tissues. When an antibody is injected into the blood stream, it passes through a number of compartments as it is metabolized and excreted. The antibody must be able to locate and bind to the target cell antigen while passing through the rest of the body. Factors that control antigen targeting include antigen location, antigen density, antigen accessibility, cellular composition of pathologic tissue, and the pharmokinetics of the targeting antibodies. Other factors that specifically affect tumor targeting by antibodies include expression of the target antigens, both in tumor and

other tissues, and bone marrow toxicity resulting from the slow blood-clearance of the radiolabeled antibodies.

The amount of targeting antibodies accreted by the targeted tumor cells is influenced by the vascularization and barriers to antibody penetration of tumors, as well as intratumoral pressure. Non-specific uptake by non-target organs such as the liver, kidneys or bone-marrow is another major limitation of the technique, especially for radioimmunotherapy, where irradiation of the bone marrow often causes the dose-limiting toxicity.

One suggested solution, referred to as the "Affinity Enhancement System" (AES), is a technique especially designed to overcome the deficiencies of tumor targeting by antibodies carrying diagnostic or therapeutic radioisotopes [U.S. 5,256,395 (1993), Barbet *et al.*, *Cancer Biotherapy & Radiopharmaceuticals* (1999) 14: 153-166]. The AES requires a radiolabeled bivalent hapten and an anti-tumor/anti-hapten bispecific antibody that recognizes both the target tumor and the radioactive hapten. The technique involves injecting the bispecific antibody into the patient and allowing the bispecific antibody to localize at the target tumor. After a sufficient amount of time for the unbound antibody to clear from the blood stream, the radiolabeled hapten is administered. The hapten binds to the antibody-antigen complex located at the site of the target cell to obtain diagnostic or therapeutic benefits. The unbound hapten clears the body. Barbet mentions the possibility that a bivalent hapten may crosslink with a bispecific antibody, when the latter is bound to the tumor surface. As a result, the radiolabeled complex is more stable and stays at the tumor for a longer period of time.

Bispecific antibodies prepared by chemically crosslinking two different Fab' fragments have been employed successfully, along with applicable bivalent haptens, to validate the utility of the AES for improved tumor targeting both in animal models and in human patients. However, there remains a need in the art for production of bispecific antibodies by recombinant DNA technology to assess whether such

engineered antibodies have merits for the AES. Specifically, there remains a need for an antibody-based agent that exhibits enhanced uptake at targeted antigens, fast clearance from the blood, and optimal protection of normal tissues and cells from toxic pharmaceuticals.

SUMMARY OF THE INVENTION

This invention relates to a kit containing a multivalent, multi-specific binding protein and a carrier molecule. The binding protein has two or more binding sites where at least one site binds with a hapten moiety and at least one site binds with a target antigen. The carrier molecule contains a linking molecule that bears a diagnostic agent and/or a therapeutic agent and two or more haptens. One embodiment of the present invention relates to bispecific diabodies that bind with hapten moieties and target antigens and to recombinant vectors useful for the expression of these functional diabodies in a microbial host.

A second embodiment is a bispecific diabody comprising a binding site that has an affinity towards molecules containing the histamine-succinyl-glycyl (HSG) moiety, and a binding site that has an affinity towards carcinoembryonic antigen (CEA). These diabodies are produced via recombinant DNA technology and create a novel AES that shows specific affinity for HSG and CEA.

A third embodiment of this invention relates to a method of delivering a diagnostic agent, a therapeutic agent, or a combination thereof to a target. The method includes administering the binding protein to a subject in need of the agent, waiting a sufficient amount of time for an amount of the non-binding protein to clear the subject's blood stream, and administering the carrier molecule which includes the diagnostic or therapeutic agent. A further embodiment of the present invention is a method of detecting and treating a human disorder with the method of delivering the agent to a target.

It is an object of the present invention to produce a binding protein that is capable of binding with hapten moieties and antigens. It is yet a further object of this invention to produce vectors that contain sequences of DNA encoding for multi-specific antibodies and that are readily expressed in microbial host cells. Moreover, this invention includes a method of producing a diabody by recombinant DNA technology. The method includes culturing the host cell in a suitable media and isolating the diabody. Further, the invention relates to DNA sequences encoding the various diabodies as specified in Figures 25-38 (Seq IDs).

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a schematic representation of the 679 single chain Fv (scFv) polypeptide that is synthesized in *E. coli* from the 679-scFv-L5 expression plasmid and forms a 679 diabody. The gene construct for the un-processed polypeptide contains the pelB signal peptide, 679V_H and V_K coding sequences coupled by a 5 amino acid linker, Gly-Gly-Gly-Gly-Ser (G₄S), and the carboxyl terminal six histidine (His) affinity tag. The figure also shows a stick figure drawing of the mature polypeptide after proteolytic removal of the pelB leader peptide and a stick figure drawing of a 679 diabody, including the HSG binding sites.

Figure 2 shows a SDS-PAGE gel stained with Coomassie blue that is used to analyze the expression of 679 scFv from 679scFv-L5-transformed *E. coli* BL21 p-LysS cultures: lanes 1- 5, induced with isopropyl- β -D-galactopyranoside (IPTG) overnight at 20°C; lanes 6 and 7, not induced. In lane 3, the culture media was concentrated 10-fold. Soluble (lanes 4 and 6) and insoluble (lanes 5 and 7) proteins were fractionated by centrifugation of cell lysates (lane 2). 679scFv was purified from the insoluble fraction by Immobilized Metal Affinity Chromatography (IMAC) following solubilization in 8M urea (lane 1).

Figure 3 shows a schematic representation of the hMN14scFv polypeptide that is synthesized in *E. coli* from the hMN14-scFv-L5 expression plasmid and forms a hMN14 diabody. The gene construct for the un-processed polypeptide contains the pelB signal peptide, hMN14V_H and V_K coding sequences coupled by a 5 amino acid linker, and the carboxyl terminal 6 histidine affinity tag. The figure also shows a stick figure drawing of the mature polypeptide following proteolytic removal of the pelB leader peptide, and a stick figure drawing of a hMN14 diabody, including CEA binding sites.

Figure 4 shows size-exclusion High Performance Liquid Chromatography (HPLC) analysis of purified hMN14 diabody. Figure A is the HPLC elution profile of IMAC-purified hMN14 diabody. The HPLC elution peaks of hMN14 diabody in figures A and B are identified with an arrow. Figure B is the HPLC elution profile of hMN14 diabody purified by WI2 anti-idiotype affinity chromatography. The *9.75 indicated on the x-axis of figure B is the HPLC retention time (9.75 min.) of control hMN14-Fab'-S-NEM (MW ~ 50 KDa).

Figure 5 shows reducing SDS-PAGE gel stained with Coomassie blue (figure A). The gel illustrates the purity of the hMN14 diabody samples following IMAC purification and WI2 anti-idiotype affinity chromatography. The positions of the M_r standards and the hMN14scFv polypeptide are indicated with arrows. Lane 1 of figure A contains IMAC-purified hMN14 diabody. Lane 2 of the same figure contains affinity purified hMN14 diabody. Figure B is an isoelectric focusing (IEF) gel. The positions of pI standards and hMN14 diabody are indicated with arrows. Lane 1 of Figure B contains the hMN14 Fab'-S-NEM used as a standard. Lane 2 of the same figure contains the

WI2 purified hMN14 diabody. Lane 3 contains the unbound flow through fraction from the WI2 affinity column and shows the proteins that are removed by this process.

Figure 6 shows the levels of ^{131}I -hMN14 diabody observed in a tumor and the blood over the first 96 hours after injection of the diabody. The concentration of ^{131}I -hMN14 diabody, measured as the percentage of the injected dose per gram of tissue (%ID/g), is plotted vs. time. Solid squares mark the data points for tumor samples and open boxes mark those of blood samples.

Figure 7 shows the biodistribution of ^{131}I -hMN14 diabody 48 hours after injection in tumors and normal tissues, including liver, spleen, kidney, lungs, blood, stomach, small intestine, and large intestine. The concentration of ^{131}I -hMN14 diabody is displayed as the percentage of the injected dose per gram of tissue (%ID/g).

Figure 8 shows a schematic representation of the creation of the pET-ER vector. Figure A illustrates the double stranded DNA sequence of MCS2. Restriction sites are indicated above the sequence. MCS2 was ligated into the BpI restriction site of pET26b vector shown in Figure B. Figure C shows the diagram of pET-ER vector, including the MCS2 sequence.

Figure 9 shows a schematic representation of the steps involved in the generation of constructs used for expression of three 679xhMN14 bispecific diabody variants represented by BS1, BS1.5 and BS2.

Figure 10 shows a schematic representation of the di-cistronic expression cassette in the pET-ER vector and also stick figures of the two heterologous polypeptides as synthesized and the formation of 679 x hMN14 bispecific diabodies. The di-cistronic

cassette codes for a single RNA message generated from T7 RNA polymerase via the T7 promoter. This message contains two ribosomal binding sites (RBS) and the coding sequences for the two heterologous polypeptides. Stick figure drawings show the two mature heterologous polypeptides, 679V_H(G₄S)hMN14V_K (Left) and hMN14V_H(G₄S)679V_K (Right) that are synthesized from the di-cistronic expression cassettes. The 679 x hMN14 bispecific diabody (BS1, BS1.5 or BS2) is represented as a stick figure drawing and is formed from the pairing of the heterologous polypeptides.

Figure 11 shows a size-exclusion HPLC analysis of BS1.5 after purification. The HPLC elution peak of BS1.5 is at 9.22 min. Soluble proteins from an induced 5L culture were purified by Ni-NTA IMAC followed by Q-Sepharose anion exchange chromatography. The flow through fraction of the Q-Sepharose column was injected for HPLC analysis.

Figure 12 shows a reducing SDS-PAGE gel stained with Coomassie blue and used to analyze the purification of BS2. Arrows indicate the positions of the M_r standards and the BS2 polypeptide constituents, 679V_H-hMN14V_K and hMN14V_H-679V_K. Soluble proteins from an induced 5L culture were loaded on a 4 ml Ni-NTA column. The column was washed/eluted with a buffer containing 40mM imidazole (lane 3) and then eluted in two fractions with 100mM imidazole (lanes 1 and 2). Impurities in the 40mM imidazole eluate were removed by passing the eluate over a Q-Sepharose anion exchange column (lane 4).

Figure 13 shows the purity of BS1, BS2 and BS1.5 through an IEF gel. These three diabodies were purified from soluble protein extracts by Ni-NTA IMAC followed by Q-Sepharose anion exchange chromatography. The positions of pI markers are indicated by arrows and the samples are identified above the lanes.

Figure 14 shows BIACore binding curves obtained for various concentrations of BS1.5 using a low-density HSG-coupled sensor chip. These data were used for calculation of the on-rates and off-rates.

Figure 15 is a graphical representation of the results of a competitive enzyme-linked immunosorbent assay (ELISA). HRP-conjugated hMN14 IgG (1 nM) was mixed with either BS1.5 or chemically linked 679 x hMN14 F (ab')₂ at concentrations ranging from 4 – 500 nM, prior to incubation in CEA-coated (0.5 µg/well) wells. The % inhibition is plotted vs. nM concentration of sample.

Figure 16 is a BIACore sensorgram showing bispecific binding properties of BS1.5 for HSG and WI2. BS1.5 (60ng) was loaded on a high-density HSG-coupled sensor chip and two 400ng injections of the hMN14-binding anti-idiotype MAb, WI2, were allowed to bind to the immobilized BS1.5. Arrows indicate injection times.

Figure 17 shows the levels of ¹³¹I-BS1.5 diabody in the tumor and the blood over the first 96 hours after injection of the diabody. The concentration of ¹³¹I-BS1.5 diabody, measured as the percentage of the injected dose per gram of tissue (%ID/g), is plotted vs. time. Diamonds mark the data points for tumor samples and filled circles mark those of blood samples.

Figure 18 shows the biodistribution of ¹³¹I-BS1.5 diabody after 12 and 24 hours post injection in tumor and normal tissue, including liver, spleen, kidney, lungs, blood, stomach, small intestine, and large intestine. The concentration of ¹³¹I-BS1.5 was measured as the percentage of the injected dose per gram of tissue (%ID/g).

Figure 19 shows the biodistribution of ^{111}In -IMP241 peptide in tumor bearing mice pretargeted with BS1.5. GW39 tumor-bearing nude mice were injected with BS1.5 diabody. After 12 hours of clearance, the ^{111}In -labeled IMP241 peptide was injected. Radioactivity in the tumor and in normal tissues, including liver, spleen, kidney, lungs, blood, stomach, small intestine, and large intestine, was measured at 3 and 24 hours post injection of ^{111}In -IMP241. The concentration of ^{111}In -IMP241 was measured as the percentage of the injected dose per gram of tissue (%ID/g).

Figure 20 shows an alignment of murine (m) and humanized (h) 679 V_H and V_K amino acid sequences using the Kabat numbering scheme. Amino acid substitutions made during humanization are indicated with arrowheads. The CDR and framework regions are indicated.

Figure 21 shows the relative locations of the PCR primers used for humanization of 679scFv-L5. Arrows signify the primers. The intermediate PCR products are also shown (A,B,C and D). All numbering represent nucleic acid positions in 679scFv-L5.

Figure 22 shows size-exclusion HPLC analysis of the BS1.5H after purification. The HPLC elution peak of BS1.5H is at 10.16 min. Soluble proteins from an induced 5L culture were purified by Ni-NTA IMAC followed by Q-Sepharose anion exchange chromatography. The flow through fraction of the Q-Sepharose column was injected for HPLC analysis.

Figure 23 is a BIACore sensorgram showing bispecific binding properties of BS1.5H for HSG and WI2. BS1.5H (60ng) was loaded on a high-density HSG-coupled sensor chip and a 1 μg injection of the hMN14-binding anti-idiotype MAb, WI2, was allowed to bind to the immobilized BS1.5H. Arrows indicate injection times.

Figure 24 shows the comparison of BIACore binding curves between BS1.5H, BS1.5 and BS2. Similar amounts of the bispecific diabodies were injected on a low density HSG-coupled sensor chip and the resulting binding curves were superimposed.

Figure 25 is the coding sequence of nucleic acids and encoded amino acids for 679-scFv-L5. 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for 679V_H. 427-441 is the coding sequence for the linker peptide (GGGGS) 442-780 is the coding sequence for 679V_K. 787-804 is the coding sequence for the 6 histidine affinity tag.

Figure 26 is the coding sequence of nucleic acids and encoded amino acids for 679-I3Q. 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for 679 V_H (I3Q). 427-441 is the coding sequence for the linker peptide (GGGGS). 442-780 is the coding sequence for 679 V_K. 787-804 is the coding sequence for the 6 histidine affinity tag.

Figure 27 is the coding sequence of nucleic acids and encoded amino acids for 679-C101S. 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for 679 V_H. 427-441 is the coding sequence for the linker peptide (GGGGS). 442-780 is the coding sequence for 679 V_K (C101S). 787-804 is the coding sequence for the 6 histidine affinity tag.

Figure 28 is the coding sequence and encoded amino acids for 679 I3Q/C101S.

Figure 29 is the coding sequence of nucleic acids and encoded amino acids for hMN14-scFv-L5. 1-66 is the coding sequence for the pelB leader peptide. 70-423 is the coding sequence for hMN14 V_H. 424-438 is the coding sequence for the linker peptide

(GGGGS). 439-759 is the coding sequence for hMN14 V_K. 766-783 is the coding sequence for the 6 histidine affinity tag.

Figure 30 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #1 of BS1 (679 x hMN14 bispecific diabody: variant 1). 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for 679 V_H. 427-441 is the coding sequence for the linker peptide (GGGGS). 442-762 is the coding sequence for hMN14 V_K. 769-786 is the coding sequence for the 6 histidine affinity tag.

Figure 31 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #2 of BS1 (679 x hMN14 bispecific diabody: variant 1). 1-66 is the coding sequence for the pelB leader peptide. 70-423 is the coding sequence for hMN14 V_H. 424-438 is the coding sequence for the linker peptide (GGGGS). 439-777 is the coding sequence for 679 V_K. 784-801 is the coding sequence for the 6 histidine affinity tag.

Figure 32 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #1 of BS1.5 (679 x hMN14 bispecific diabody: variant 2). 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for 679 V_H (I3Q). 427-441 is the coding sequence for the linker peptide (GGGGS). 442-762 is the coding sequence for hMN14 V_K. 769-786 is the coding sequence for the 6 histidine affinity tag.

Figure 33 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #2 of BS1.5 (679 x hMN14 bispecific diabody: variant 2). 1-66 is the coding sequence for the pelB leader peptide. 70-423 is the coding sequence for hMN14V_H. 424-438 is the coding sequence for the linker peptide (GGGGS). 439-777

is the coding sequence for 679V_K. 784-801 is the coding sequence for the 6 histidine affinity tag.

Figure 34 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #1 of BS2 (679 x hMN14 bispecific diabody: variant 3). 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for 679V_H (I3Q). 427-441 is the coding sequence for the linker peptide (GGGGS). 442-762 is the coding sequence for hMN14V_K. 769-786 is the coding sequence for the 6 histidine affinity tag.

Figure 35 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #2 of BS2 (679 x hMN14 bispecific diabody: variant 3). 1-66 is the coding sequence for the pelB leader peptide. 70-423 is the coding sequence for hMN14V_H. 424-438 is the coding sequence for the linker peptide (GGGGS). 439-777 is the coding sequence for 679V_K C101S. 784-801 is the coding sequence for the 6 histidine affinity tag.

Figure 36 is the coding sequence of nucleic acids and encoded amino acids for h679-scFv-L5. 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for h679V_H. 427-441 is the coding sequence for the linker peptide (GGGGS). 442-780 is the coding sequence for h679V_K. 787-804 is the coding sequence for the 6 histidine affinity tag.

Figure 37 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #1 of BS1.5H (h679 x hMN14 bispecific diabody). 1-66 is the coding sequence for the pelB leader peptide. 70-426 is the coding sequence for h679V_H. 427-441 is the coding sequence for the linker peptide (GGGGS). 442-762 is the coding sequence for hMN14V_K. 769-786 is the coding sequence for the 6 histidine affinity tag.

Figure 38 is the coding sequence of nucleic acids and encoded amino acids for polypeptide #2 of BS1.5H (h679 x hMN14 bispecific diabody). 1-66 is the coding sequence for the pelB leader peptide. 70-423 is the coding sequence for hMN14V_H. 424-438 is the coding sequence for the linker peptide (GGGGS). 439-777 is the coding sequence for h679V_K C101S. 784-801 is the coding sequence for the 6 histidine affinity tag.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

This invention relates to a multivalent, multi-specific binding protein comprising at least one binding site for a hapten moiety and at least one binding site for a target antigen. The hapten is connected to a small molecule that carries a diagnostic agent and/or a therapeutic agent. The present invention further relates to bispecific diabodies that bind with hapten moieties and target antigens and to recombinant vectors useful for the expression of these functional diabodies in a microbial host.

Structurally, whole antibodies are composed of one or more copies of an Y-shaped unit that contains four polypeptides chains. Two chains are identical copies of a polypeptide, referred to as the heavy chain, and two chains are identical copies of a polypeptide, referred to as the light chain. The two heavy chains are linked together by one or more disulfide bonds and each light chain is linked to one of the heavy chains by one disulfide bond. Each chain has a N-terminal variable domains, referred to as V_H and V_L for the heavy and the light chains, respectively, and the non-covalent association of a pair of V_H and V_L, referred to as the Fv fragment, forms one antigen-binding site.

Discrete Fv fragments are prone to dissociation at low protein concentrations and under physiological conditions [Glockshuber *et al.*, *Biochemistry* (1990) 29: 1362-1367], and therefore are not of much practical use. To improve stability and enhance potential utility, recombinant single-chain Fv (scFv) fragments have been produced and studied extensively, in which the C-terminal of the V_H domain (or V_L) is joined to the

N-terminal of the V_L domain (or V_H) via a peptide linker of variable length. [For a recent review, see Hudson and Kortt, *J. Immunological methods* (1999) 231: 177-189].

ScFvs with linkers greater than 12 amino acid residues in length (for example, 15-or 18-residue linkers) allow interaction between the V_H and V_L domains on the same chain and generally form a mixture of monomers, dimers (termed diabodies) and small amounts of higher mass multimers, [Kortt *et al.*, *Eur. J. Biochem.* (1994) 221: 151-157]. ScFvs with linkers of 5 or less amino acid residues, however, prohibit intramolecular pairing of the V_H and V_L domains on the same chain, forcing pairing with V_H and V_L domains on a different chain. Linkers between 3- and 12-residues form predominantly dimers [Atwell *et al.*, *Protein Engineering* (1999) 12: 597-604]. With linkers between 0 and 2 residues, trimeric (termed triabodies), tetrameric (termed tetrabodies) or higher oligomeric structures of scFvs are in favor; however, the exact patterns of oligomerization appear to depend on the composition as well as the orientation of the V-domains, in addition to the linker length. For example, scFvs of the anti-neuraminidase antibody NC10 formed predominantly trimers (V_H to V_L orientation) or tetramers (V_L to V_H orientation) with 0-residue linkers [Dolezal *et al.*, *Protein Engineering* (2000) 13: 565-574]. For scFvs constructed from NC10 with 1- and 2-residue linkers, the V_H to V_L orientation formed predominantly diabodies [Atwell *et al.*, *Protein Engineering* (1999) 12: 597-604]; in contrast, the V_L to V_H orientation formed a mixture of tetramers, trimers, dimers, and higher mass multimers [Dolezal *et al.*, *Protein Engineering* (2000) 13: 565-574]. For scFvs constructed from the anti-CD19 antibody HD37 in the V_H to V_L orientation, the 0-residue linker formed exclusively trimers and the 1-residue linker formed exclusively tetramers [Le Gall *et al.*, *FEBS Letters* (1999) 453: 164-168].

As the non-covalent association of two or more identical scFv molecules can form functional diabodies, triabodies and tetrabodies, which are multivalent but monospecific, a similar association of two or more different scFv molecules, if

constructed properly, may form functional multispecific scFv multimers. Bispecific diabodies are heterodimers of two different scFvs, each scFv consisting of the V_H domain from one antibody connected by a short linker to the V_L domain of another antibody. Several bispecific diabodies have been made using a di-cistronic expression vector that contains in one cistron a recombinant gene construct comprising V_{H1} -linker- V_{L2} and in the other cistron a second recombinant gene construct comprising V_{H2} -linker- V_{L1} . [See Holliger *et al.*, Proc. Natl. Acad. Sci. USA (1993) 90: 6444-6448; Atwell *et al.*, Molecular Immunology (1996) 33: 1301-1302; Holliger *et al.*, Nature Biotechnology (1997) 15: 632-631; Helfrich *et al.*, Int. J. Cancer (1998) 76: 232-239; Kipriyanov *et al.*, Int. J. Cancer (1998) 77: 763-772; Holiger *et al.*, Cancer Research (1999) 59: 2909-2916]. More recently, a tetravalent tandem diabody (termed tandab) with dual specificity has also been reported [Cochlovius *et al.*, Cancer Research (2000) 60: 4336-4341]. The bispecific tandab is a homodimer of two polypeptides, each containing four variable domains of two different antibodies (V_{H1} , V_{L1} , V_{H2} , V_{L2}) linked in an orientation to facilitate the formation of two potential binding sites for each of the two different specificities upon self-association. Methods of constructing scFvs are disclosed in U.S. 4,946,778 (1990) and U.S. 5,132,405 (1992). Methods of producing scFv-based agents of multivalency and multispecificity as described above are disclosed in U.S. 5,837,242 (1998), U.S. 5,844,094 (1998) and WO 98/44001 (1998) for bispecific diabodies, and in PCT/DE99/01350 for tandem diabodies.

Alternative methods of manufacturing multispecific and multivalent antigen-binding proteins from V_H and V_L domains are disclosed in U.S. 5,989,830 and U.S. 6,239,259. Such multivalent and multispecific antigen-binding proteins are obtained by expressing a dicistronic vector which encodes two polypeptide chains, with one polypeptide chain consisting of two or more V_H domains (from the same or different antibodies) connected in series by a peptide linker and the other polypeptide chain consisting of complementary V_L domains connected in series by a peptide linker.

The present invention utilizes two monoclonal antibodies, 679 and hMN14, and two point mutations of 679, (679-V_H (I3Q) and 679-V_K(C101S)), to produce antigen specific diabodies. In addition, a bispecific diabody is produced from hMN14 and h679, which is obtained by grafting the CDRs of 679 onto a framework of amino acid residues found in human antibodies. The murine monoclonal antibody designated 679 (an IgG1, K) binds with high affinity to molecules containing the moiety histamine-succinyl-glycyl (HSG) (Morel *et al.*, Molecular Immunology, 27, 995-1000, 1990). The nucleotide sequence pertaining to the variable domains (V_H and V_K) of 679 has been determined (Qu *et al.*, unpublished results). V_K is one of two isotypes of the antibody light chains, V_L. As depicted in Figure 1, the design of the gene construct (679-scFv-L5) for expressing a 679 diabody possesses the following features: 1) The carboxyl terminal end of V_H is linked to the amino terminal end of V_K by the peptide linker Gly-Gly-Gly-Gly-Ser (G₄S). The use of the G₄S peptide linker enables the secreted polypeptide to dimerize into a diabody, forming two binding sites for HSG. 2) A pelB leader signal peptide sequence precedes the V_H gene to facilitate the transport of the polypeptide to the periplasmic space of *E. coli*. 3) Six histidine (His) residues are added to the carboxyl terminus to allow purification by IMAC. The DNA coding sequence and the corresponding encoded amino acids for 679-scFv-L5 are contained in Figure 25 (Seq IDs). The DNA coding sequence and the corresponding encoded amino acids for 679-I3Q are contained in Figure 26 (Seq IDs). The DNA coding sequence and the corresponding encoded amino acids for 679-C101S are contained in Figure 27 (Seq IDs). Figure 1 also includes a stick figure drawing of the mature polypeptide after proteolytic removal of the pelB leader peptide and a stick figure drawing of a 679 diabody, including the HSG binding sites.

Two site-directed point mutations were made to increase the amount of 679 diabodies in soluble extracts. Specifically, converting residue 3 in the 679V_H sequence from Ile to Gln (I3Q), or residue 101 in the 679V_K sequence from Cys to Ser (C101S),

or both (I3Q/C101S), resulted in at least a ten-fold increase in soluble expression levels. Moreover, 679 can be humanized or fully human to help avoid an adverse response to the murine antibody.

hMN14 is a humanized monoclonal antibody (Mab) that binds specifically to CEA (Shevitz *et al*, J. Nucl. Med., Supp., 34, 217P, 1993; U.S. 6,254,868 (2001)). While the original Mabs were murine, humanized antibody reagents are now utilized to reduce the human anti-mouse antibody response. The variable regions of this antibody were engineered into an expression construct (hMN14-scFv-L5) in a similar fashion to 679-scFv-L5 as described in Example 1. As depicted in Figure 3, the design of the gene construct (hMN14-scFv-L5) for expressing an hMN14 diabody possesses the following features: 1) The carboxyl terminal end of V_H is linked to the amino terminal end of V_K by the peptide linker Gly-Gly-Gly-Gly-Ser (G4S). The use of the G4S peptide linker enables the secreted polypeptide to dimerize into a diabody, forming two binding sites for CEA. 2) A pelB leader sequence precedes the V_H gene to facilitate the transport of the polypeptide to the periplasmic space of *E. coli*. 3) Six histidine (His) residues are added to the carboxyl terminus to allow purification by IMAC. The DNA coding sequence and the corresponding encoded amino acids for hMN14-scFv-L5 are contained in Figure 29 (Seq IDs). Figure 3 also shows a stick figure drawing of the mature polypeptide following proteolytic removal of the pelB leader peptide, and a stick figure drawing of a hMN14 diabody, including CEA binding sites.

Di-cistronic expression vectors were constructed through a series of sub-cloning procedures outlined in Figures 8 and 9 and described in Example 6. The di-cistronic expression cassette for bispecific hMN14x679 diabody is shown schematically in Figure 10. The expression cassette may be contained in a plasmid, which is a small, double-stranded DNA forming an extra-chromosomal self-replicating genetic element in many bacteria and some eukaryotes and is widely used in genetic engineering as a cloning vector. A cloning vector is a DNA molecule that can replicate on its own in a

microbial host cell. This invention describes a vector that expresses bispecific diabodies. A host cell accepts a vector for reproduction and the vector replicates each time the host cell divides. A commonly used host cell is *Escherichia Coli* (E. Coli), however, other host cells are available.

When the di-cistronic cassette as shown in Figure 10 is expressed in *E. coli*, some of the polypeptides fold and spontaneously form soluble bispecific diabodies. The bispecific diabody shown in Figure 10 forms one binding site having high affinity for HSG and one binding site having high affinity for CEA.

In this instance, the carboxyl terminal end of the V_H segment of the 679 MAb is connected to the amino terminal end of the V_K segment of the hMN14 MAb by a five amino acid residue linker, and the carboxyl terminal end of the V_H segment of the hMN14 MAb is connected to the amino terminal end of the V_K segment of the 679 MAb by the same five amino acid residue linker. Three variants of 679 x hMN14 bispecific diabodies have been produced and tested. BS1 is composed of the wild-type sequences for both 679 and hMN14 variable regions. BS1.5 incorporates the 679 V_H I3Q mutation. BS2 incorporates both the 679 V_H I3Q and the 679 V_K C101S mutations. The DNA coding sequences and the corresponding encoded amino acids for the two polypeptides of BS1, BS1.5, and BS2 are contained in Figures 30 & 31, 32 & 33, and 34 & 35 (Seq IDs), respectively. Additionally, a bispecific diabody of h679xhMN14 has been constructed and named BS1.5H (See Figures 37 & 38).

The ultimate use of these bispecific diabodies is for pre-targeting CEA positive tumors for subsequent specific delivery of therapeutic radioisotopes carried by HSG containing peptides. These diabodies bind selectively to targeted antigens and when combined with a bivalent di-HSG hapten allow for increased affinity and a longer residence time at the desired location. Moreover, non-antigen bound diabodies are cleared from the body quickly and exposure of normal tissues is minimized.

Delivering a diagnostic or a therapeutic agent to a target for diagnosis or treatment in accordance with the invention includes administering a patient with the binding protein, waiting a sufficient amount of time for an amount of the non-binding protein to clear the patient's blood stream, and administering a diagnostic or therapeutic agent that binds to a binding site of the binding protein. Diagnosis further requires the step of detecting the bound proteins with known techniques. The diagnostic or therapeutic carrier molecule comprises a diagnostically or therapeutically efficient agent, a linking moiety, and one or more hapten moieties. The hapten moieties are positioned to permit simultaneous binding of the hapten moieties with the binding protein.

Administration of the binding protein and diagnostic or therapeutic agents of the present invention to a mammal may be intravenous, intraarterial, intraperitoneal, intramuscular, subcutaneous, intrapleural, intrathecal, by perfusion through a regional catheter, or by direct intralesional injection. When administering the binding moiety by injection, the administration may be by continuous infusion or by single or multiple boluses.

The unmixed diagnostic or therapeutic agent and bispecific antibody may be provided as a kit for human therapeutic and diagnostic use in a pharmaceutically acceptable injection vehicle, preferably phosphate-buffered saline (PBS) at physiological pH and concentration. The preparation preferably will be sterile, especially if it is intended for use in humans. Optional components of such kits would normally be containers of stabilizers, buffers, labeling reagents, radioisotopes, paramagnetic compounds, second antibody for enhanced clearance, and conventional syringes, columns, vials and the like.

EXAMPLES

The examples below are illustrative of embodiments of the current invention and should not be used, in any way, to limit the scope of the claims.

Example 1 - Construction of Plasmids for expression of 679 diabody in *E. coli*

Standard recombinant DNA methods were used to obtain 679-scFv-L5 as follows. A plasmid containing the V_H sequence of 679 was used as the template for polymerase chain reaction (PCR) using Pfu polymerase and the two oligonucleotide primers specified below:

679V_H-Left

5'-TCAGCCATGGAAGTGATCCTGGTGGAGTCAGGGGGAGACT-3'

679V_H-Right (G₄S)

5'-TGAGGATCCGCCACCTCCTGAGGAGACGGAGACCGTGGTC-3'

The left PCR primer contains a 5' NcoI restriction site. The right PCR primer contains the sequence for a 5 amino acid residue linker (G₄S) and a BamHI restriction site. The PCR product was digested with NcoI and BamHI and ligated in frame with the pelB leader sequence into NcoI/BamHI digested pET-26b vector (Novagen) to generate 679V_HL5-pET26.

A plasmid containing the V_K sequence of 679 was used as the template for PCR using Pfu polymerase and the two oligonucleotide primers specified below:

679V_K-Left

5'-CTGAGGATCCGACATTGTGATGTCACAATCT-3'

679V_K-Right

5'- ATCCTCGAGCCGTTTCAGCTCCAGCTTGGT-3'

The left and right PCR primers contain BamHI and XhoI restriction sites, respectively. The PCR product was digested with XhoI and BamHI and ligated (in frame with the 679V_H, G₄S linker, and 6His sequences) into the XhoI/BamHI digested 679V_HL5-pET26 to generate the expression construct 679-scFv-L5. The DNA sequence of the inserted gene confirmed that the V_H and V_k sequences were identical to those of the original cDNA clones and the sequences of the ligation sites and linker regions were as designed. The gene construct, 679-scFv-L5, is illustrated in Figure 1.

Example 2 - Expression of 679 diabody in *E. coli*

Competent *E. coli* BL21(P-Lys-S) cells were transformed with 679-scFv-L5 by standard methods. Cultures were shaken in 2xYT media supplemented with 100 μ g/ml kanamycin sulphate and 34 μ g/ml chloramphenicol and grown at 37°C to OD₆₀₀ of 1.6 - 1.8. An equal volume of room temperature 2xYT media supplemented with antibiotics and 0.8M sucrose was added to the cultures, which were then transferred to 20°C. After 30 minutes at 20°C, expression was induced by the addition of 40 μ M IPTG and continued at 20°C for 15-18 hours.

The expression of 679 diabody was examined in (1) cell culture conditioned media, (2) soluble proteins extracted under non-denaturing conditions from the cell pellet following centrifugation, and (3) insoluble material remained in the pellet following several cycles of extraction and centrifugation.

Soluble proteins were extracted from bacterial cell pellets as follows. Pellets were frozen and thawed then re-suspended in lysis buffer (2% Triton-X 100; 300mM NaCl; 10mM imidazole; 5mM MgSO₄; 25 units/ml benzonase; 50mM NaH₂PO₄, pH 8.0) using an amount equal to 1% of the culture volume. The suspension was homogenized by sonication, clarified by centrifugation, and loaded onto Ni-NTA IMAC columns. After being washed with buffer containing 20mM imidazole, the

columns were eluted with 100mM imidazole buffer (100mM imidazole; 50mM NaCl; 25mM Tris, pH 7.5) and the eluate obtained was further purified on a Q-Sepharose column.

The insoluble material was solubilized in denaturing Ni-NTA binding buffer (8M urea; 10mM imidazole; 0.1M NaH₂PO₄; 10mM Tris, pH 8.0) and mixed with 1ml of Ni-NTA agarose (Qiagen, inc.). The mixture was rocked at room temperature for 1 hour then the resin was washed once with 50ml of the same buffer and loaded onto a column. The column was washed with 20ml of the same buffer followed by 20ml of wash buffer (8M urea; 20mM imidazole; 0.1M NaH₂PO₄; 10mM Tris, pH 8.0). Bound proteins were eluted with 5ml of denaturing elution buffer (8M urea; 250mM imidazole; 0.1M NaH₂PO₄; 10mM Tris, pH 8.0).

As shown by the results of reducing SDS-PAGE in Figure 2, a robust induction was evident in the whole cell lysate (lane 2), which displayed a predominant band corresponding to a protein of approximately 28 kD (the predicted MW for 679 scFv). However, virtually all of the induced protein was present in the insoluble fraction (lane 5), and none was detected in the 10x concentrated culture media (lane 3). The induced protein was purified from the insoluble fraction following solubilization and elution of the bound material off a Ni-NTA column under denaturing conditions (lane 1). The soluble extract contained a trace amount of HSG-binding material, estimated to be about 1 ug per liter of culture by BIACore analysis.

Example 3 - 679 Diabodies formed from scFv mutants

Two site-directed point mutations were made to increase the amount of 679 diabodies in soluble extracts. Specifically, converting residue 3 in the 679V_H sequence from Ile to Gln (I3Q), or residue 101 in the 679V_K sequence from Cys to Ser (C101S), or both (I3Q/C101S), resulted in at least a ten-fold increase in soluble expression levels. The mutations were introduced in synthetic oligonucleotides used for PCR. The V_H-I3Q mutation was incorporated in the oligonucleotide primer depicted below:

679V_H I3Q-Left

5'- CCATGGAAGTGCAGCTGGTGGAGTCAGGG-3'

This primer was paired with 679V_H-Right (Example 1) to generate the V_H-I3Q mutant by PCR from 679-scFv-L5 template using Pfu polymerase.

The 679V_K-C101S mutation was incorporated in the oligonucleotide primer specified below:

679V_K C101S-Right

5'GCTCGAGCCGTTTCAGCTCCAGCTTGGTCCCAGCACCACGTGCT
CAGATAATAAACTTGAG-3'

This primer was paired with 679-V_K Left (Example 1) to generate 679V_K-C101S mutant by PCR from 679-scFv-L5 template using Pfu polymerase. The PCR products were cloned into pET26b following the same procedure as described above in Example 1.

Expression levels in the soluble fractions were estimated by BIACore analysis using a HSG coupled sensor chip. The expression levels of I3Q, C101S, or I3Q/C101S mutant 679 diabody were about 10 ug/L as compared to about 1 ug/L for the wild type.

Example 4 - Construction of plasmids for expression of hMN14 diabody in *E. coli*

Standard recombinant DNA methods were used to obtain hMN14-scFv-L5 as follows. The hMN14 V_H and V_K sequences were amplified from a vector constructed for expressing hMN14 Fab' (Leung *et al.*, Cancer Research, Supp., 55, 5968s-5972s, 1995) by PCR with Pfu polymerase. The hMN14V_H sequence was amplified using the oligonucleotide primers specified below:

hMN14V_H-Left

5'- CGTACCATGGAGGTCCA ACTGGTGGAGA-3'

hMN14V_H-Right (G₄S)

5'-CATAGGATCCACCGCCTCCGGAGACGGTGACCGGGT-3'

The left PCR primer contains a 5' NcoI restriction site. The right PCR primer contains a sequence for a 5 amino acid residue linker (G₄S) and a BamHI restriction site. The PCR product was digested with NcoI and BamHI and ligated, in frame with the pelB leader sequence, into NcoI/BamHI digested pET-26b vector to generate hMN14V_HL5-pET26. The hMN14V_K sequence was amplified using the oligonucleotide primers specified below:

hMN14V_K-Left

5'- CTGAGGATCCGACATCCAGCTGACCCAGAG-3'

hMN14V_K-Right

5'-GCTACTCGAGACGTTGATTCCACCTTGG-3'

The left and right PCR primers contain BamHI and XhoI restriction sites, respectively. The PCR product was digested with XhoI and BamHI and ligated, in frame with the hMN14V_H, G₄S linker and 6His sequences, into the XhoI/BamHI digested hMN14V_HL5-pET26 construct to generate the expression construct hMN14-

scFv-L5. The DNA sequence of this construct was verified by automated DNA sequencing. The gene construct, hMN14-scFv-L5, is illustrated in Figure 3.

Example 5 - Expression of hMN14 diabody in *E. coli*

The hMN14-scFv-L5 construct was used to transform BL21(P-LysS) *E. coli*. Culture conditions, induction, and purification were carried out similar to those described for the 679 diabody in Example 1, except that the hMN14 diabody was purified by affinity chromatography, instead of Q-Sepharose anion exchange chromatography, via binding to an anti-id antibody immobilized on Affi-gel. Soluble proteins that bound and eluted from Ni-NTA resin were loaded on a WI2 anti-idiotype affinity column. The column was washed with PBS and the product was eluted with 0.1M Glycine; 0.1M NaCl, pH 2.5 and neutralized immediately.

Although most of the hMN14scFv expressed was present as insoluble protein, approximately 1.5 mg/L culture of soluble hMN14scFv was purified from the soluble fraction. As shown by size-exclusion high performance liquid chromatography (HPLC), a predominant peak was observed in Figures 4A and 4B at 9.8 min for the IMAC purified as well as the affinity purified material. The retention time of hMN14 Fab', which has a molecular weight of approximately 50 kDa, was 9.75 minutes as indicated on the x-axis of Figure 4B. The very similar retention time of hMN14scFv indicates that it exists in solution as a dimer or diabody since the calculated molecular weight of the monomeric hMN14scFv is 26kDa. SDS-PAGE gel analysis in Figure 5A shows a single band of the predicted Mr at 26kDa, and the isoelectric focusing (IEF) gel analysis in Figure 5B yields a band with pI of 8.2, close to the calculated pI of 7.9. A competitive ELISA showed that the hMN14 diabody is functionally active and displays excellent binding properties.

Nude mice bearing the CEA positive GW39 tumor were injected with ^{131}I -labeled hMN14 diabody and the biodistribution was analyzed at various times post injection. While a significant amount of the diabody remained associated with the tumor for more than 96 hours, much of the free diabody cleared the blood rapidly as illustrated in Figure 6. Figure 7 shows the percentage of the injected dose that is associated with the tumor and with normal tissues, such as liver, spleen, kidney, lungs, blood, stomach, small intestine, and large intestine, at 48 hours after the injection. The amount of the injected dose in each normal tissue is very low when compared to the amount in the tumor. Table 1 summarizes the relative amounts of activity found in normal tissues compared to that in the tumor at 24, 48 and 72 hours.

Table 1. Tumor to non-tumor ratios

	24hrs	48hrs	72hrs
Tumor	1.00	1.00	1.00
Liver	22.47	31.85	28.32
Spleen	25.41	39.51	41.03
Kidney	9.12	12.12	10.54
Lung	15.49	25.70	31.75
Blood	9.84	17.32	21.80
Stomach	9.98	17.50	23.13
Sm. Int.	37.23	65.60	50.58
Lg. Int.	35.87	66.54	45.66

Example 6 - 679 x hMN14 bispecific diabody (BS1, BS1.5 and BS2)**Construction of PET-ER**

Before proceeding to expression vectors that direct the synthesis of bispecific diabodies capable of binding to both HSG and CEA, a new vector (pET-ER) was generated by the addition of a multiple cloning site, MCS2, shown in Figure 8A, into the pET-26b vector, shown in Figure 8B. Two complimentary oligonucleotides were synthesized and phosphorylated with T4 polynucleotide kinase. The oligonucleotides were mixed in equal molar concentrations, heated to 95°C then allowed to anneal as the mixture was slowly cooled to room temperature. The duplex structure, MCS2, was ligated into the BlnI restriction site of pET-26b to generate the pET-ER vector as illustrated in Figure 8C. This vector facilitates the construction of di-cistronic expression cassettes and allows for stoichiometric expression of two heterologous polypeptides in a single *E. coli* cell.

Construction and expression of 679xhMN14 diabodies in *E. coli*

The di-cistronic expression vectors were constructed through a series of sub-cloning procedures that are outlined in Figure 9. Initially, the V_κ sequences of 679-scFv-L5 and hMN14-scFv-L5 were exchanged by excision with BamHI and XhoI to generate two intermediate constructs in pET26b. A DNA fragment containing the sequence 679V_H-L5-hMN14V_κ, excised from a pET26b construct with NcoI and XhoI, was ligated into the same restriction sites in pET-ER vector to generate an intermediate clone (679V_H-L5-hMN14V_κ- pET-ER). A 900bp DNA fragment, which includes a ribosomal binding site in addition to the coding sequence for polypeptide 2 (below), was excised from hMN14V_H-L5-679V_κ- pET26b with XbaI and BlnI. This fragment was ligated into the SpeI and BlnI restriction sites of 679V_H-L5-hMN14V_κ- pET-ER to create the final bispecific expression constructs. The di-cistronic expression cassette

for bispecific hMN14x679 diabody is shown schematically in Figure 10. The DNA coding sequence of nucleic acids and the corresponding encoded amino acids for the first and second polypeptide sequences of BS1, BS1.5, and BS2 are contained in Figures, 30 & 31, 32 & 33, and 34 & 35 (Seq IDs), respectively. The di-cistronic expression cassette codes for two polypeptides that are arranged as follows:

Polypeptide 1

Pel B; 679V_H; GGGGS linker; hMN14V_K; 6 His

Polypeptide 2

Pel B; hMN14V_H; GGGGS linker; 679V_K; 6His

When this cassette is expressed in *E. coli*, some of the polypeptides fold and spontaneously form soluble bispecific diabodies. The bispecific diabody, having four polypeptides interacting with each other, is shown in Figure 10. In this instance, the carboxyl terminal end of the V_H segment of the 679 MAb is connected to the amino terminal end of the V_K segment of the hMN14 MAb by a five amino acid residue linker, and the carboxyl terminal end of the V_H segment of the hMN14 MAb is connected to the amino terminal end of the V_K segment of the 679 MAb by the same five amino acid residue linker. Each chain forms one half of the 679xhMN14 diabody. The three constructs for expression of 679 x hMN14 bispecific diabodies, BS1, BS1.5, and BS2 were expressed and purified as described for 679scFv in Example 1. The results are described in detail below for BS1.5.

Following IPTG induction, BS1.5-transformed *E. coli* (BL21-pLysS) cultures expressed 0.5 mg of soluble bispecific diabody per liter of culture. From 5L induction, 2.4 mg of highly purified BS1.5 diabody was isolated following the procedures similar to those described in Example 1. Soluble cell extracts were loaded onto a 4ml of Ni-NTA agarose column (Qiagen), which was washed with 20 bed volumes of 10mM

imidazole buffer and 5 bed volumes of 20mM imidazole buffer. The diabody was eluted from the IMAC column in 15 ml of 100mM imidazole elution buffer. The eluate was directly passed over a 4-ml Q-Sepharose anion exchange column and the highly purified BS1.5 was collected in the flow through fraction. HPLC analysis showed a single peak illustrated in Figure 11 with a retention time of 9.2 minutes demonstrating that the two heterologous polypeptides, 679V_H-GGGGS-hMN14V_K and hMN14V_H-GGGGS-679V_K, exclusively form a dimer or diabody. The purity of the three 679xhMN14 bispecific diabodies was further demonstrated by reducing SDS-PAGE and IEF. A single protein band is seen in Figure 12 at approximately 27 kDa in a Coomassie blue-stained SDS-PAGE gel for BS2. The two polypeptides essentially co-migrate, since their calculated MWs are 26.5 kDa and 27.2 kDa. On IEF gel, as shown in Figure 13, BS1, BS1.5 and BS2 each shows the presence of a single band with a pI of approximately 8.3, which is close to the predicted pI of 7.9 for the three bispecific diabodies.

The binding kinetics of BS1.5 was evaluated by BIACore using a low density HSG-coupled sensor chip. Binding sensograms were obtained for BS1.5 concentrations from 0 to 54 nM and the resulting data were analyzed with the BIACore BiaEvaluation software using 1:1 Langmuir binding model, yielding an association constant of the interaction, K_d , of 2.4 nM for the binding of BS1.5 to immobilized HSG. Figure 14 shows the BIACore binding curves at various concentrations of BS1.5. Using the same method, a chemically prepared 679 x hMN14 F(ab')₂ conjugate yields a K_d of 1.55 nM. The binding properties for BS1.5 as compared to BS1 and BS2 are summarized in Table 2. A lower K_d suggests a higher affinity to the antigen. BS1.5 has the lowest K_d and therefore exhibits the greatest affinity to HSG. K_d is a measure of the ratio of the off rate and on rate constants, K_{off} and K_{on} , where $K_d = K_{off}/K_{on}$.

Table 2. Properties of bispecific diabodies

	K _d	k _{on} (1/Ms)	k _{off} (1/s)	Expression
BS1	4.7nM	2.12e5	1.01e-3	0.25 mg/L
BS1.5	2.5nM	4.05e5	1.01e-3	0.5 mg/L
BS2	10.6nM	3.58e5	3.81e-3	1.0 mg/L

The binding of BS1.5 to CEA was demonstrated by competitive ELISA.

Microtiter plates were coated with 0.5 µg/well with soluble CEA (Scripps Laboratories). BS1.5 at concentrations ranging from 4 - 500 nM were allowed to compete for CEA binding with HRP-conjugated hMN14 IgG (1nM). BS1.5 shows a competitive binding curve similar to that of the 679 x hMN14 F(ab')₂ chemical conjugate. These data indicate that the BS1.5 has a CEA binding affinity similar to the parental hMN14 antibody. The bispecific binding properties of BS1.5 was also analyzed by BIACore with a high-density HSG-coupled biosensor chip. BS1.5 was pre-bound to the sensor chip before injection of an anti-idiotype MAb designated WI2 that is highly specific for hMN14. Soluble CEA was also used in place of WI2 and gave similar results. As shown in Figure 16, injection of 60 ng of BS1.5 gave a relative response of 620 RU. Subsequent injection of 400ng of WI2 increased the signal by 400 RU. Binding approached saturation with a second WI2 injection (400ng), as a total of 520 RU were added to the 620RU signal of BS1.5. Injection of WI2 following pre-binding with 679 F(ab')₂ or without pre-binding yielded a negligible response. These data demonstrate that BS1.5 has the capability of binding HSG and CEA simultaneously.

BS1 and BS2 each differ from BS1.5 by single point mutations in the 679 component of the diabody. Some of the properties of these molecules are summarized in Table 2. ELISA experiments demonstrate that each of these proteins exhibits similar

CEA binding properties, which is not surprising given that the hMN14 component of the diabody is consistent among the three diabodies. Further, BS1 and BS2 are demonstrated by BIACore analysis to be bispecific and capable of binding to CEA and HSG simultaneously. BS1.5 includes the 679V_H I3Q mutation that is not included in BS1, which is composed entirely of the wildtype sequences. This mutation doubles the yield of soluble diabody that is expressed without compromising the binding affinity for HSG. BS2 includes the additional 679V_K C101S mutation as well as the 679V_H I3Q. With this second change, soluble BS2 is expressed at twice the level of BS1.5, however, the binding affinity for HSG decreased measurably.

Example 7 – In Vivo Targeting

The potential of these bispecific diabodies for use as pre-targeting CEA positive tumors for subsequent specific delivery of therapeutic radioisotopes carried by HSG containing peptides is demonstrated by BS1.5. Nude mice bearing GW39 (CEA positive) tumors were pre-targeted with BS1.5. Initially, the bio-distribution was followed with ¹³¹I-labeled BS1.5. The results are shown in Figure 17. The diabody rapidly accumulated in the tumor within one hour and slowly cleared. The diabody also accumulated in the blood within one hour, however, significant blood clearance occurred within 8 to 12 hours. At 12 and 24 hour clearance times, the tumors were enriched appreciably with ¹³¹I-BS1.5 as compared to normal tissues, such as liver, spleen, kidney, lungs, blood, stomach, small intestine, and large intestine, as illustrated in Figure 18. Pre-targeting experiments were performed with 12 or 24 hour clearance times following injection of BS1.5 (unlabeled). IMP241, a peptide containing two HSG groups and a DOTA moiety, was loaded with ¹¹¹Indium and injected in BS1.5 pre-targeted mice. The bio-distribution of the ¹¹¹In-IMP241 was examined at 3 and 24 hours after injection. Figure 19 shows the activity in the tumor and normal tissues in

pre-targeted mice with 12 hour clearance. Substantial radioactivity accumulates in tumors within 3 hours with only minimal loss after 24 hours. Small amounts of radioactivity was detected in all normal tissues besides the kidney at both time points, suggesting that the diabody is specific to the tumor and radioactive isotopes, but avoids uptake into normal tissues. The tumor to non-tumor ratios of ^{111}In -IMP241 are summarized in Table 3.

Table 3. Tumor to non-tumor ratios for ^{111}In -IMP241 after BS1.5 injection and 12- hour clearance.

	3 hrs post ^{111}I -IMP241	24 hrs post ^{111}I -IMP241
Tumor	1.00	1.00
Kidney	3.30	4.96
Liver	82.34	60.66
Spleen	179.23	67.79
Lung	28.57	74.75
Blood	154.78	157.18
Stomach	494.84	328.03
Sm. Int.	132.72	184.14
Lg Int.	34.60	172.47

Example 8 - Humanization of 679 V domains

A humanized version of 679-based diabody has been generated that exhibits HSG binding affinity comparable to the murine forms. The strategy employed was to retain all CDR residues and those residues known to interact with the CDR residues while substituting only those residues of the mouse frameworks that are not found in the database of human frameworks at corresponding positions. In such cases if more than one amino acid residue of the human frameworks is known for the same position, the most common one is selected for humanization.

The amino acid sequence for each of the framework regions of m679V_H or m679V_K were used to query the NCBI database and aligned with human antibody (h-Ab) sequences. Most amino acid residues of the murine 679 frameworks are identical with some or all of the human frameworks in the database at corresponding positions and therefore they are conserved for h679. For those amino acid residues of the murine 679 frameworks that are not found in any of the human frameworks, they are substituted with the most common residue found in the homologous h-Abs at the corresponding positions. However, if a residue in a particular position is likely to interact with the CDRs or to be involved in the V_H and V_K association (E.A. Padlan, *Molecular Immunology*, 31, 169-217, 1994), the residue in m679 is retained in h679.

Substitutions

Figure 20 shows an alignment of m679 and humanized h679. The Kabat numbering system is used and framework regions (FR) as well as CDRs are indicated. Arrows signify amino acid substitutions. For all of the considerations below, human sequences with high levels of sequence identity were compared to m679.

V_H framework region 1 (V_HFR-1)

All but one of the m679 V_HFR-1 amino acids is commonly found in the h-Abs and were therefore left unchanged in h679. At position V_H-3, glutamine (Q), which is always in this position in the h-Abs, was substituted for isoleucine (I), which is not found in the h-Abs. The V_HI3Q substitution has previously been introduced into both m679 diabodies and bi-specific diabodies and was found to increase the solubility levels of expressed products.

V_H framework region 2 (V_HFR-2)

This region is small yet divergent. Residues found in three positions in V_HFR-2 of m679 are not found in h-Abs. In m679, leucine (L) is in position V_H-37, which in h-Abs is almost always valine. However, the leucine was retained in h679 because this position is known to be strongly involved in V_H to V_K association and often is in contact with CDR residues. Positions V_H 42 and 44 are always glycine in the h-Abs and do not contact the V_K or CDRs. Therefore, glutamic acid (E) at V_H-42 and arginine (R) at V_H-44 were each substituted with glycine.

V_H framework region 3 (V_HFR-3)

Substitutions at three of 32 positions in V_HFR-3 made this region of h679 entirely humanized. None of the three positions are known to be involved in V_H-V_K or CDR contact so the following substitutions were made with the most common h-Ab amino acid for the respective positions; serine (S) for asparagine (N) at V_H-77; alanine (A) for serine (S) at V_H-84; and glutamic acid (E) for alanine (A) at V_H-85.

V_H framework region 4 (V_HFR-4)

Substitution of threonine (T) for serine (S) at V_H-110 would make this region completely humanized. However, for technical reasons, we chose to keep T in the V_HFR-4 of h679.

V_K framework region 1 (V_KFR-1)

This region has considerable variability amongst the h-Abs. The m679 amino acids at 20 of the 23 positions in V_KFR-1 are acceptable for h-Abs. The following substitutions were made at three positions with the most common h-Ab amino acid for the respective positions: threonine (T) for serine (S) at V_K-5; arginine (R) for lysine (K) at V_K-18; and leucine (L) for methionine (M) at V_K-21. These positions are not known to be involved in V_H-V_K or CDR contacts.

V_K framework region 2 (V_KFR-2)

This short region resembles the human sequences and is acceptable as is.

V_K framework region 3 (V_KFR-3)

This large (31 amino acids) region requires four substitutions for complete humanization. Serine (S), always found in h-Abs at V_K-63, replaced threonine (T). Leucine (L), always found in h-Abs at V_K-78, replaced valine (V). Alanine (A), usually found in h-Abs at V_K-80, replaced serine (S). Valine (V), always found in h-Abs at V_K-83, replaced leucine (L). None of these positions are known to be involved in V_H-V_K or CDR contacts.

V_K framework region 4 (V_KFR-4)

This short region resembles the human sequences and is acceptable as is.

With a total of only 13 amino acid substitutions made in the V_H and V_K frameworks of m679 as described above, the new frameworks contain all residues

found in h-Abs, except two, namely, leucine at position V_H -37, which is retained due to its involvement in the V_H and V_K contact, and threonine at position V_H -110, which is retained because of technical reasons.

Methods

Eight oligonucleotide PCR primers, which together contain 12 of the 13 mutations described above to convert m679scFv into h679 diabody, were synthesized and used to generate 4 PCR products. The mutant sequences were amplified from the 679scFv-L5 plasmid construct using Taq polymerase. Restriction sites were engineered into the primers to allow ligation of the PCR products while conserving the encoded amino acid sequence. The sequences, coding regions, restriction sites and specific mutations contained on each of the primers are summarized in Table 4. The relative location of the primers and the PCR products are shown schematically in Figure 21. The PCR products were each cloned into the PCR cloning vector pGemT (Promega). Through several rounds of sub-cloning using standard methods, the four PCR sequences were assembled and added to the first 120 nucleotides of 679 V_H I3Q to generate the h679scFv-L5-pGemT construct. From this construct the V_H and V_K domains were transferred together into the pET26b expression vector for h679 diabody or individually to make fully humanized bi-specific diabodies. The sub-cloning process is described in detail below.

Table 4. PCR Primers for humanization of 679scFv-L5

Primer	Base Pairs	Restriction Site	Mutations	Sequence
A-Left	121 - 150	Xma I	V_H -E42G V_H -R44G	5'GCTTCCCGGGAAAGGGCTGGA GTGGGTCGCAACC3'
A-Right	212 - 247	Pst I	V_H -N77S	5'CGATCTGCAGATATAGGCTGTT

				CTTGGCATTGTCTCTGG3'
B-Left	241 - 284	Pst I	V _H -S84A V _H -A85E	5'CTGCAGATGAACAGTCTAAGG GCTGAGGACACGGCCTTGTATTA3'
B-Right	365 - 421	Xma I	V _K -S5T	5'CCCCGGGTGACACAGCCAGGGAG GATGGAGATTGTGTCATCACAATGT CGGATCCGC3'
C-Left	414 - 455	Xma I	V _K -K18R V _K -M21L	5'ACCCGGGGAGAGGGTCACTCTGA CCTGCAAATCCAGTCAGAG3'
C-Right	565 - 595	Bsp EI	V _K -T63S	5'TTCCGGATCCACTGCCTGAGAAG CGATCAGGGACCCCAGA3'
D-Left	588 - 659	Bsp EI	V _K -V78L V _K -S80A V _K -L83V	5'ATCCGGAACAGATTTCACTCTCAC CATCAACAGTCTGCAGGCTGAAGAC GTGGCAGTTATTACTGCCTCA3'
D-Right	687 -717	Xho I	None	5'ATCCTCGAGCCGTTTCAGCTCCAG CTTGGT3'

Construct A. 1-247 with 3 V_H mutations

A plasmid clone containing the 679V_H-I3Q mutation (679V_HI3Q-pGemT) was digested with the restriction enzymes BspEI (base pair 121) and PstI (in pGemT vector 3' of the insert), leaving the first 121 base pairs of 679V_HI3Q with the vector. This vector fragment was ligated with PCR product A that was digested with XmaI (5' end) and Pst I (3' end) to generate construct A. It is important to note that the BspEI-XmaI ligation destroys both sites as each of these restriction enzymes was used in subsequent steps.

Construct B. 1-415 with 2 additional V_H and 1 V_K mutations

PCR product B was cloned into pGem T and screened for clones in the T7 orientation. The B fragment was excised from the pGemT clone with PstI and ligated

into the PstI site of construct A. Clones were screened for proper insert orientation for construct B.

Construct C. 1-589 with 3 additional V_k mutations

PCR product C was cloned into pGem T and screened for clones in the T7 orientation. The C fragment was excised from the pGemT clone with XmaI and NdeI (vector site) and then ligated into construct B that was digested with the same enzymes.

Construct D. Humanized 679scFv in pGemT

PCR product D was cloned into pGem T and screened for clones in the T7 orientation. The D fragment was excised from the pGemT clone with BspEI and NdeI and then ligated into construct C that was digested with the same enzymes.

H679scFv-L5 construction and production of h679 diabody

The h679scFv-L5 sequence was excised from the pGemT construct with NcoI and XhoI and ligated into similarly digested pET26b vector. This construct was used to transform BL21(P-LysS) *E. coli*. Culture conditions, induction, and purification were carried out similar to those described for the m679 diabody in Example 2. Expression levels in the soluble fractions were estimated by BIAcore analysis using a HSG coupled sensor chip. The expression level of h679 diabody was 50 µg/L as compared to 1 µg/L for the wild type m679 diabody or 10 µg/L for m679I3Q diabody. The h679 diabody displayed comparable binding properties to the m679I3Q diabody with BIAcore analysis.

Example 9 - BS1.5H

Using the methods described in Example 6, the h679V_H and h679V_K domains were incorporated into the pET-ER vector with the V_H and V_K of hMN14 to make the fully humanized BS1.5H bispecific diabody construct. The di-cistronic expression vector was constructed through a series of sub-cloning procedures that are outlined in Figure 9. Initially, the V_K sequences of h679-scFv-L5 and hMN14-scFv-L5 were exchanged by excision with BamHI and XhoI to generate two intermediate constructs in pET26b. A DNA fragment containing the sequence h679V_H-L5-hMN14V_K, excised from a pET26b construct with NcoI and XhoI, was ligated into the same restriction sites in pET-ER vector to generate an intermediate clone (h679V_H-L5-hMN14V_K- pET-ER). A 900bp DNA fragment, which includes a ribosomal binding site in addition to the coding sequence for polypeptide 2 (below), was excised from hMN14V_H-L5-h679V_K- pET26b with XbaI and BpI. This fragment was ligated into the SpeI and BpI restriction sites of h679V_H-L5-hMN14V_K- pET-ER to create the final bispecific expression construct, BS1.5H. The di-cistronic expression cassette codes for two polypeptides that are arranged as follows:

Polypeptide 1

Pel B; h679V_H; GGGGS linker; hMN14V_K; 6 His

Polypeptide 2

Pel B; hMN14V_H; GGGGS linker; h679V_K; 6His

When this cassette is expressed in *E. coli*, some of the polypeptides fold and spontaneously form soluble bispecific diabodies.

The BS1.5H construct was used to transform *E. coli* (BL21-pLysS) cells. The recombinant BS1.5H protein was expressed and purified as described in Example 6. The level of soluble protein expression was 0.55 mg/L, about 10% higher than BS1.5. Size exclusion HPLC analysis of the purified BS1.5H yielded a single protein peak at 10.16 minutes (Fig 22). Comparatively, BS2 had a retention time of 10.04 minutes under identical conditions, indicating that BS1.5H polypeptides exclusively form diabodies. The bispecific (CEA/HSG) binding properties of BS1.5H were confirmed by BIAcore analysis (Fig 23). BS1.5H was pre-bound to a HSG-coupled sensor chip before injection of WI2 (hMN14-specific anti-idiotype MAb). As shown in Figure 23, injection of 60 ng of BS1.5H gave a relative response of 660 RU. Subsequent injection of 1 μ g of WI2 increased the signal by 760 RU. Injection of WI2 following pre-binding with 679 F(ab')₂ or without pre-binding yielded a negligible response. These data demonstrate that BS1.5H has the capability of binding HSG and CEA simultaneously. BS1.5H differs from BS1.5 by the humanization of the 679 moiety, which was accomplished by substitutions of 13 amino acid residues. To determine if the HSG binding affinity was affected by these changes, BIAcore binding curves for HSG binding of BS1.5H were compared with those of BS1.5 and BS2. As exemplified in Figure 24, the off rates for BS1.5H were very similar to those of BS1.5 and not BS2, which has lower HSG binding affinity. This was consistently the case over a range of analyte concentrations, demonstrating that the HSG binding affinity was largely unaffected by the humanization.

Example 10 - Linking Moiety / Hapten Conjugate for Carrier Molecule

The therapeutic agents may take the following form:

(Drug)_m-Linking Moiety-(Hapten)_n

The therapeutic agent comprises at least two haptens which are covalently linked via a peptidic, proteinaceous or non-proteinaceous moiety. Non-limiting examples of haptens are fluorescein isothiocyanate, vitamin B-12, DTPA (diethylenetriamine-pentaacetic acid) and DOTA (1,4,7,10-tetraazacyclododecanetetraacetic acid) residues.

This example relates to the preparation of carboxylesterase-DTPA conjugate. Two vials of rabbit liver carboxylesterase (about 8.5 mg protein content/vial) were reconstituted with 2.3 mL of 50 mM potassium phosphate buffer pH 7.5, and the solution was made 4.2 mM in DTPA using 0.1 mL of a 0.1 M stock solution of DTPA pH 6.7. The pH of the resultant solution was adjusted to be in the 7.7-7.8 range, and then reacted with 10 mg of cyclic DTPA dianhydride. After 1 h of stirring at the room temperature, the reaction mixture was passed through two successive SEC columns equilibrated in 0.1 M sodium phosphate pH 7.3. The eluate was further purified by preparative HPLC on a TSK G3000SW column using 0.2 M sodium phosphate pH 6.8, at 4 mL/min flow, as the eluent. The purified conjugate was made 0.1 M in sodium phosphate pH 6.8, and concentrated. The DTPA-to-carboxylesterase molar substitution ratio, determined by a metal-binding assay, was in the range of 2.95-to-1 to 4.43-to-1.

It will be apparent to those skilled in the art that various modifications and variations can be made to the compositions and processes of this invention. Thus, it is intended that the present invention cover such modifications and variations, provided they come within the scope of the appended claims and their equivalents.

The disclosure of all publications cited above are expressly incorporated herein by reference in their entireties to the same extent as if each were incorporated by reference individually.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A multivalent, multi-specific binding protein comprising a histamine-succinyl-glycyl (HSG) binding site having an affinity towards molecules containing a HSG moiety and a carcinoembryonic antigen (CEA) binding site having an affinity towards CEA,

wherein said HSG antigen binding site comprises a first and second polypeptide segment that must associate with each other to form said HSG antigen binding site, and

wherein said first polypeptide segment comprises the heavy chain complementarity-determining region (CDR) sequences: CDR1 IYTMS; CDR2 TLSGDGDDIYYPDSVKG; and CDR3 VRLGDWDFDV; and said second polypeptide segment comprises the light chain CDR sequences: CDR1 KSSQSLFNSRTRKNYLG; CDR2 WASTRES; and CDR3 TQVYYLCT of the 679 MAb.

2. The binding protein of claim 1, wherein said first polypeptide segment comprises a V_H polypeptide of 679 MAb, including residues 70-426 of Figure 25 and said second polypeptide segment comprises a V_K polypeptide of 679 MAb, including residues 442-780 of Figure 25.

3. The binding protein of claim 1, wherein said first polypeptide segment comprises a V_H polypeptide of h679 MAb, including residues 70-426 of Figure 36, and said second polypeptide segment comprises a V_K polypeptide of h679 MAb, including residues 442-780 of Figure 36.

4. The binding protein of claim 1, wherein said first polypeptide segment comprises a V_H polypeptide of 679 V_H I3Q, including residues 70-426 of Figure 26, and said second polypeptide segment comprises a V_K polypeptide of 679 MAb, including residues 442-780 of Figure 25.

5. The binding protein of claim 1, wherein said first polypeptide segment comprises a V_H polypeptide of 679 V_H I3Q, including residues 70-426 of Figure 26 and said second polypeptide segment comprises a V_K polypeptide of 679 V_K C101S, including residues 442-780 of Figure 27.

6. The binding protein of claim 1, wherein said CEA antigen binding site comprises a third and fourth polypeptide segment that must associate with each other to form said CEA antigen binding site.
7. The binding protein of claim 6, wherein said third polypeptide segment comprises a V_H polypeptide of hMN14 MAb, including residues 70-423 of Figure 29, and said fourth polypeptide segment comprises a V_K polypeptide of hMN14 MAb, including residues 439-759 of Figure 29.
8. The binding protein of claim 6, wherein said first and third polypeptide segments are connected by a first linker and said second and fourth polypeptide segments are connected by a second linker.
9. The binding protein of claim 8, wherein said first linker and said second linker each comprise zero to five amino acid residues.
10. The binding protein of claim 6, wherein said binding protein is a diabody.
11. The binding protein of claim 10 wherein said diabody is selected from the group consisting of a diabody comprising amino acid sequences shown in Figure 30 and Figure 31, a diabody comprising amino acid sequences shown in Figure 32 and Figure 33, a diabody comprising amino acid sequences shown in Figure 34 and Figure 35, and a diabody comprising amino acid sequences shown in Figure 37 and Figure 38.
12. The binding protein of claim 6, wherein said first, second, third and fourth polypeptide segments are each encoded by a first, second, third and fourth cDNA, respectively.
13. The binding protein of claim 12, wherein said first cDNA comprises nucleotide sequences shown in Figure 30 and Figure 31, wherein said second cDNA comprises nucleotide sequences shown in Figure 32 and Figure 33, wherein said third cDNA comprises nucleotide sequences shown in Figure 34 and Figure 35, and wherein said fourth cDNA comprises nucleotide sequences shown in Figure 37 and Figure 38.

14. The binding protein of claim 12, wherein said first and third cDNAs are contained on a single nucleic acid molecule.
15. The binding protein of claim 12, wherein said second and fourth cDNAs are contained on a single nucleic acid molecule.
16. The binding protein of claim 12, wherein said first, second, third and fourth cDNAs are on a single expression cassette.
17. The binding protein of claim 16, wherein said expression cassette is contained in a plasmid.
18. A host cell comprising the plasmid of claim 17.
19. A method of producing a binding protein, comprising culturing the host cell of claim 18 in a suitable medium, and separating said binding protein from said media.
20. A method of delivering a diagnostic agent, a therapeutic agent, or a combination thereof to a target, comprising:
 - a. administering to a subject in need thereof the binding protein of claim 1;
 - b. waiting a sufficient amount of time for an amount of the non-binding protein to clear the subject's blood stream; and
 - c. administering to said subject a carrier molecule comprising a diagnostic agent, a therapeutic agent, or a combination thereof, that binds to a binding site of the binding protein.
21. The method of claim 20, wherein said carrier molecule binds to more than one binding site of the binding protein.

22. The method of claim 20, wherein said therapeutic agent is selected from the group comprising, drugs, toxins, cytokines, hormones, growth factors, conjugates and radionuclides.
23. A method of detecting or treating a human disorder, comprising:
 - a. administering to a subject in need thereof, the binding protein of claim 1;
 - b. waiting a sufficient amount of time for an amount of the non-binding protein to clear the subject's blood stream; and
 - c. administering to said subject a carrier molecule comprising a diagnostic agent, a therapeutic agent, or a combination thereof, that binds to a binding site of the binding protein.
24. The method of claim 23, wherein said human disorder is selected from the group comprising cancer, autoimmune diseases, infectious diseases, cardiovascular diseases and inflammatory diseases.
25. A kit for delivering a diagnostic agent, a therapeutic agent, or a combination thereof to a target, comprising the multivalent, multispecific binding protein of claim 1.
26. The binding protein according to any one of claim 1 to 17, or the host cell according to claim 18, or the method according to any one of claims 19 to 24, or the kit according to claim 25, substantially as hereinbefore described with reference to the figures and/or examples.

679scFv polypeptide

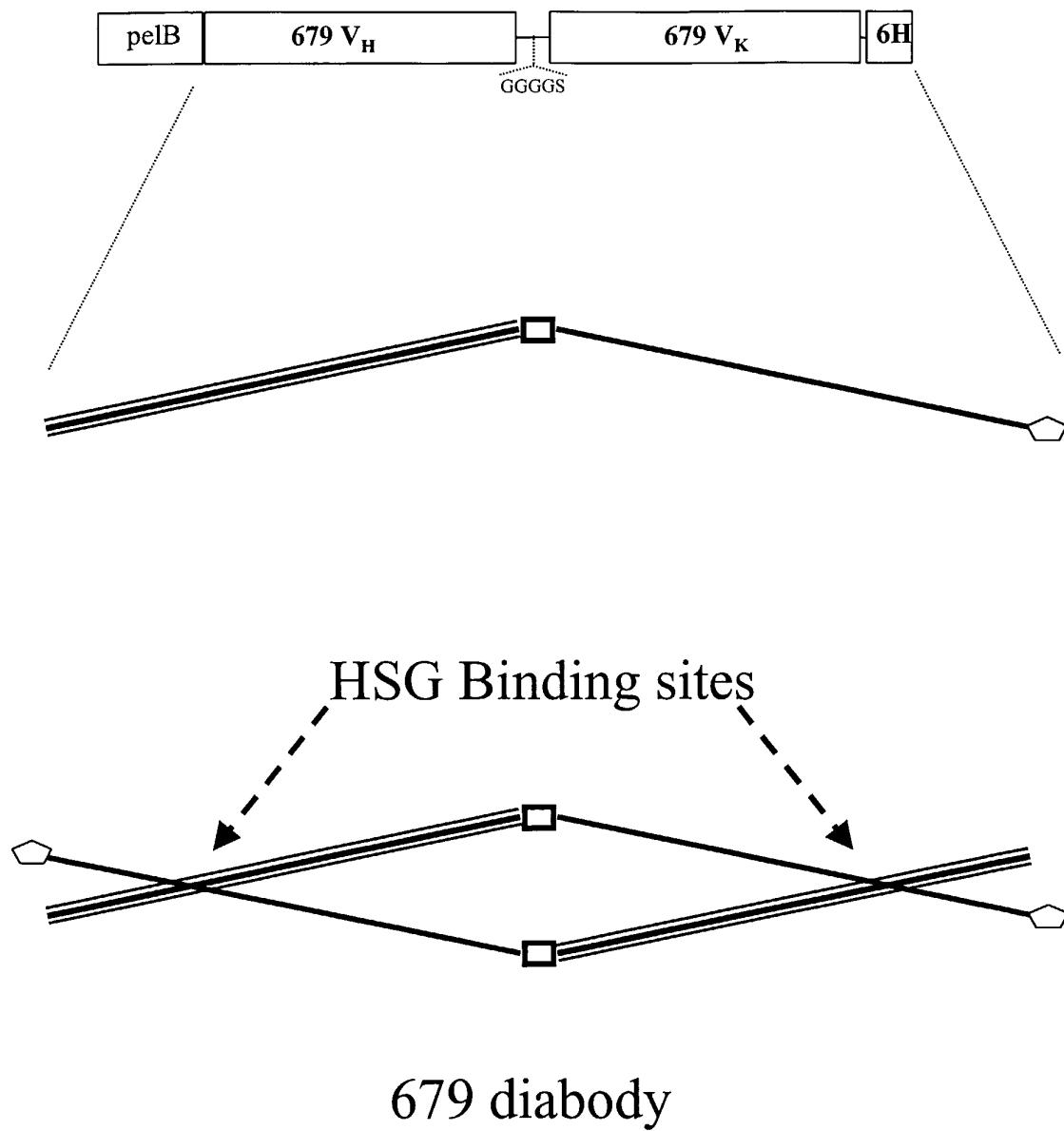
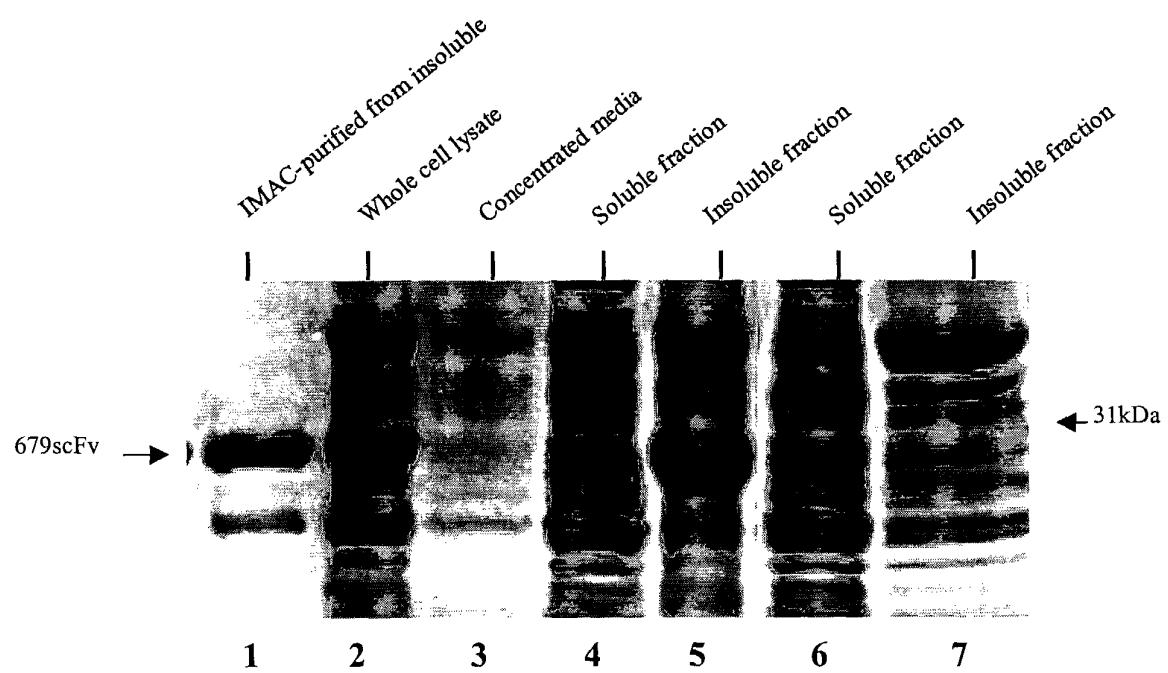
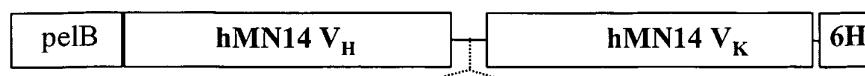


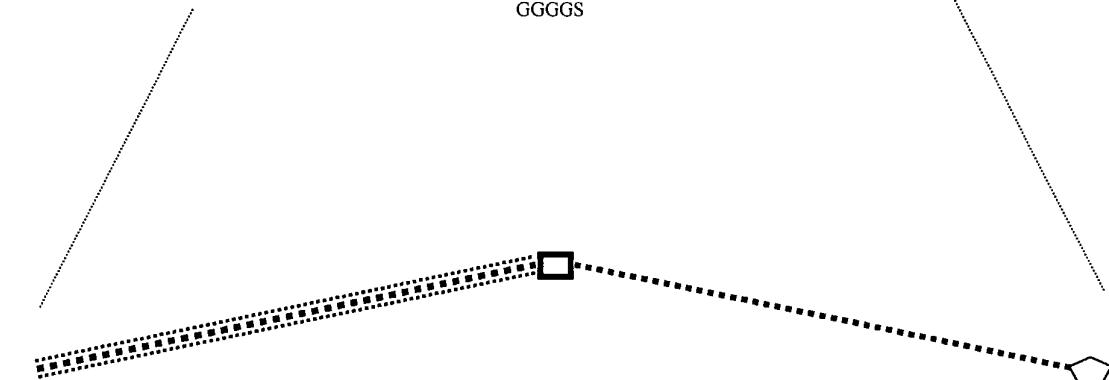
FIGURE 1

**FIGURE 2**

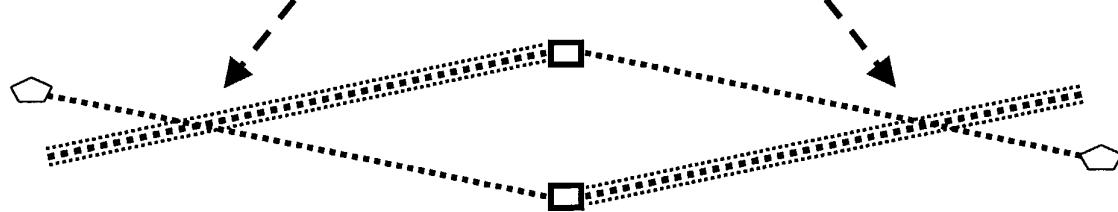
hMN14scFv polypeptide



GGGGS



CEA Binding sites



hMN14 diabody

FIGURE 3

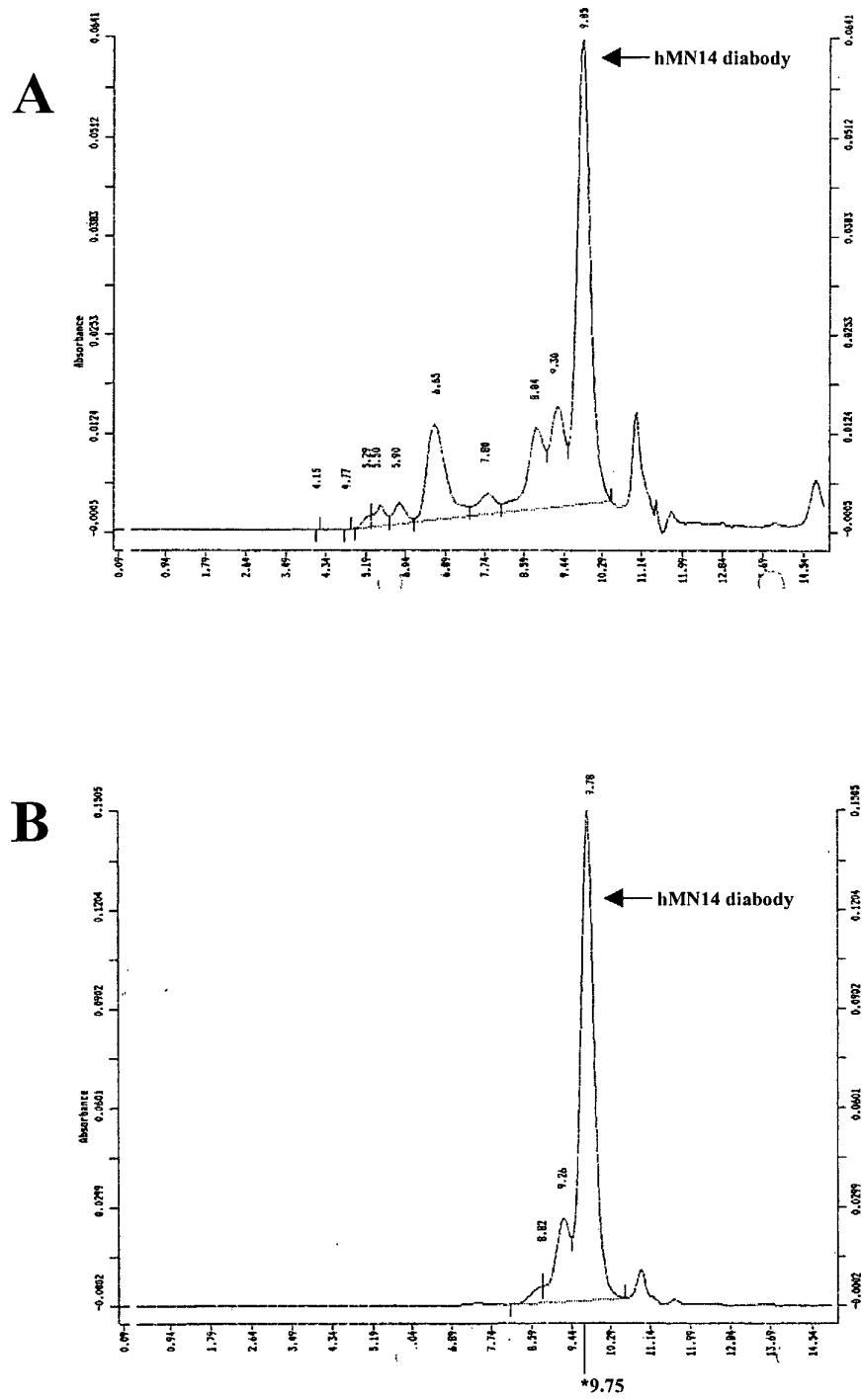


FIGURE 4

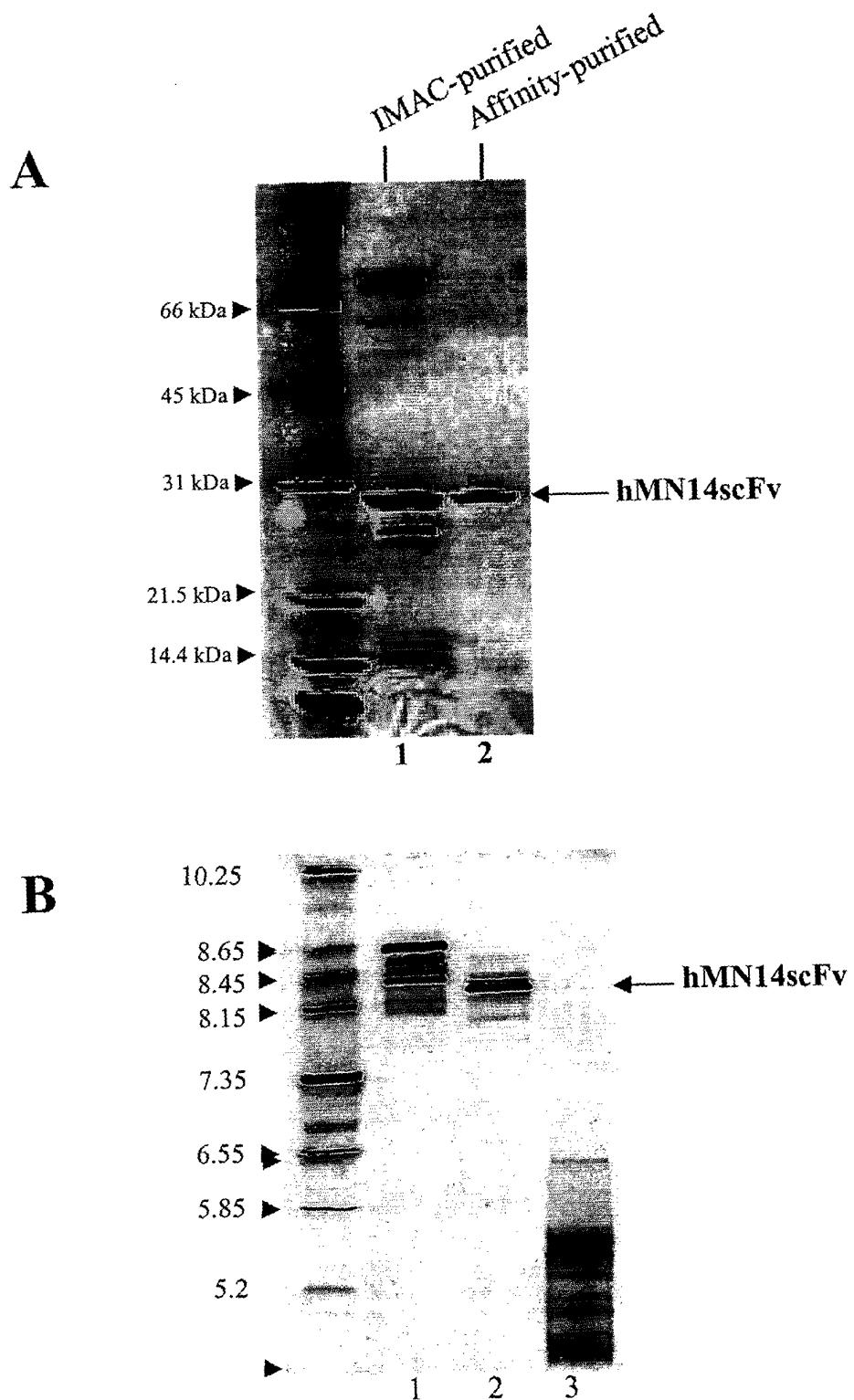


FIGURE 5

^{131}I -hMN-14 diabody
tumor and blood uptake

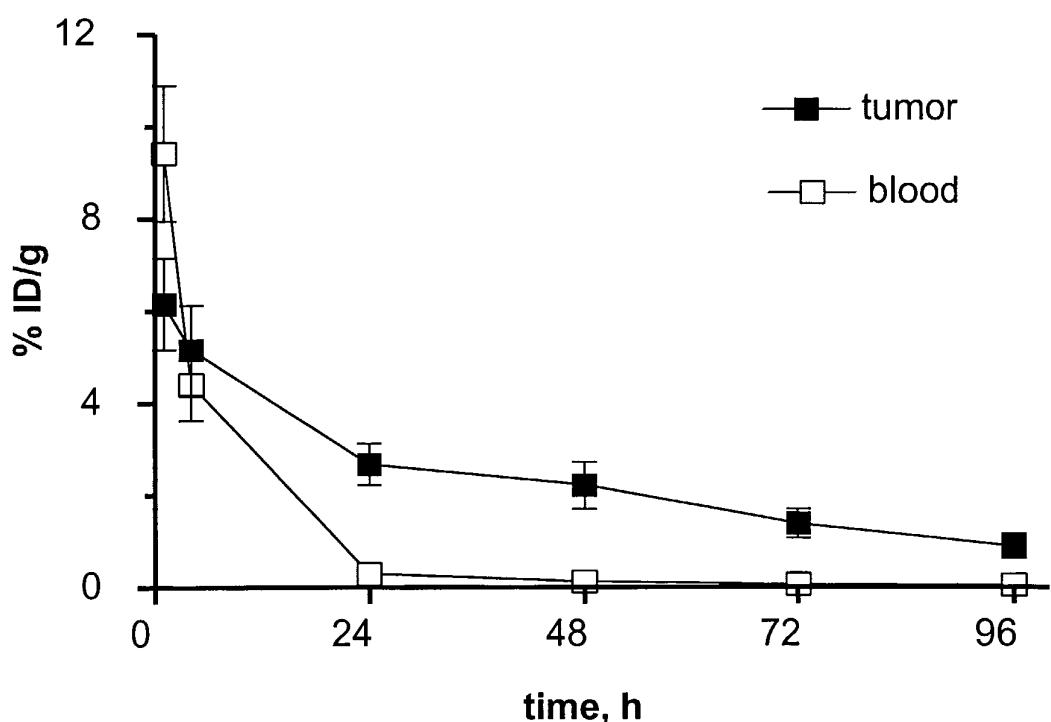


FIGURE 6

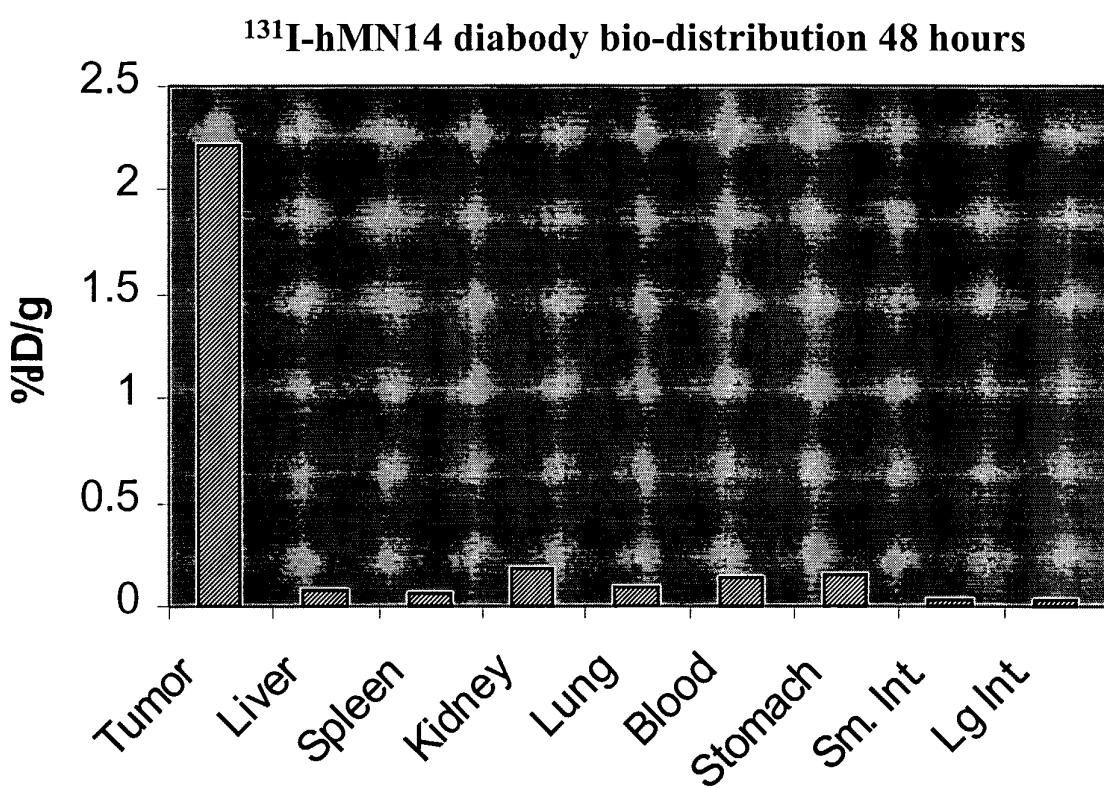
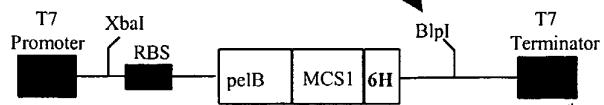
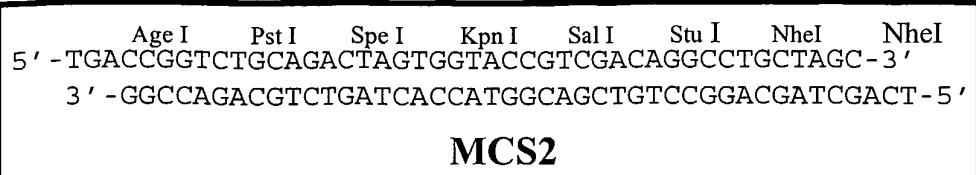
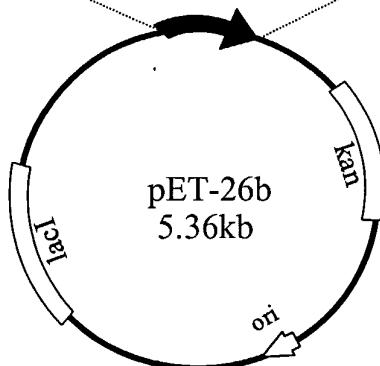
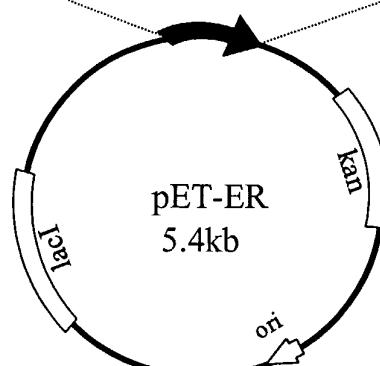
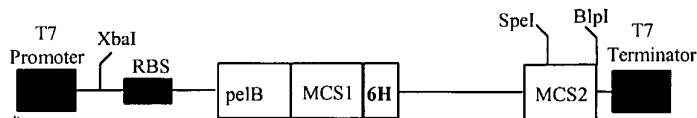
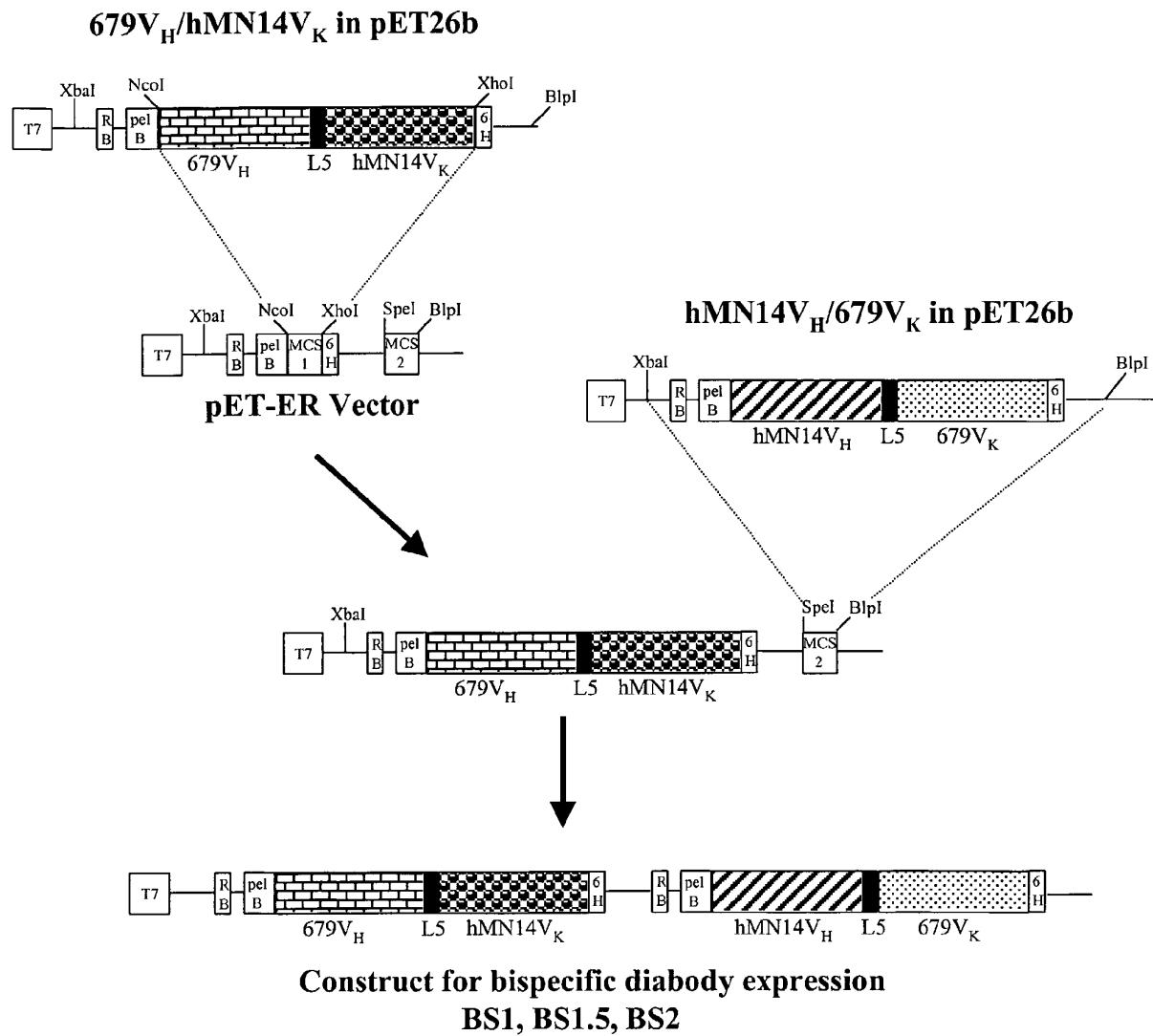
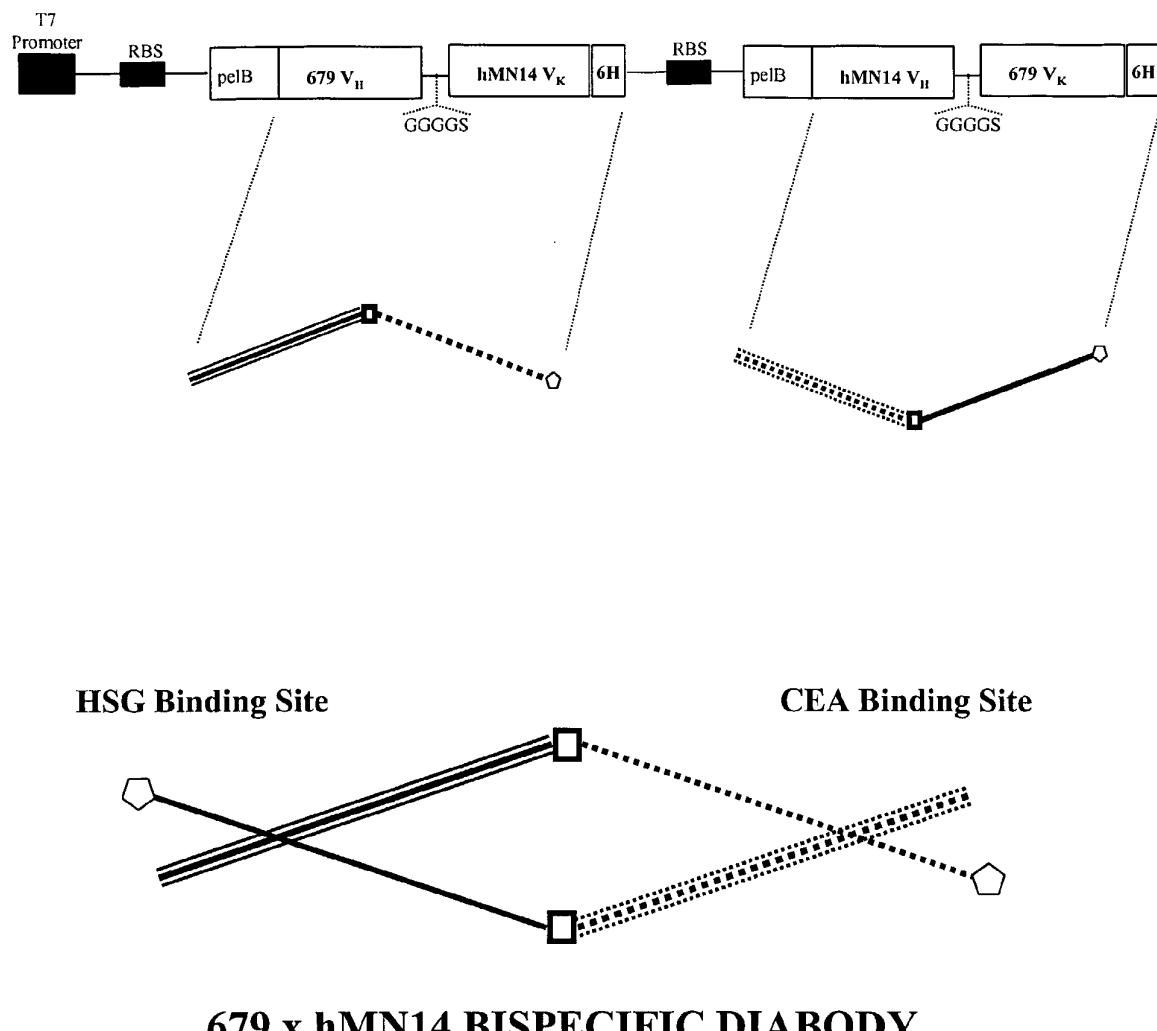
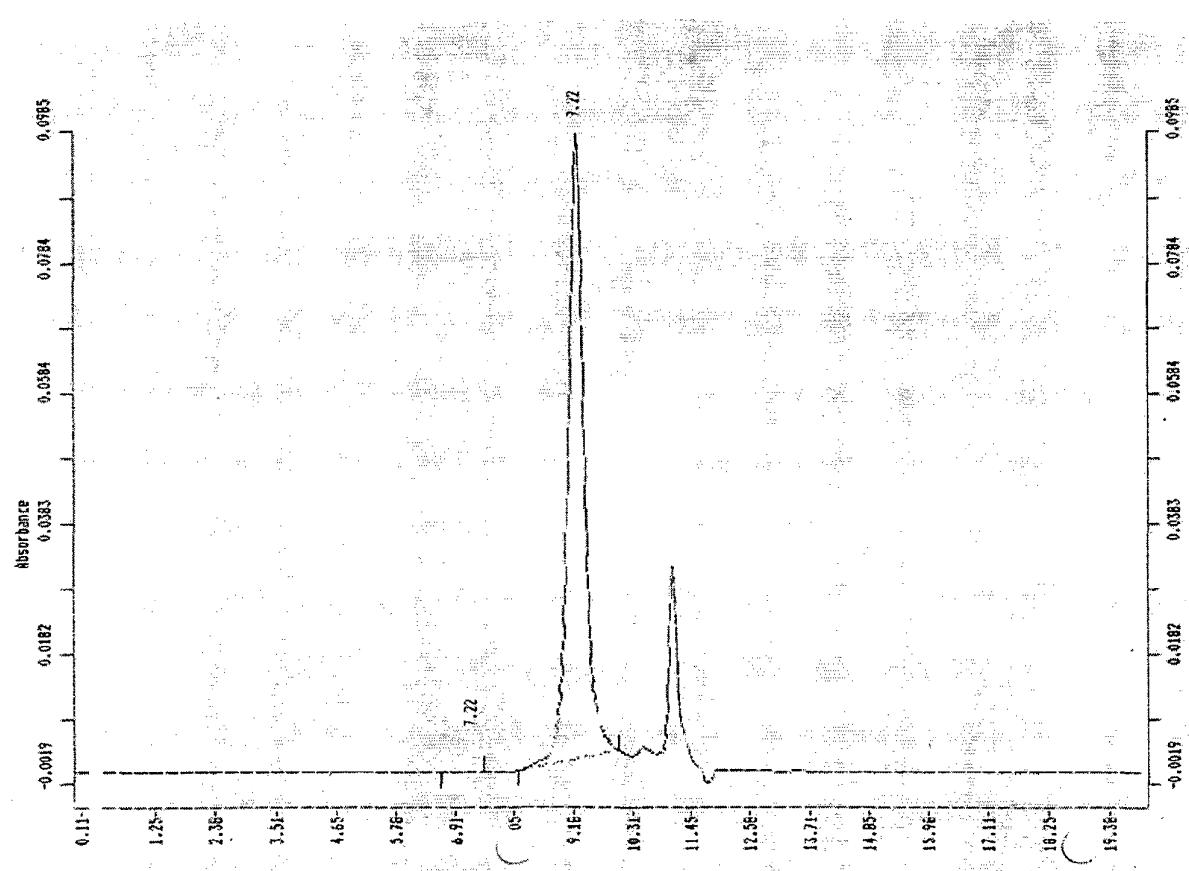


FIGURE 7

A**B****C****FIGURE 8**

**FIGURE 9**

**FIGURE 10**

**FIGURE 11**

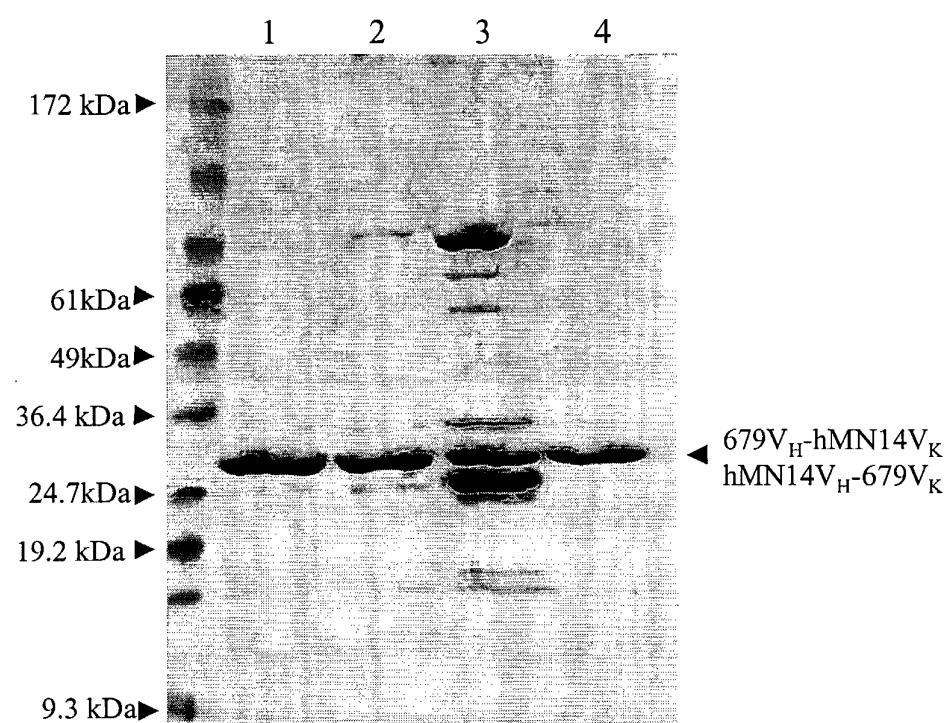
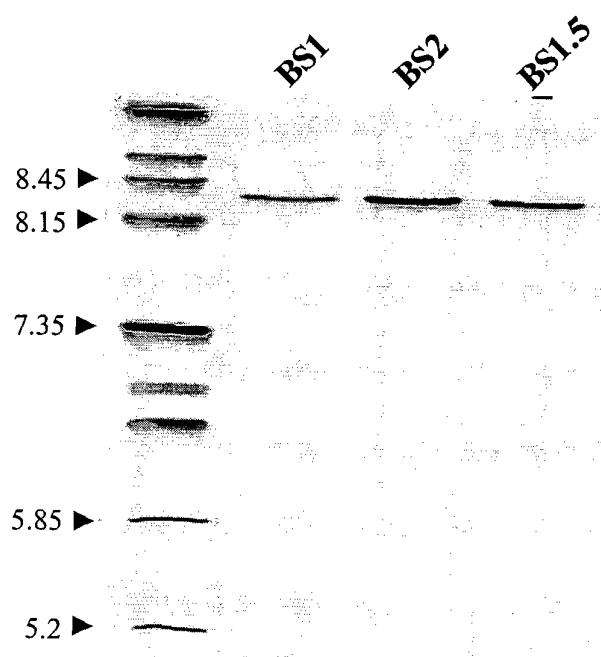


FIGURE 12

**FIGURE 13**

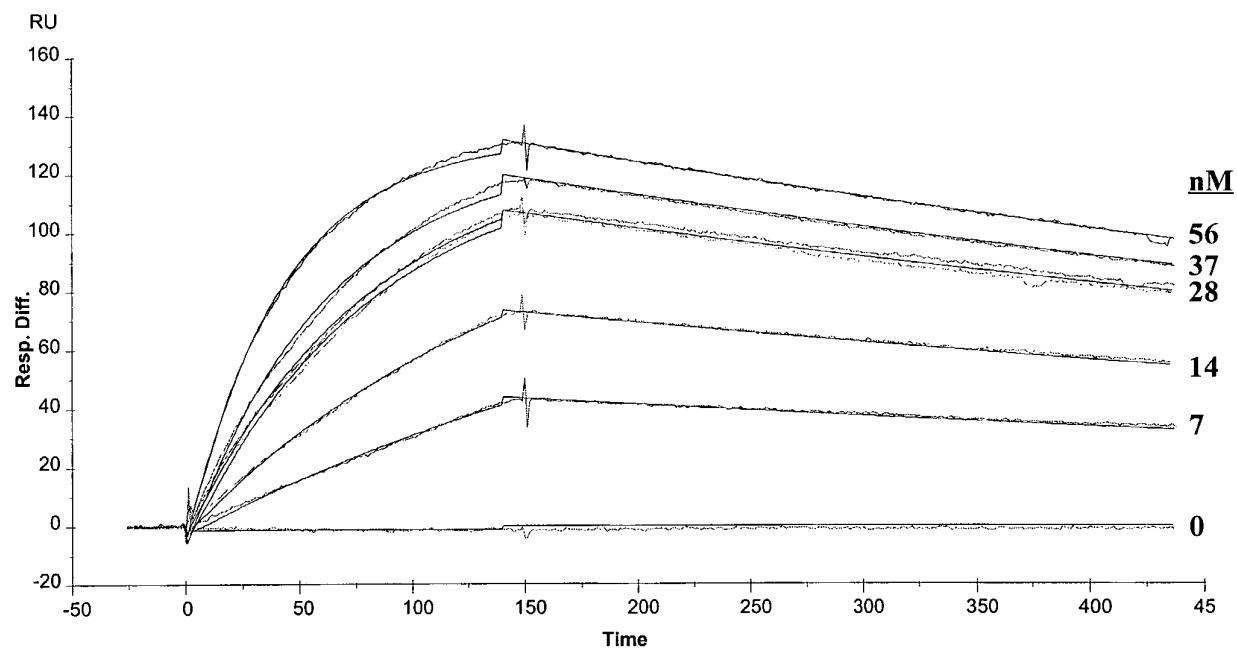
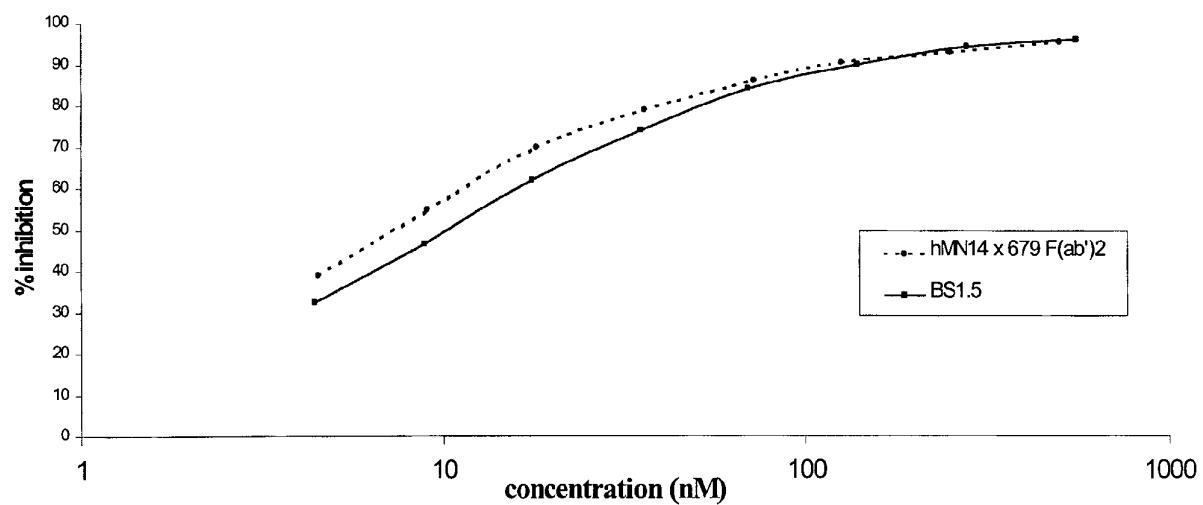
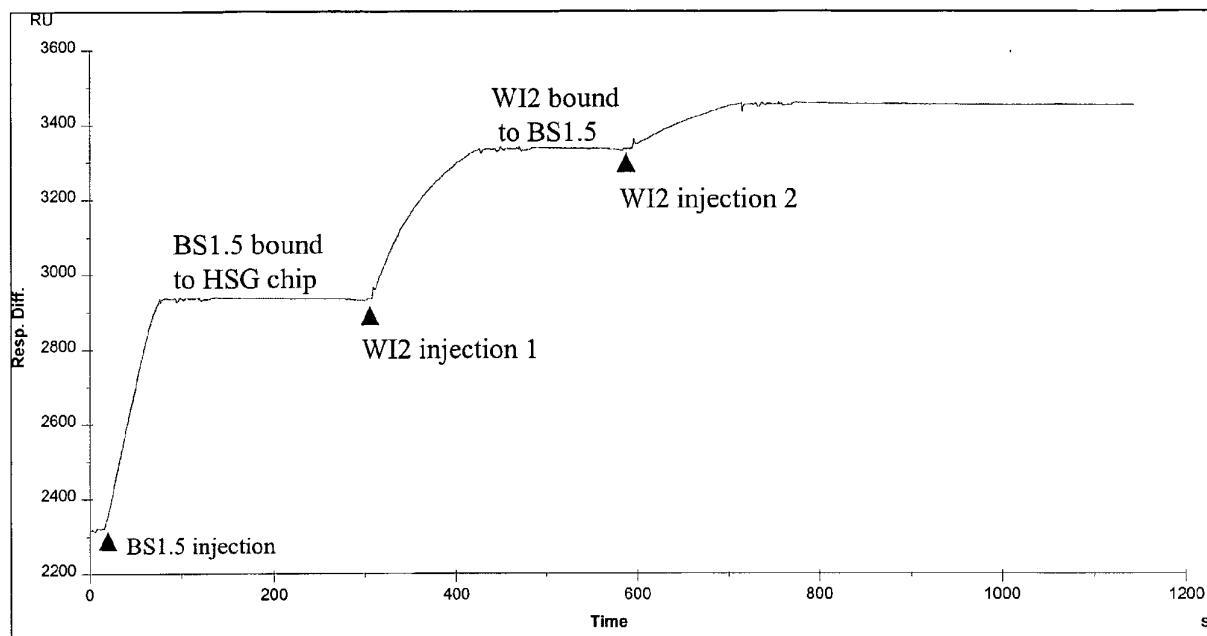


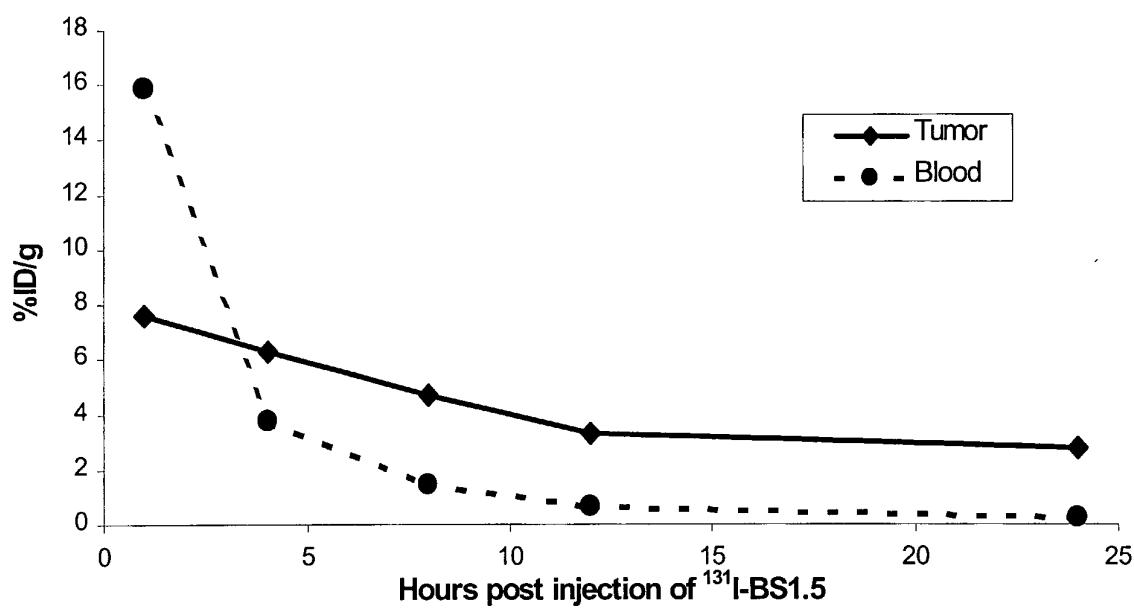
FIGURE 14

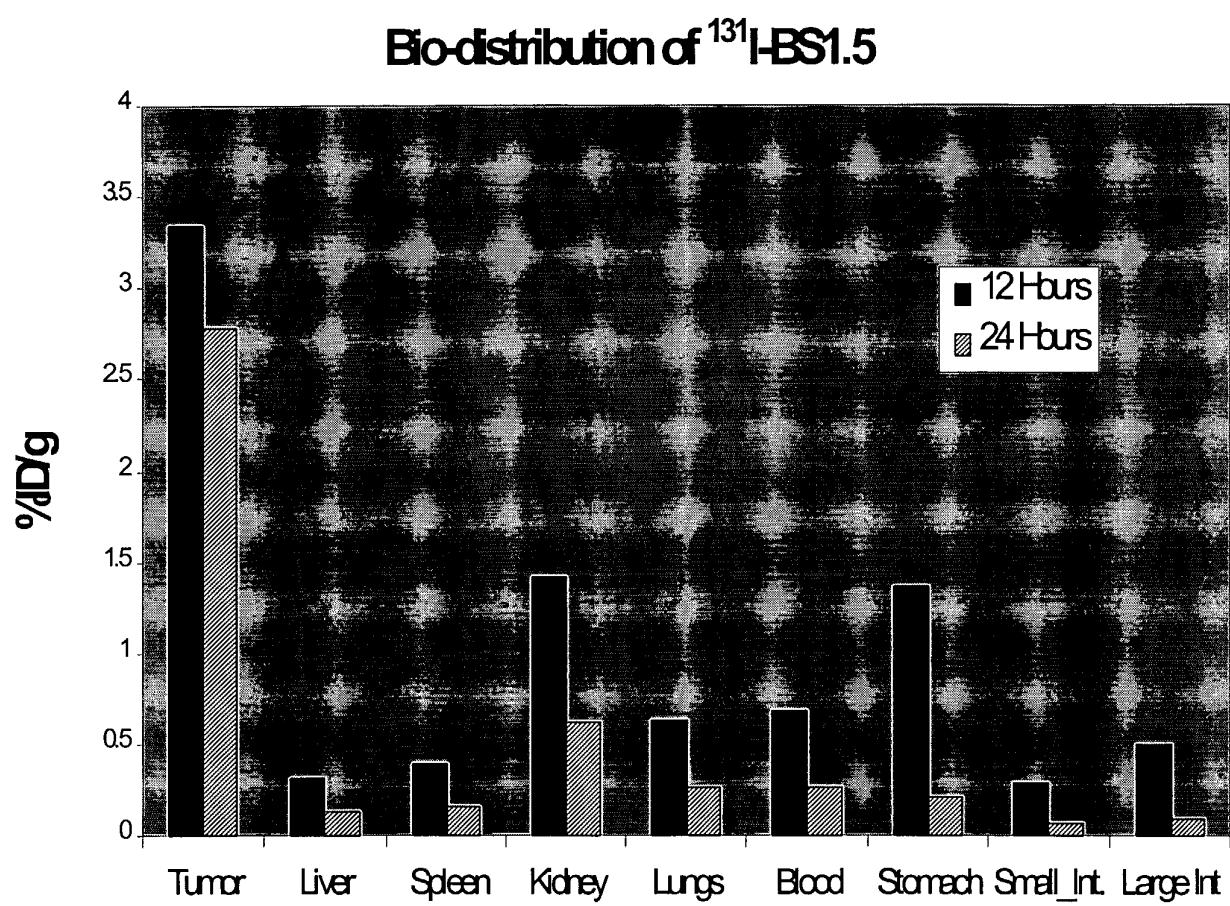
Competition for CEA binding with HRP-hMN14 IgG

$$\% \text{ inhibition} = 1 - \frac{\text{sample OD}}{\text{non-competition OD}}$$

FIGURE 15

Simultaneous bi-specific binding of BS1.5**FIGURE 16**

**FIGURE 17**

**FIGURE 18**

Bio-distribution of ^{111}In -IMP241
with BS1.5 pre-targeting and 12 hour clearance

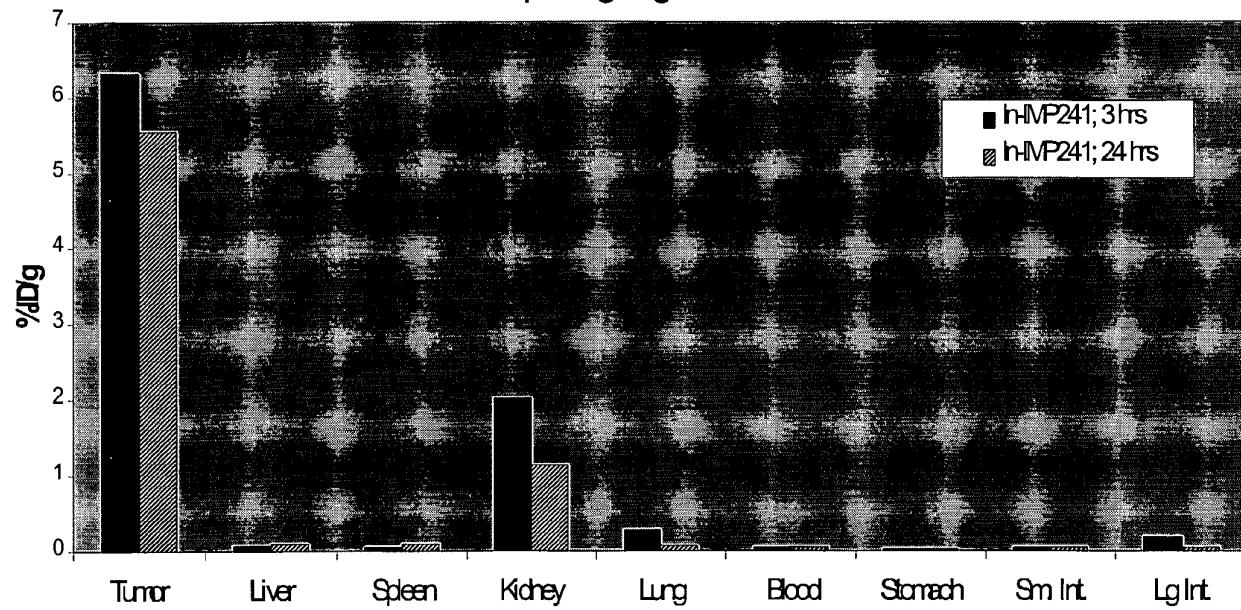


FIGURE 19

	V_HFR-1	CDR-H1	V_HFR-2
m679VH	1 EVILVESGGDLVKGPGSLKLSCAAASGFTFS 11 20 30	33 IYTMS	36 41 49 WLRQTPERKLEWVA ▼ ▼
h679VH	EVQLVESGGDLVKGPGSLKLSCAAASGFTFS	IYTMS	WLRQTPGKGLEWVA

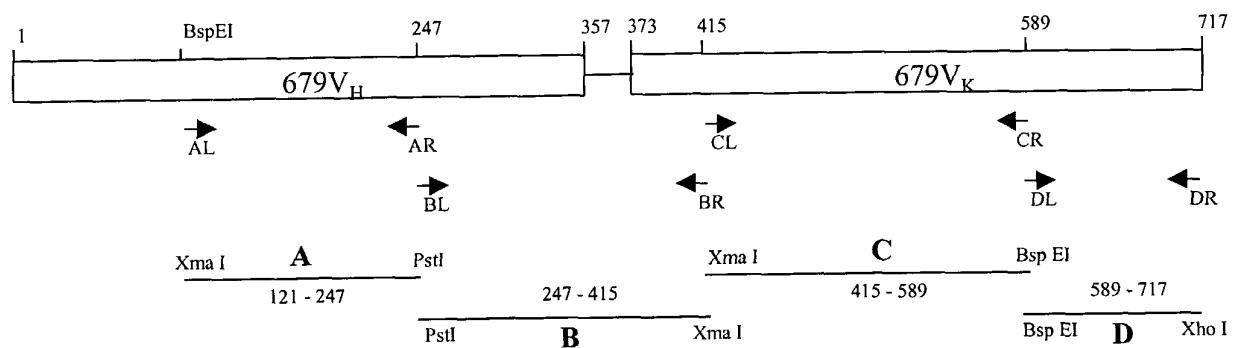
CDR-H2				V _H FR-3			
m679VH	52A	61	65	66	71	81	82 abc
h679VH	TLSGDGDDIYYPDSVKG			RFTISRDNAKNLYLQMNSLRSADTALYYCAR			

	CDR-H3 ₁₀₀	V_HFR-4
m679VH	⁹⁵ VRLGDWDFDV	¹⁰³ WGQGTTVSVSS
h679VH	VRLGDWDFDV	WGQGTTVSVSS

	V _k FR-1	CDR-K1	V _k FR-2	CDR-K2
679VK	1 DIVMSQSPSSLAVSPGEKVTMTC 11 ▼ 21	24 ab cd ef 34 KSSQSLFNSRTRKNYLG	41 WYQQKPGQSPKLLIY 49 WASTRES	53
h679VK	DIVMTQSPSSLAVSPGERVTLTC	KSSQSLFNSRTRKNYLG	WYQQKPGQSPKLLIY WASTRES	

	V_kFR-3	CDR-K3	V_kFR-4
m679VK	57 61 71 81 88 GVPDRFTGSGSGTDFTLTINSVQSEDLAVYYC ▼ ▼ ▼	TQVYLYCT	98 108 FGAGTKLELKR
h679VK	GVPDRFTGSGSGTDFTLTINSVQSEDLAVYYC	TQVYLYCT	FGAGTKLELKR

Figure 20

**Figure 21**

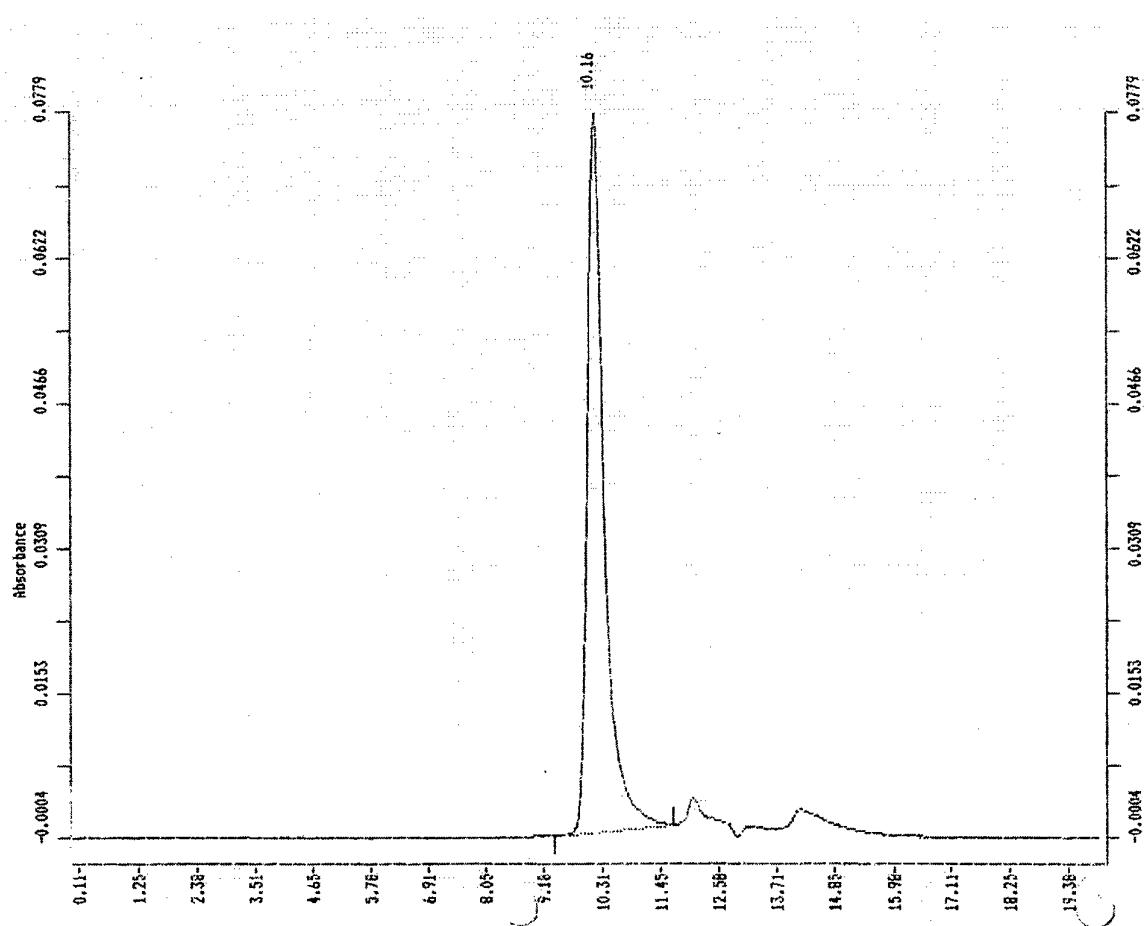


Figure 22

Simultaneous bi-specific binding of BS1.5H

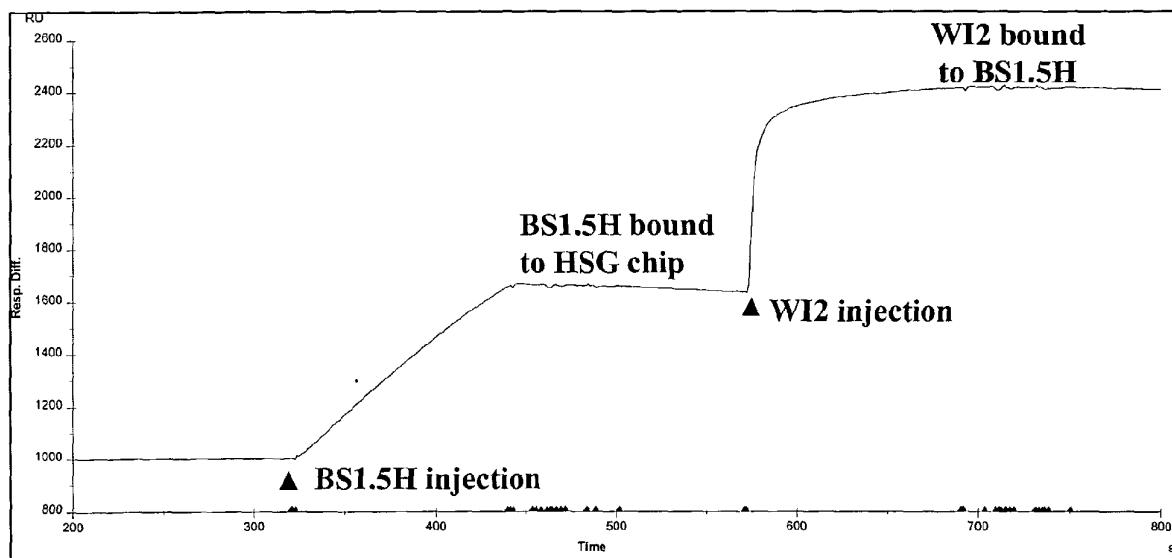


Figure 23

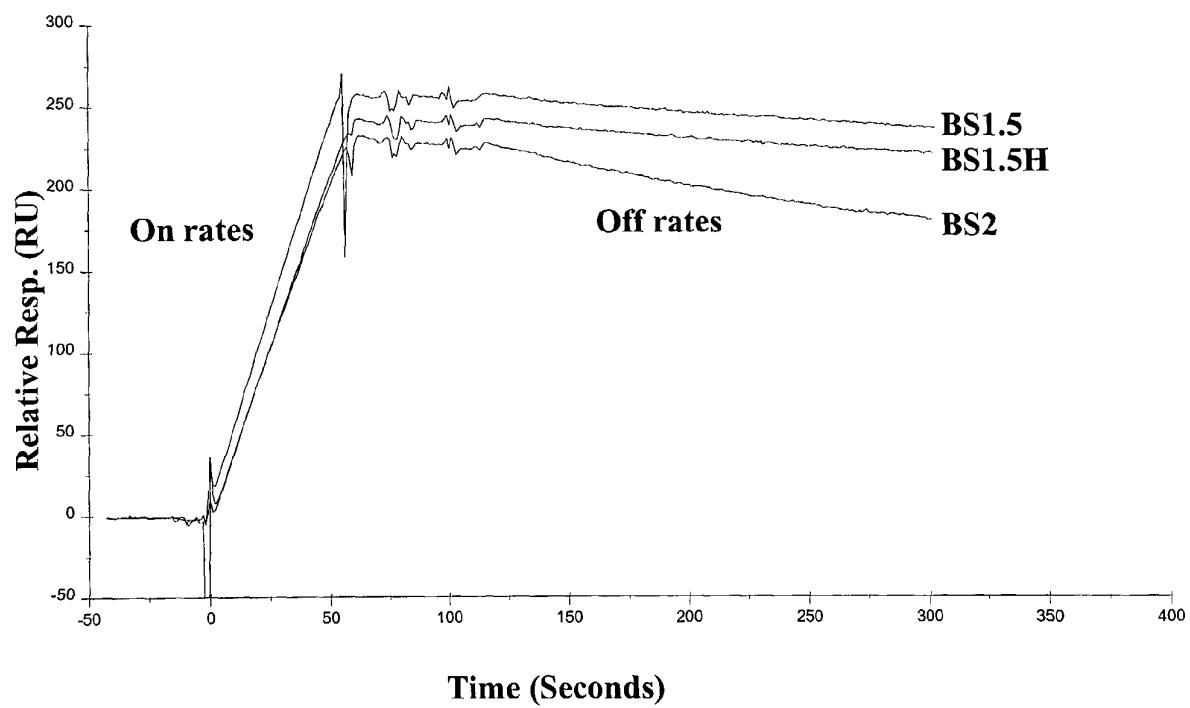


Figure 24

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG ATC CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly
 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GAT GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala
 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly
 433 GGC GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG
 Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
 481 TCA CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG
 Ser Pro Gly Glu Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu
 529 TTC AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA
 Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys
 577 CCA GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
 625 TCT GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe
 673 ACT CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC
 Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr
 721 TGC ACT CAA GTT TAT TAC CTG TGC ACG TTC GGT GCT GGG ACC AAG CTG
 Cys Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu
 769 GAG CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Glu Leu Lys Arg Leu Glu His His His His His His His ---

Nucleic acids and encoded amino acids for 679-scF_v-L5

Figure 25

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG CAG CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly

 433 GGC GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG
 Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val

 481 TCA CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG
 Ser Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu

 529 TTC AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA
 Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys

 577 CCA GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu

 625 TCT GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe

 673 ACT CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC
 Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr

 721 TGC ACT CAA GTT TAT TAC CTG TGC ACG TTC GGT GCT GGG ACC AAG CTG
 Cys Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu

 769 GAG CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Glu Leu Lys Arg Leu Glu His His His His His His His ---

Nucleic acids and encoded amino acids for 679-I3Q

Figure 26

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG ATC CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly

 433 GGC GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG
 Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val

 481 TCA CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG
 Ser Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu

 529 TTC AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA
 Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys

 577 CCA GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu

 625 TCT GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe

 673 ACT CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC
 Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr

 721 TGC ACT CAA GTT TAT TAC CTG **AGC** ACG TTC GGT GCT GGG ACC AAG CTG
 Cys Thr Gln Val Tyr Tyr Leu **Ser** Thr Phe Gly Ala Gly Thr Lys Leu

 769 GAG CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Glu Leu Lys Arg Leu Glu His His His His His His ---

Nucleic acids and encoded amino acids for 679-C101S

Figure 27

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG CAG CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Gly Gly

 433 GGC GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG
 Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val

 481 TCA CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG
 Ser Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu

 529 TTC AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA
 Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys

 577 CCA GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu

 625 TCT GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe

 673 ACT CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC
 Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr

 721 TGC ACT CAA GTT TAT TAT CTG AGC ACG TTC GGT GCT GGG ACC AAG CTG
 Cys Thr Gln Val Tyr Tyr Leu Ser Thr Phe Gly Ala Gly Thr Lys Leu

 769 GAG CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Glu Leu Lys Arg Leu Glu His His His His His His His ---

Coding sequence and encoded amino acids for 679 I3Q/C101S

Figure 28

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAG GTC CAA CTG GTG GAG AGC GGT GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GGT GTT GTG CAA CCT GGC CGG TCC CTG CGC CTG TCC TGC TCC GCA TCT
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser

 145 GGC TTC GAT TTC ACC ACA TAT TGG ATG AGT TGG GTG AGA CAG GCA CCT
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro

 193 GGA AAA GGT CTT GAG TGG ATT GGA GAA ATT CAT CCA GAT AGC AGT ACG
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr

 241 ATT AAC TAT GCG CCG TCT CTA AAG GAT AGA TTT ACA ATA TCG CGA GAC
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp

 289 AAC GCC AAG AAC ACA TTG TTC CTG CAA ATG GAC AGC CTG AGA CCC GAA
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu

 337 GAC ACC GGG GTC TAT TTT TGT GCA AGC CTT TAC TTC GGC TTC CCC TGG
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp

 385 TTT GCT TAT TGG GGC CAA GGG ACC CCG GTC ACC GTC TCC GGA GGC GGT
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly

 433 GGA TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC
 Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser

 481 GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG GAT GTG GGT
 Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly

 529 ACT TCT GTA GCC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG
 Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu

 577 CTG ATC TAC TGG ACA TCC ACC CGG CAC ACT GGT GTG CCA AGC AGA TTC
 Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe

 625 AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu

 673 CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AGC CTC TAT
 Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu Tyr

 721 CGG TCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT CTC GAG CAC
 Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu His

 769 CAC CAC CAC CAC CAC TGA
 His His His His ---

Nucleic acids and encoded amino acids for hMN14-scF_v-L5

Figure 29

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG ATC CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly

 433 GGC GGA TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

 481 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG GAT GTG
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val

 529 GGT ACT TCT GTA GCC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG
 Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

 577 CTG CTG ATC TAC TGG ACA TCC ACC CGG CAC ACT GGT GTG CCA AGC AGA
 Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

 625 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC
 Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

 673 CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AGC CTC
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu

 721 TAT CGG TCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT CTC GAG
 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu

 769 CAC CAC CAC CAC CAC TGA
 His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #1 of BS1
(679 x hMN14 bispecific diabody)**

Figure 30

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAG GTC CAA CTG GTG GAG AGC GGT GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GGT GTT GTG CAA CCT GGC CGG TCC CTG CGC CTG TCC TGC TCC GCA TCT
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser

 145 GGC TTC GAT TTC ACC ACA TAT TGG ATG AGT TGG GTG AGA CAG GCA CCT
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro

 193 GGA AAA GGT CTT GAG TGG ATT GGA GAA ATT CAT CCA GAT AGC AGT ACG
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr

 241 ATT AAC TAT GCG CCG TCT CTA AAG GAT AGA TTT ACA ATA TCG CGA GAC
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp

 289 AAC GCC AAG AAC ACA TTG TTC CTG CAA ATG GAC AGC CTG AGA CCC GAA
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu

 337 GAC ACC GGG GTC TAT TTT TGT GCA AGC CTT TAC TTC GGC TTC CCC TGG
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp

 385 TTT GCT TAT TGG GGC CAA GGG ACC CCG GTC ACC GTC TCC GGA GGC GGT
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly

 433 GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG TCA
 Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser

 481 CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG TTC
 Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe

 529 AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA CCA
 Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

 577 GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA TCT
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser

 625 GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr

 673 CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC TGC
 Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys

 721 ACT CAA GTT TAT TAT CTG TGC ACG TTC GGT GCT GGG ACC AAG CTG GAG
 Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu

 769 CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Leu Lys Arg Leu Glu His His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #2 of BS1
(679 x hMN14 bispecific diabody)**

Figure 31

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG CAG CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GAC GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly

 433 GGC GGA TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

 481 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG GAT GTG
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val

 529 GGT ACT TCT GTA GCC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG
 Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

 577 CTG CTG ATC TAC TGG ACA TCC ACC CCG CAC ACT GGT GTG CCA AGC AGA
 Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

 625 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC
 Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

 673 CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AGC CTC
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Cys Gln Gln Tyr Ser Leu

 721 TAT CGG TCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT CTC GAG
 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu

 769 CAC CAC CAC CAC CAC TGA
 His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #1 of BS1.5
(679 x hMN14 bispecific diabody)**

Figure 32

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAG GTC CAA CTG GTG GAG AGC GGT GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GGT GTT GTG CAA CCT GGC CGG TCC CTG CGC CTG TCC TGC TCC GCA TCT
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser

 145 GGC TTC GAT TTC ACC ACA TAT TGG ATG AGT TGG GTG AGA CAG GCA CCT
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro

 193 GGA AAA GGT CTT GAG TGG ATT GGA GAA ATT CAT CCA GAT AGC AGT ACG
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr

 241 ATT AAC TAT GCG CCG TCT CTA AAG GAT AGA TTT ACA ATA TCG CGA GAC
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp

 289 AAC GCC AAG AAC ACA TTG TTC CTG CAA ATG GAC AGC CTG AGA CCC GAA
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu

 337 GAC ACC GGG GTC TAT TTT TGT GCA AGC CTT TAC TTC GGC TTC CCC TGG
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp

 385 TTT GCT TAT TGG GGC CAA GGG ACC CCG GTC ACC GTC TCC GGA GGC GGT
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly

 433 GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG TCA
 Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser

 481 CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG TTC
 Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe

 529 AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA CCA
 Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

 577 GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA TCT
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser

 625 GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr

 673 CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC TGC
 Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys

 721 ACT CAA GTT TAT TAT CTG TGC ACG TTC GGT GCT GGG ACC AAG CTG GAG
 Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu

 769 CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Leu Lys Arg Leu Glu His His His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #2 of BS1.5
(679 x hMN14 bispecific diabody)**

Figure 33

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG **CAG** CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val **Gln** Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GAA AAG AGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AAC CTA TAT CTG CAA ATG AAC AGT CTA AGG TCT GCG
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly

 433 GGC GGA TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

 481 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG GAT GTG
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val

 529 GGT ACT TCT GTA GCC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG
 Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

 577 CTG CTG ATC TAC TGG ACA TCC ACC CGG CAC ACT GGT GTG CCA AGC AGA
 Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

 625 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC
 Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

 673 CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AGC CTC
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu

 721 TAT CGG TCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT CTC GAG
 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu

 769 CAC CAC CAC CAC CAC CAC TGA
 His His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #1 of BS2
(679 x hMN14 bispecific diabody)**

Figure 34

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAG GTC CAA CTG CTG GAG AGC GGT GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GGT GTT GTG CAA CCT GGC CGG TCC CTG CGC CTG TCC TGC TCC GCA TCT
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser

 145 GGC TTC GAT TTC ACC ACA TAT TGG ATG AGT TGG GTG AGA CAG GCA CCT
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro

 193 GGA AAA GGT CTT GAG TGG ATT GGA GAA ATT CAT CCA GAT AGC AGT ACG
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr

 241 ATT AAC TAT GCG CCG TCT CTA AAG GAT AGA TTT ACA ATA TCG CGA GAC
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp

 289 AAC GCC AAG AAC ACA TTG TTC CTG CAA ATG GAC AGC CTG AGA CCC GAA
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu

 337 GAC ACC GGG GTC TAT TTT TGT GCA AGC CTT TAC TTC GGC TTC CCC TGG
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp

 385 TTT GCT TAT TGG GGC CAA GGG ACC CCG GTC ACC GTC TCC GGA GGC GGT
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly

 433 GGA TCC GAC ATT GTG ATG TCA CAA TCT CCA TCC TCC CTG GCT GTG TCA
 Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser

 481 CCA GGA GAG AAG GTC ACT ATG ACC TGC AAA TCC AGT CAG AGT CTG TTC
 Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe

 529 AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA CCA
 Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

 577 GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA TCT
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser

 625 GGG GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr

 673 CTC ACC ATC AAC AGT GTG CAG TCT GAA GAC CTG GCA GTT TAT TAC TGC
 Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys

 721 ACT CAA GTT TAT TAT CTG AGC ACG TTC GGT GCT GGG ACC AAG CTG GAG
 Thr Gln Val Tyr Tyr Leu Ser Thr Phe Gly Ala Gly Thr Lys Leu Glu

 769 CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Leu Lys Arg Leu Glu His His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #2 of BS2
(679 x hMN14 bispecific diabody)**

Figure 35

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG CAG CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GGA AAG GGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AGC CTA TAT CTG CAG ATG AAC AGT CTA AGG GCT GAG
 Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly

 433 GGC GGA TCC GAC ATT GTG ATG ACA CAA TCT CCA TCC TCC CTG GCT GTG
 Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val

 481 TCA CCC GGG GAG AGG GTC ACT CTG ACC TGC AAA TCC AGT CAG AGT CTG
 Ser Pro Gly Glu Arg Val Thr Leu Thr Cys Lys Ser Ser Gln Ser Leu

 529 TTC AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA
 Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys

 577 CCA GGG CAG CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu

 625 TCT GGG GTC CCT GAT CGC TTC TCA GGC AGT GGA TCC GGA ACA GAT TTC
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe

 673 ACT CTC ACC ATC AAC AGT CTG CAG GCT GAA GAC GTG GCA GTT TAT TAC
 Thr Leu Thr Ile Asn Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr

 721 TGC ACT CAA GTT TAT TAT CTG TGC ACG TTC GGT GCT GGG ACC AAG CTG
 Cys Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu

 769 GAG CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Glu Leu Lys Arg Leu Glu His His His His His His ---

Nucleic acids and encoded amino acids for h679-scF_v-L5

Figure 36

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala

 49 GCC CAG CCG GCG ATG GCC ATG GAA GTG CAG CTG GTG GAG TCA GGG GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly

 97 GAC TTA GTG AAG CCT GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser

 145 GGA TTC ACT TTC AGT ATT TAC ACC ATG TCT TGG CTT CGC CAG ACT CCG
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro

 193 GGA AAG GGG CTG GAG TGG GTC GCA ACC CTG AGT GGT GAT GGT GAT GAC
 Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp

 241 ATC TAC TAT CCA GAC AGT GTG AAG GGT CGA TTC ACC ATC TCC AGA GAC
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp

 289 AAT GCC AAG AAC AGC CTA TAT CTG CAG ATG AAC AGT CTA AGG GCT GAG
 Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu

 337 GAC ACG GCC TTG TAT TAC TGT GCA AGG GTG CGA CTT GGG GAC TGG GAC
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp

 385 TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC TCC GTC TCC TCA GGA GGT
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Gly Gly

 433 GGC GGA TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

 481 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG GAT GTG
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val

 529 GGT ACT TCT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG
 Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

 577 CTG CTG ATC TAC TGG ACA TCC ACC CGG CAC ACT GGT GTG CCA AGC AGA
 Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

 625 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC
 Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

 673 CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AGC CTC
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu

 721 TAT CGG TCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT CTC GAG
 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu

 769 CAC CAC CAC CAC CAC CAC TGA
 His His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #1 of BS1.5H
(h679 x hMN14 bispecific diabody)**

Figure 37

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT GGT CTG CTG CTC CTC GCT
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 49 GCC CAG CCG GCG ATG GCC ATG GAG GTC CAA CTG GTG GAG AGC GGT GGA
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 97 GGT GTT GTG CAA CCT GGC CGG TCC CTG CGC CTG TCC TGC TCC GGA TCT
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
 145 GGC TTC GAT TTC ACC ACA TAT TGG ATG AGT TGG GTG AGA CAG GCA CCT
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
 193 GGA AAA GGT CTT GAG TGG ATT GGA GAA ATT CAT CCA GAT AGC AGT ACG
 Gly Lys Gly Leu Glu Trp Ile Gly Ile Glu His Pro Asp Ser Ser Thr
 241 ATT AAC TAT GCG CCG TCT CTA AAG GAT AGA TTT ACA ATA TCG CGA GAC
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
 289 AAC GCC AAG AAC ACA TTG TTC CTG CAA ATG GAC AGC CTG AGA CCC GAA
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 337 GAC ACC GGG GTC TAT TTT TGT GCA AGC CTT TAC TTC GGC TTC CCC TGG
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
 385 TTT GCT TAT TGG GGC CAA GGG ACC CCG GTC ACC GTC TCC GGA GGC GGT
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
 433 GGA TCC GAC ATT GTG ATG ACA CAA TCT CCA TCC TCC CTG GCT GTG TCA
 Gly Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser
 481 CCC GGG GAG AGG GTC ACT CTG ACC TGC AAA TCC AGT CAG AGT CTG TTC
 Pro Gly Glu Arg Val Thr Leu Thr Cys Lys Ser Ser Gln Ser Leu Phe
 529 AAC AGT AGA ACC CGA AAG AAC TAC TTG GGT TGG TAC CAG CAG AAA CCA
 Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
 577 GGG CAG TCT CCT AAA CTT CTG ATC TAC TGG GCA TCT ACT CGG GAA TCT
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
 625 GGG GTC CCT GAT CGC TTC TCA GGC AGT GGA TCC GGA ACA GAT TTC ACT
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
 673 CTC ACC ATC AAC AGT CTG CAG GCT GAA GAC GTG GCA GTT TAT TAC TGC
 Leu Thr Ile Asn Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
 721 ACT CAA GTT TAT TAT CTG TGC ACG TTC GGT GCT GGG ACC AAG CTG GAG
 Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu
 769 CTG AAA CGG CTC GAG CAC CAC CAC CAC CAC TGA
 Leu Lys Arg Leu Glu His His His His His His ---

**Nucleic acids and encoded amino acids for polypeptide #2 of BS1.5H
(h679 x hMN14 bispecific diabody)**

Figure 38