



(86) Date de dépôt PCT/PCT Filing Date: 2002/10/15
(87) Date publication PCT/PCT Publication Date: 2003/04/24
(45) Date de délivrance/Issue Date: 2011/07/12
(85) Entrée phase nationale/National Entry: 2004/04/14
(86) N° demande PCT/PCT Application No.: US 2002/032717
(87) N° publication PCT/PCT Publication No.: 2003/033653
(30) Priorités/Priorities: 2001/10/15 (US60/328,835);
2001/12/21 (US60/341,881)

(51) Cl.Int./Int.Cl. *C07K 16/00* (2006.01),
A61K 39/395 (2006.01), *A61K 45/06* (2006.01),
C07K 16/30 (2006.01), *C07K 16/44* (2006.01),
C12N 15/00 (2006.01), *C12N 15/85* (2006.01),
C12N 15/86 (2006.01)

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(54) Titre : AGENTS D'AUGMENTATION DE L'AFFINITE
(54) Title: AFFINITY ENHANCEMENT AGENTS

(57) **Abrégé/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.



(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
24 April 2003 (24.04.2003)

PCT

(10) International Publication Number
WO 2003/033653 A3

(51) International Patent Classification⁷: **C07K 16/00**,
A61K 39/395, C12N 15/00, 15/85, 15/86

(21) International Application Number:
PCT/US2002/032717

(22) International Filing Date: 15 October 2002 (15.10.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/328,835 15 October 2001 (15.10.2001) US
60/341,881 21 December 2001 (21.12.2001) US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- with amended claims

(88) Date of publication of the international search report:
13 November 2003

Date of publication of the amended claims: 12 February 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(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.



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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 GSCC.

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 pharmacokinetics 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.

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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 ID NOS: 9-36, respectively).

In one aspect, the invention relates to a humanized monoclonal antibody comprising the light chain variable region complementarity determining region (CDR) sequences CDR1 (KSSQSLFNSRTKNYLG) CDR2 (WASTRES) and CDR3 (TQVYYLCT) and heavy chain CDR sequences CDR1 (IYTMS) CDR2 (TLSGDGDDIYYPDSVKG) and CDR3 (VRLGDWDFDV) and human antibody framework region (FR) and constant region sequences.

In another aspect, the invention relates to a fusion protein comprising a humanized monoclonal antibody or fragment thereof, wherein said antibody or fragment comprises the light chain variable region complementarity determining region (CDR) sequences CDR1 (KSSQSLFNSRTKNYLG) CDR2 (WASTRES) and CDR3 (TQVYYLCT) and heavy chain CDR sequences CDR1 (IYTMS) CDR2 (TLSGDGDDIYYPDSVKG) and CDR3 (VRLGDWDFDV) and human antibody framework region (FR) sequences.

In another aspect, the invention relates to a multivalent, multispecific binding protein comprising a histamine-succinyl-glycyl binding humanized monoclonal antibody or fragment thereof, wherein said antibody or fragment

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comprises the light chain variable region complementarity determining region (CDR) sequences CDR1 (KSSQSLFNSRTKNYLG) CDR2 (WASTRES) and CDR3 (TQVYYLCT) and heavy chain CDR sequences CDR1 (IYTMS) CDR2 (TLSGDGDDIYYPDSVKG) and CDR3 (VRLGDWDFDV) and human antibody
5 framework region (FR) sequences.

In another aspect, the invention relates to a kit comprising an antibody as described above, a fusion protein as described above, or a multivalent binding protein as described above.

In another aspect, the invention relates to a pharmaceutical
10 composition comprising an antibody as described above, a fusion protein as described above or a multivalent binding protein as described above, in a pharmaceutically acceptable excipient.

In another aspect, the invention relates to an isolated nucleic acid encoding an antibody as described above, a fusion protein as described above, or
15 a multivalent binding protein as described above.

In another aspect, the invention relates to an expression vector comprising a nucleic acid as described above.

In another aspect, the invention relates to a host cell comprising an expression vector as described above.

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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) (SEQ ID NO: 1), and the carboxyl terminal six histidine (His) affinity tag (SEQ ID NO: 2). 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 (SEQ ID NO: 1), and the carboxyl terminal 6 histidine affinity tag (SEQ ID NO: 2). 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-idiotypic 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-idiotypic 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 (SEQ ID NOS: 3-4, respectively, in order of appearance). Restriction sites are indicated above the sequence. MCS2 was ligated into the BlnI restriction site of pET26b vector shown in figure B. Figure C shows the diagram of pET-ER vector, including the MCS2 sequence.. The 6 Histidine tags correspond to SEQ ID NO: 2.

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. The 6 Histidine tags correspond to SEQ ID NO: 2.

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. The G₄S linker has been assigned SEQ ID NO: 1.

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-idiotypic 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) (SEQ ID NOS: 5 and 7, respectively, in order of appearance) and humanized (h) (SEQ ID NOS: 6 and 8, respectively, in order of appearance) 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-idiotypic 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-scF_v-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) (SEQ ID NO: 1) 442-780 is the coding sequence for 679V_K. 787-804 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 9 & 10)

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) (SEQ ID NO: 1). 442-780 is the coding sequence for 679 V_K. 787-804 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 11 & 12)

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) (SEQ ID NO: 1). 442-780 is the coding sequence for 679 V_K (C101S). 787-804 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 13 & 14)

Figure 28 is the coding sequence and encoded amino acids for 679 I3Q/C101S. (SEQ ID NOS: 15 & 16)

Figure 29 is the coding sequence of nucleic acids and encoded amino acids for hMN14-scF_v-L5. 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) (SEQ ID NO: 1). 439-759 is the coding sequence for hMN14 V_K. 766-783 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 17 & 18)

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) (SEQ ID NO: 1). 442-762 is the coding sequence for hMN14 V_K. 769-786 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 19 & 20)

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) (SEQ ID NO: 1). 439-777 is the coding sequence for 679 V_K. 784-801 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 21 & 22)

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) (SEQ ID NO: 1). 442-762 is the coding sequence for hMN14 V_K. 769-786 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 23 & 24)

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) (SEQ ID NO: 1). 439-777

is the coding sequence for 679V_K. 784-801 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 25 & 26)

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) (SEQ ID NO: 1). 442-762 is the coding sequence for hMN14V_K. 769-786 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 27 & 28)

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) (SEQ ID NO: 1). 439-777 is the coding sequence for 679V_K C101S. 784-801 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 29 & 30)

Figure 36 is the coding sequence of nucleic acids and encoded amino acids for h679-scF_v-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) (SEQ ID NO: 1). 442-780 is the coding sequence for h679V_K. 787-804 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 31 & 32)

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) (SEQ ID NO: 1). 442-762 is the coding sequence for hMN14V_K. 769-786 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 33 & 34)

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) (SEQ ID NO: 1). 439-777 is the coding sequence for h679V_K C101S. 784-801 is the coding sequence for the 6 histidine affinity tag. (SEQ ID NOS: 35 & 36)

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 discistronic 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) (SEQ ID NO: 1). 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 ID NOS: 9 & 10). The DNA coding sequence and the corresponding encoded amino acids for 679-I3Q are contained in Figure 26 (SEQ ID NOS: 11 & 12). The DNA coding sequence and the corresponding encoded amino acids for 679-C101S are contained in Figure 27 (SEQ ID NOS: 13 & 14). 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) (SEQ ID NO:1). 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 ID NOS: 17 & 18). 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 679V_H I3Q mutation. BS2 incorporates both the 679V_H I3Q and the 679V_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 ID NOS: 19-30), respectively. Additionally, a bispecific diabody of h679 x hMN14 has been constructed and named BS1.5H (See Figures 37 & 38) (SEQ ID NOS 33 & 34).

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 (SEQ ID NO: 37)

5'-TCAGCCATGGAAGTGATCCTGGTGGAGTCAGGGGGAGACT-3'

679V_H-Right (G₄S) (SEQ ID NO: 38)

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) (SEQ ID NO: 1) 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 (SEQ ID NO: 39)

5'-CTGAGGATCCGACATTGTGATGTCACAATCT-3'

679V_K-Right (SEQ ID NO: 40)

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 (SEQ ID NO: 1) linker, and 6His (SEQ ID NO: 2) 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 µg/ml kanamycin sulphate and 34µg/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 40µM 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; 10 mM 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

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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.

*Trade-mark

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 (SEQ ID NO: 41)

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_KC101S-Right (SEQ ID NO: 42)

5'GCTCGAGCCGTTTCAGCTCCAGCTTGGTCCCAGCACCGAACGTGCT
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 (SEQ ID NO: 43)

5'-CGTACCATGGAGGTCCAACCTGGTGGAGA-3'

hMN14V_H-Right (G₄S) (SEQ ID NO: 44)

5'-CATAGGATCCACCGCCTCCGGAGACGGTGACCGGGGT-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) (SEQ ID NO: 1) 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 (SEQ ID NO: 45)

5'-CTGAGGATCCGACATCCAGCTGACCCAGAG-3'

hMN14V_K-Right (SEQ ID NO: 46)

5'-GCTACTCGAGACGTTTGATTTCACCTTGG-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 (SEQ ID NO: 1) linker and 6His (SEQ ID NO:2) 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-idiotypic 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 M_r 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 BspI 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_K 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_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 (679V_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-L5-679V_K- pET26b with XbaI and BspI. This fragment was ligated into the SpeI and BspI restriction sites of 679V_H-L5-hMN14V_K- 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 ID NOS: 19-30), respectively. The dicistronic expression cassette codes for two polypeptides that are arranged as follows:

Polypeptide 1

Pel B; 679V_H; GGGGS (SEQ ID NO; 1) linker; hMN14V_K; 6His (SEQ ID NO: 2)

Polypeptide 2

Pel B;hMN14V_H; GGGGS (SEQ ID NO; 1) linker; 679V_K; 6His (SEQ ID NO: 2)

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 679 x hMN14 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 NiNTA 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 (SEQ ID NO: 1)-hMN14V_K and hMN14V_H- GGGGS (SEQ ID NO: 1)-679V_K, exclusively form a dimer or diabody. The purity of the three 679 x hMN14 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 μ g/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-idiotypic 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_HI3Q 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_KC101S mutation as well as the 679V_HI3Q. 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}In -IMP241	24 hrs post ^{111}In -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 679V_HI3Q 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	Mutations	Sequence
A-Left	121 - 150	Xma I	V _H -E42G V _H -R44G	5'GCTTCCCGGGAAAGGGGCTGGA GTGGGTCGCAACC3' (SEQ ID NO: 47)
A-Right	212 - 247	Pst I	V _H -N775	5'CGATCTGCAGATATAGGCTGTT CTTGGCATTGTCTCTGG3' (SEQ ID NO: 48)

B-Left	241 - 284	Pst I	V _H -S84A V _H -A85E	5'CTGCAGATGAACAGTCTAAGG GCTGAGGACACGGCCTTGTATTA3' (SEQ ID NO: 49)
B-Right	365 – 421	Xma I	V _K -S5T	5'CCCCGGGTGACACAGCCAGGGAG GATGGAGATTGTGTCATCACAATGT CGGATCCGC3' (SEQ NO: 50)
C-left	414 – 455	Xma I	V _K -K18R V _K -M21L	5'ACCCGGGGAGAGGGTCACTCTGA CCTGCAAATCCAGTCAGAG3' (SEQ ID NO: 51)
C-Right	565 - 595	Bsp EI	V _K -T63S	5'TTCCGGATCCACTGCCTGAGAAG CGATCAGGGACCCCAGA3' (SEQ ID NO: 52)
D-Left	588 – 659	Bsp EI	V _K -V78L V _K -S80A V _K -L83V	5'ATCCGGAACAGATTTCACTCTCAC CATCAACAGTCTGCAGGCTGAAGAC GTGGCAGTTTATTACTGCACTCA3' (SEQ ID NO: 53)
D-Right	687 - 717	Xho I	None	5'ATCCTCGAGCCGTTTCAGCTCCAG CTTGGT3' (SEQ ID NO: 54)

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 PstI (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 ug/L for the wild type m679 diabody or 10 ug/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 BlnI. This fragment was ligated into the SpeI and BlnI 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 (SEQ ID NO: 1) linker; hMN14V_K; 6 His (SEQ ID NO: 2)

Polypeptide 2

Pel B; hMN14V_H; GGGGS (SEQ ID NO: 1) linker; h679V_K; 6His (SEQ ID NO: 2)

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-idiotypic MAb). As shown in Figure 23, injection of 60 ng of BS1.5H gave a relative response of 660 RU. Subsequent injection of 1 µg 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:



52392-36

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.

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 35 40 45
 Ala Thr Leu Ser Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ser Ala Asp Thr Ala Leu Tyr Tyr Cys
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr					
	65		70		75
Leu Gln Met Asn Ser Leu Arg Ser Ala Asp Thr Ala Leu Tyr Tyr Cys					
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			20					25					30		

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

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

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

Ile	Asn	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Thr	Gln
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gcc	cag	ccg	gcg	atg	gcc	atg	gaa	gtg	atc	ctg	gtg	gag	tca	ggg	gga	96
Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Ile	Leu	Val	Glu	Ser	Gly	Gly	
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gac	tta	gtg	aag	cct	gga	ggg	tcc	ctg	aaa	ctc	tcc	tgt	gca	gcc	tct	144
Asp	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	
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gga	ttc	act	ttc	agt	att	tac	acc	atg	tct	tgg	ctt	cgc	cag	act	ccg	192
Gly	Phe	Thr	Phe	Ser	Ile	Tyr	Thr	Met	Ser	Trp	Leu	Arg	Gln	Thr	Pro	
	50					55					60					

gaa	aag	agg	ctg	gag	tgg	gtc	gca	acc	ctg	agt	ggt	gat	ggt	gat	gac	240
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Glu 65	Lys	Arg	Leu	Glu	Trp 70	Val	Ala	Thr	Leu	Ser 75	Gly	Asp	Gly	Asp	Asp 80	
atc	tac	tat	cca	gac	agt	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	288
Ile	Tyr	Tyr	Pro	Asp 85	Ser	Val	Lys	Gly	Arg 90	Phe	Thr	Ile	Ser	Arg 95	Asp	
aat	gcc	aag	aac	aac	cta	tat	ctg	caa	atg	aac	agt	cta	agg	tct	gcg	336
Asn	Ala	Lys	Asn 100	Asn	Leu	Tyr	Leu	Gln 105	Met	Asn	Ser	Leu	Arg 110	Ser	Ala	
gac	acg	gcc	ttg	tat	tac	tgt	gca	agg	gtg	cga	ctt	ggg	gac	tgg	gac	384
Asp	Thr	Ala 115	Leu	Tyr	Tyr	Cys	Ala 120	Arg	Val	Arg	Leu	Gly 125	Asp	Trp	Asp	
ttc	gat	gtc	tgg	ggc	caa	ggg	acc	acg	gtc	tcc	gtc	tcc	tca	gga	ggc	432
Phe	Asp 130	Val	Trp	Gly	Gln	Gly 135	Thr	Thr	Val	Ser	Val 140	Ser	Ser	Gly	Gly	
ggc	gga	tcc	gac	att	gtg	atg	tca	caa	tct	cca	tcc	tcc	ctg	gct	gtg	480
Gly 145	Gly	Ser	Asp	Ile	Val 150	Met	Ser	Gln	Ser	Pro 155	Ser	Ser	Leu	Ala	Val 160	
tca	cca	gga	gag	aag	gtc	act	atg	acc	tgc	aaa	tcc	agt	cag	agt	ctg	528
Ser	Pro	Gly	Glu	Lys 165	Val	Thr	Met	Thr	Cys 170	Lys	Ser	Ser	Gln	Ser 175	Leu	
ttc	aac	agt	aga	acc	cga	aag	aac	tac	ttg	ggc	tgg	tac	cag	cag	aaa	576
Phe	Asn	Ser	Arg 180	Thr	Arg	Lys	Asn	Tyr 185	Leu	Gly	Trp	Tyr	Gln 190	Gln	Lys	
cca	ggg	cag	tct	cct	aaa	ctt	ctg	atc	tac	tgg	gca	tct	act	cgg	gaa	624
Pro	Gly	Gln 195	Ser	Pro	Lys	Leu	Leu 200	Ile	Tyr	Trp	Ala	Ser 205	Thr	Arg	Glu	
tct	ggg	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	672
Ser	Gly 210	Val	Pro	Asp	Arg	Phe 215	Thr	Gly	Ser	Gly	Ser 220	Gly	Thr	Asp	Phe	
act	ctc	acc	atc	aac	agt	gtg	cag	tct	gaa	gac	ctg	gca	gtt	tat	tac	720
Thr 225	Leu	Thr	Ile	Asn	Ser 230	Val	Gln	Ser	Glu	Asp 235	Leu	Ala	Val	Tyr	Tyr 240	
tgc	act	caa	gtt	tat	tat	ctg	tgc	acg	ttc	ggc	gct	ggg	acc	aag	ctg	768
Cys	Thr	Gln	Val	Tyr 245	Tyr	Leu	Cys	Thr	Phe 250	Gly	Ala	Gly	Thr	Lys 255	Leu	
gag	ctg	aaa	cgg	ctc	gag	cac	cac	cac	cac	cac	cac	tga				807
Glu	Leu	Lys	Arg 260	Leu	Glu	His	His 265	His	His	His	His					

<210> 10

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
sequence of 679-scFv-L5

<400> 10

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly
 20 25 30

Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 35 40 45

Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
 50 55 60

Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
 65 70 75 80

Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 85 90 95

Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala
 100 105 110

Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
 115 120 125

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

Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
 145 150 155 160

Ser Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu
 165 170 175

Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys
 180 185 190

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
 195 200 205

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
 210 215 220

Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr
 225 230 235 240

Cys Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu
 245 250 255

Glu Leu Lys Arg Leu Glu His His His His His His
 260 265

<210> 11

<211> 807

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(804)

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide sequence of 679-I3Q

<400> 11

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

act ctc acc atc aac agt gtg cag tct gaa gac ctg gca gtt tat tac 720
 Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr
 225 230 235 240

tgc act caa gtt tat tat ctg tgc acg ttc ggt gct ggg acc aag ctg 768
 Cys Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu
 245 250 255

gag ctg aaa cgg ctc gag cac cac cac cac cac tga 807
 Glu Leu Lys Arg Leu Glu His His His His His His
 260 265

<210> 12

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
 sequence of 679-I3Q

<400> 12

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30

Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 35 40 45

Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
 50 55 60

Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
 65 70 75 80

Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 85 90 95

Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala
 100 105 110

Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
 115 120 125

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

Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
 145 150 155 160

Ser Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu
 165 170 175

Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys
 180 185 190

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu

195					200					205					
Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
210						215					220				
Thr	Leu	Thr	Ile	Asn	Ser	Val	Gln	Ser	Glu	Asp	Leu	Ala	Val	Tyr	Tyr
225					230					235					240
Cys	Thr	Gln	Val	Tyr	Tyr	Leu	Cys	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu
				245					250					255	
Glu	Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His				
			260					265							

<210> 13
 <211> 807
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(804)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide sequence of 679-C101S

<400> 13

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Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	
1				5					10					15		
gcc	cag	ccg	gcg	atg	gcc	atg	gaa	gtg	atc	ctg	gtg	gag	tca	ggg	gga	96
Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Ile	Leu	Val	Glu	Ser	Gly	Gly	
			20					25					30			
gac	tta	gtg	aag	cct	gga	ggg	tcc	ctg	aaa	ctc	tcc	tgt	gca	gcc	tct	144
Asp	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	
			35				40					45				
gga	ttc	act	ttc	agt	att	tac	acc	atg	tct	tgg	ctt	cgc	cag	act	ccg	192
Gly	Phe	Thr	Phe	Ser	Ile	Tyr	Thr	Met	Ser	Trp	Leu	Arg	Gln	Thr	Pro	
	50					55					60					
gaa	aag	agg	ctg	gag	tgg	gtc	gca	acc	ctg	agt	ggt	gat	ggt	gat	gac	240
Glu	Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Leu	Ser	Gly	Asp	Gly	Asp	Asp	
65					70					75					80	
atc	tac	tat	cca	gac	agt	gtg	aag	ggt	cga	ttc	acc	atc	tcc	aga	gac	288
Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
				85					90					95		
aat	gcc	aag	aac	aac	cta	tat	ctg	caa	atg	aac	agt	cta	agg	tct	gcg	336
Asn	Ala	Lys	Asn	Asn	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ser	Ala	
			100					105					110			
gac	acg	gcc	ttg	tat	tac	tgt	gca	agg	gtg	cga	ctt	ggg	gac	tgg	gac	384
Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Leu	Gly	Asp	Trp	Asp	
			115				120					125				

ttc gat gtc tgg ggc caa ggg acc acg gtc tcc gtc tcc tca gga ggt	432
Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly	
130 135 140	
ggc gga tcc gac att gtg atg tca caa tct cca tcc tcc ctg gct gtg	480
Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val	
145 150 155 160	
tca cca gga gag aag gtc act atg acc tgc aaa tcc agt cag agt ctg	528
Ser Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu	
165 170 175	
ttc aac agt aga acc cga aag aac tac ttg ggt tgg tac cag cag aaa	576
Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys	
180 185 190	
cca ggg cag tct cct aaa ctt ctg atc tac tgg gca tct act cgg gaa	624
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu	
195 200 205	
tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttc	672
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
act ctc acc atc aac agt gtg cag tct gaa gac ctg gca gtt tat tac	720
Thr Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr	
225 230 235 240	
tgc act caa gtt tat tat ctg agc acg ttc ggt gct ggg acc aag ctg	768
Cys Thr Gln Val Tyr Tyr Leu Ser Thr Phe Gly Ala Gly Thr Lys Leu	
245 250 255	
gag ctg aaa cgg ctc gag cac cac cac cac cac tga	807
Glu Leu Lys Arg Leu Glu His His His His His His	
260 265	

<210> 14

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
sequence of 679-C101S

<400> 14

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly
20 25 30

Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
35 40 45

Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
50 55 60

Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
65 70 75 80

Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
				85					90					95		
Asn	Ala	Lys	Asn	Asn	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ser	Ala	
			100					105					110			
Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Leu	Gly	Asp	Trp	Asp	
		115					120					125				
Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ser	Val	Ser	Ser	Gly	Gly	
	130					135					140					
Gly	Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	
145					150					155					160	
Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	
				165					170					175		
Phe	Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	
			180					185					190			
Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	
		195					200					205				
Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
	210					215					220					
Thr	Leu	Thr	Ile	Asn	Ser	Val	Gln	Ser	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	
225					230					235					240	
Cys	Thr	Gln	Val	Tyr	Tyr	Leu	Ser	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	
				245					250					255		
Glu	Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His					
			260					265								

<210> 15
 <211> 807
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(804)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide
 sequence of 679 I3Q/C101S

<400> 15																
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Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	
1				5					10					15		
gcc	cag	ccg	gcg	atg	gcc	atg	gaa	gtg	cag	ctg	gtg	gag	tca	ggg	gga	96
Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	
			20					25					30			
gac	tta	gtg	aag	cct	gga	ggg	tcc	ctg	aaa	ctc	tcc	tgt	gca	gcc	tct	144

Asp	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser		
		35					40					45					
gga	ttc	act	ttc	agt	att	tac	acc	atg	tct	tgg	ctt	cgc	cag	act	ccg	192	
Gly	Phe	Thr	Phe	Ser	Ile	Tyr	Thr	Met	Ser	Trp	Leu	Arg	Gln	Thr	Pro		
	50					55					60						
gaa	aag	agg	ctg	gag	tgg	gtc	gca	acc	ctg	agt	ggg	gat	ggg	gat	gac	240	
Glu	Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Leu	Ser	Gly	Asp	Gly	Asp	Asp		
	65				70					75					80		
atc	tac	tat	cca	gac	agt	gtg	aag	ggg	cga	ttc	acc	atc	tcc	aga	gac	288	
Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp		
				85					90					95			
aat	gcc	aag	aac	aac	cta	tat	ctg	caa	atg	aac	agt	cta	agg	tct	gcg	336	
Asn	Ala	Lys	Asn	Asn	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ser	Ala		
			100					105					110				
gac	acg	gcc	ttg	tat	tac	tgt	gca	agg	gtg	cga	ctt	ggg	gac	tgg	gac	384	
Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Leu	Gly	Asp	Trp	Asp		
		115					120					125					
ttc	gat	gtc	tgg	ggc	caa	ggg	acc	acg	gtc	tcc	gtc	tcc	tca	gga	ggg	432	
Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ser	Val	Ser	Ser	Gly	Gly		
	130					135					140						
ggc	gga	tcc	gac	att	gtg	atg	tca	caa	tct	cca	tcc	tcc	ctg	gct	gtg	480	
Gly	Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val		
	145				150					155					160		
tca	cca	gga	gag	aag	gtc	act	atg	acc	tgc	aaa	tcc	agt	cag	agt	ctg	528	
Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu		
				165					170					175			
ttc	aac	agt	aga	acc	cga	aag	aac	tac	ttg	ggg	tgg	tac	cag	cag	aaa	576	
Phe	Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys		
			180					185					190				
cca	ggg	cag	tct	cct	aaa	ctt	ctg	atc	tac	tgg	gca	tct	act	cgg	gaa	624	
Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu		
		195				200						205					
tct	ggg	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	672	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
	210					215						220					
act	ctc	acc	atc	aac	agt	gtg	cag	tct	gaa	gac	ctg	gca	gtt	tat	tac	720	
Thr	Leu	Thr	Ile	Asn	Ser	Val	Gln	Ser	Glu	Asp	Leu	Ala	Val	Tyr	Tyr		
	225				230					235					240		
tgc	act	caa	gtt	tat	tat	ctg	agc	acg	ttc	ggg	gct	ggg	acc	aag	ctg	768	
Cys	Thr	Gln	Val	Tyr	Tyr	Leu	Ser	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu		
				245					250					255			
gag	ctg	aaa	cgg	ctc	gag	cac	cac	cac	cac	cac	cac	tga				807	
Glu	Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His						
			260					265									

<210> 16

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
sequence of 679 I3Q/C101S

<400> 16

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala
1				5					10					15	

Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly
			20					25					30		

Asp	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser
		35					40					45			

Gly	Phe	Thr	Phe	Ser	Ile	Tyr	Thr	Met	Ser	Trp	Leu	Arg	Gln	Thr	Pro
	50					55					60				

Glu	Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Leu	Ser	Gly	Asp	Gly	Asp	Asp
65					70					75					80

Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp
				85					90					95	

Asn	Ala	Lys	Asn	Asn	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ser	Ala
			100					105					110		

Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Leu	Gly	Asp	Trp	Asp
		115					120					125			

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

Gly	Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val
145					150					155					160

Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu
				165					170					175	

Phe	Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys
			180					185					190		

Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu
		195				200						205			

Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
	210					215					220				

Thr	Leu	Thr	Ile	Asn	Ser	Val	Gln	Ser	Glu	Asp	Leu	Ala	Val	Tyr	Tyr
225					230					235					240

Cys	Thr	Gln	Val	Tyr	Tyr	Leu	Ser	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu
				245					250					255	

Glu	Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His	His
			260					265				

<210> 17
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(783)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide
 sequence of hMN14VK

<400> 17
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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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 gcc cag ccg gcg atg gcc atg gag gtc caa ctg gtg gag agc ggt gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct 144
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
 35 40 45
 ggc ttc gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct 192
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
 50 55 60
 gga aaa ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg 240
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
 65 70 75 80
 att aac tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac 288
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
 85 90 95
 aac gcc aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa 336
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 100 105 110
 gac acc ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg 384
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
 115 120 125
 ttt gct tat tgg ggc caa ggg acc ccg gtc acc gtc tcc gga ggc ggt 432
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
 130 135 140
 gga tcc gac atc cag ctg acc cag agc cca agc agc ctg agc gcc agc 480
 Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 145 150 155 160
 gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag gat gtg ggt 528
 Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly
 165 170 175
 act tct gta gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg 576
 Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 180 185 190

ctg atc tac tgg aca tcc acc cgg cac act ggt gtg cca agc aga ttc	624
Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe	
195 200 205	
agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc	672
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu	
210 215 220	
cag cca gag gac atc gcc acc tac tac tgc cag caa tat agc ctc tat	720
Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu Tyr	
225 230 235 240	
cgg tcg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt ctc gag cac	768
Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu His	
245 250 255	
cac cac cac cac cac tga	786
His His His His His	
260	

<210> 18
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide
 sequence of hMN14VK

<400> 18
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 1 5 10 15
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
 35 40 45
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
 50 55 60
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
 65 70 75 80
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
 85 90 95
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 100 105 110
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
 115 120 125
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
 130 135 140
 Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 145 150 155 160

Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly
 165 170 175
 Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 180 185 190
 Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe
 195 200 205
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu
 210 215 220
 Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu Tyr
 225 230 235 240
 Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu His
 245 250 255
 His His His His His
 260

<210> 19
 <211> 789
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(786)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide
 sequence of polypeptide 1 of BS1

<400> 19
 atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct 48
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 gcc cag ccg gcg atg gcc atg gaa gtg atc ctg gtg gag tca ggg gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly
 20 25 30
 gac tta gtg aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct 144
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 35 40 45
 gga ttc act ttc agt att tac acc atg tct tgg ctt cgc cag act ccg 192
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
 50 55 60
 gaa aag agg ctg gag tgg gtc gca acc ctg agt ggt gat ggt gat gac 240
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
 65 70 75 80
 atc tac tat cca gac agt gtg aag ggt cga ttc acc atc tcc aga gac 288
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 85 90 95

aat gcc aag aac aac cta tat ctg caa atg aac agt cta agg tct gcg	336
Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala	
100 105 110	
gac acg gcc ttg tat tac tgt gca agg gtg cga ctt ggg gac tgg gac	384
Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp	
115 120 125	
ttc gat gtc tgg ggc caa ggg acc acg gtc tcc gtc tcc tca gga ggt	432
Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly	
130 135 140	
ggc gga tcc gac atc cag ctg acc cag agc cca agc agc ctg agc gcc	480
Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala	
145 150 155 160	
agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag gat gtg	528
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val	
165 170 175	
ggc act tct gta gcc tgg tac cag cag aag cca ggt aag gct cca aag	576
Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
180 185 190	
ctg ctg atc tac tgg aca tcc acc cgg cac act ggt gtg cca agc aga	624
Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg	
195 200 205	
ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc	672
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
210 215 220	
ctc cag cca gag gac atc gcc acc tac tac tgc cag caa tat agc ctc	720
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu	
225 230 235 240	
tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt ctc gag	768
Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu	
245 250 255	
cac cac cac cac cac cac tga	789
His His His His His His	
260	

<210> 20

<211> 262

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
sequence of polypeptide 1 of BS1

<400> 20

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15Ala Gln Pro Ala Met Ala Met Glu Val Ile Leu Val Glu Ser Gly Gly
20 25 30

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Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
    35                                40                                45

Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
    50                                55                                60

Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
    65                                70                                75                                80

Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    85                                90                                95

Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala
    100                               105                               110

Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
    115                               120                               125

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

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

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
    165                               170                               175

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
    180                               185                               190

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
    195                               200                               205

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
    210                               215                               220

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

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
    245                               250                               255

His His His His His His
    260

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<210> 21
<211> 804
<212> DNA
<213> Artificial Sequence

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<220>
<221> CDS
<222> (1)..(801)

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<220>
<223> Description of Artificial Sequence: Synthetic nucleotide
      sequence of polypeptide 2 of BS1

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<400> 21

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Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	
1				5					10						15	
gcc	cag	ccg	gcg	atg	gcc	atg	gag	gtc	caa	ctg	gtg	gag	agc	ggg	gga	96
Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	
			20					25					30			
ggg	gtt	gtg	caa	cct	ggc	cgg	tcc	ctg	cgc	ctg	tcc	tgc	tcc	gca	tct	144
Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	
			35				40					45				
ggc	ttc	gat	ttc	acc	aca	tat	tgg	atg	agt	tgg	gtg	aga	cag	gca	cct	192
Gly	Phe	Asp	Phe	Thr	Thr	Tyr	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	
	50					55					60					
gga	aaa	ggg	ctt	gag	tgg	att	gga	gaa	att	cat	cca	gat	agc	agt	acg	240
Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	His	Pro	Asp	Ser	Ser	Thr	
65					70					75					80	
att	aac	tat	gcg	ccg	tct	cta	aag	gat	aga	ttt	aca	ata	tcg	cga	gac	288
Ile	Asn	Tyr	Ala	Pro	Ser	Leu	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
				85					90					95		
aac	gcc	aag	aac	aca	ttg	ttc	ctg	caa	atg	gac	agc	ctg	aga	ccc	gaa	336
Asn	Ala	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	
			100					105					110			
gac	acc	ggg	gtc	tat	ttt	tgt	gca	agc	ctt	tac	ttc	ggc	ttc	ccc	tgg	384
Asp	Thr	Gly	Val	Tyr	Phe	Cys	Ala	Ser	Leu	Tyr	Phe	Gly	Phe	Pro	Trp	
		115					120					125				
ttt	gct	tat	tgg	ggc	caa	ggg	acc	ccg	gtc	acc	gtc	tcc	gga	ggc	ggg	432
Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Gly	Gly	Gly	
	130					135					140					
gga	tcc	gac	att	gtg	atg	tca	caa	tct	cca	tcc	tcc	ctg	gct	gtg	tca	480
Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	Ser	
145					150					155					160	
cca	gga	gag	aag	gtc	act	atg	acc	tgc	aaa	tcc	agt	cag	agt	ctg	ttc	528
Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Phe	
				165					170					175		
aac	agt	aga	acc	cga	aag	aac	tac	ttg	ggg	tgg	tac	cag	cag	aaa	cca	576
Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	
			180					185					190			
ggg	cag	tct	cct	aaa	ctt	ctg	atc	tac	tgg	gca	tct	act	cgg	gaa	tct	624
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	
		195					200					205				
ggg	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	act	672
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
	210					215					220					
ctc	acc	atc	aac	agt	gtg	cag	tct	gaa	gac	ctg	gca	gtt	tat	tac	tgc	720
Leu	Thr	Ile	Asn	Ser	Val	Gln	Ser	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	
225					230					235					240	
act	caa	gtt	tat	tat	ctg	tgc	acg	ttc	ggg	gct	ggg	acc	aag	ctg	gag	768

225		230		235		240									
Thr	Gln	Val	Tyr	Tyr	Leu	Cys	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu
				245					250					255	
Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His					
			260					265							

<210> 23
 <211> 789
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(786)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide sequence of polypeptide 1 of BS1.5

<400> 23
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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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 gcc cag ccg gcg atg gcc atg gaa gtg cag ctg gtg gag tca ggg gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 gac tta gtg aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct 144
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 35 40 45
 gga ttc act ttc agt att tac acc atg tct tgg ctt cgc cag act ccg 192
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
 50 55 60
 gaa aag agg ctg gag tgg gtc gca acc ctg agt ggt gat ggt gat gac 240
 Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
 65 70 75 80
 atc tac tat cca gac agt gtg aag ggt cga ttc acc atc tcc aga gac 288
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 85 90 95
 aat gcc aag aac aac cta tat ctg caa atg aac agt cta agg tct gcg 336
 Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala
 100 105 110
 gac acg gcc ttg tat tac tgt gca agg gtg cga ctt ggg gac tgg gac 384
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
 115 120 125
 ttc gat gtc tgg ggc caa ggg acc acg gtc tcc gtc tcc tca gga ggt 432
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly
 130 135 140
 ggc gga tcc gac atc cag ctg acc cag agc cca agc agc ctg agc gcc 480
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

145	150	155	160	
agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag gat gtg				528
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val	165	170	175	
ggt act tct gta gcc tgg tac cag cag aag cca ggt aag gct cca aag				576
Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	180	185	190	
ctg ctg atc tac tgg aca tcc acc cgg cac act ggt gtg cca agc aga				624
Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg	195	200	205	
ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc				672
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	210	215	220	
ctc cag cca gag gac atc gcc acc tac tac tgc cag caa tat agc ctc				720
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu	225	230	235	240
tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt ctc gag				768
Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu	245	250	255	
cac cac cac cac cac cac tga				789
His His His His His His	260			

<210> 24
 <211> 262
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide
 sequence of polypeptide 1 of BS1.5

<400> 24
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15
Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
20 25 30
Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
35 40 45
Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
50 55 60
Glu Lys Arg Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
65 70 75 80
Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
85 90 95
Asn Ala Lys Asn Asn Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Ala
100 105 110

Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
 115 120 125
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly
 130 135 140
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
 145 150 155 160
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
 165 170 175
 Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 180 185 190
 Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
 195 200 205
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 210 215 220
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
 225 230 235 240
 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
 245 250 255
 His His His His His His
 260

<210> 25
 <211> 804
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(801)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide
 sequence of polypeptide 2 of BS1.5

<400> 25
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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
 1 5 10 15
 gcc cag ccg gcg atg gcc atg gag gtc caa ctg gtg gag agc ggt gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct 144
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
 35 40 45
 ggc ttc gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct 192
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
 50 55 60

gga	aaa	ggt	ctt	gag	tgg	att	gga	gaa	att	cat	cca	gat	agc	agt	acg	240
Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	His	Pro	Asp	Ser	Ser	Thr	
65					70					75					80	
att	aac	tat	gcg	ccg	tct	cta	aag	gat	aga	ttt	aca	ata	tcg	cga	gac	288
Ile	Asn	Tyr	Ala	Pro	Ser	Leu	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
				85				90						95		
aac	gcc	aag	aac	aca	ttg	ttc	ctg	caa	atg	gac	agc	ctg	aga	ccc	gaa	336
Asn	Ala	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	
			100					105					110			
gac	acc	ggg	gtc	tat	ttt	tgt	gca	agc	ctt	tac	ttc	ggc	ttc	ccc	tgg	384
Asp	Thr	Gly	Val	Tyr	Phe	Cys	Ala	Ser	Leu	Tyr	Phe	Gly	Phe	Pro	Trp	
		115					120					125				
ttt	gct	tat	tgg	ggc	caa	ggg	acc	ccg	gtc	acc	gtc	tcc	gga	ggc	ggt	432
Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Gly	Gly	Gly	
	130					135					140					
gga	tcc	gac	att	gtg	atg	tca	caa	tct	cca	tcc	tcc	ctg	gct	gtg	tca	480
Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	Ser	
145					150					155					160	
cca	gga	gag	aag	gtc	act	atg	acc	tgc	aaa	tcc	agt	cag	agt	ctg	ttc	528
Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Phe	
				165					170					175		
aac	agt	aga	acc	cga	aag	aac	tac	ttg	ggt	tgg	tac	cag	cag	aaa	cca	576
Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	
			180					185					190			
ggg	cag	tct	cct	aaa	ctt	ctg	atc	tac	tgg	gca	tct	act	cgg	gaa	tct	624
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	
		195					200					205				
ggg	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	act	672
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
	210					215					220					
ctc	acc	atc	aac	agt	gtg	cag	tct	gaa	gac	ctg	gca	gtt	tat	tac	tgc	720
Leu	Thr	Ile	Asn	Ser	Val	Gln	Ser	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	
225					230					235					240	
act	caa	gtt	tat	tat	ctg	tgc	acg	ttc	ggt	gct	ggg	acc	aag	ctg	gag	768
Thr	Gln	Val	Tyr	Tyr	Leu	Cys	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	
				245					250					255		
ctg	aaa	cgg	ctc	gag	cac	cac	cac	cac	cac	cac	tga					804
Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His						
			260					265								

<210> 26

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

sequence of polypeptide 2 of BS1.5

<400> 26

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1           5           10           15

Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
      20           25           30

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
      35           40           45

Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
      50           55           60

Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
      65           70           75           80

Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
      85           90           95

Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
      100          105          110

Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
      115          120          125

Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
      130          135          140

Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser
      145          150          155          160

Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe
      165          170          175

Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
      180          185          190

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
      195          200          205

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
      210          215          220

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

Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu
      245          250          255

Leu Lys Arg Leu Glu His His His His His His
      260          265

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<210> 27

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(786)

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide
sequence of polypeptide 1 of BS2

<400> 27

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

Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser		
210						215					220						
ctc	cag	cca	gag	gac	atc	gcc	acc	tac	tac	tgc	cag	caa	tat	agc	ctc	720	
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Leu		
225					230					235					240		
tat	cgg	tcg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc	aaa	cgt	ctc	gag	768	
Tyr	Arg	Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Leu	Glu		
				245					250					255			
cac	cac	cac	cac	cac	cac	tga										789	
His	His	His	His	His	His												
				260													

<210> 28
 <211> 262
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide
 sequence of polypeptide 1 of BS2

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala		
1				5					10					15			
Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly		
			20					25					30				
Asp	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser		
		35					40					45					
Gly	Phe	Thr	Phe	Ser	Ile	Tyr	Thr	Met	Ser	Trp	Leu	Arg	Gln	Thr	Pro		
	50					55					60						
Glu	Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Leu	Ser	Gly	Asp	Gly	Asp	Asp		
65					70					75					80		
Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp		
				85					90					95			
Asn	Ala	Lys	Asn	Asn	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ser	Ala		
			100					105					110				
Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Leu	Gly	Asp	Trp	Asp		
		115					120					125					
Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ser	Val	Ser	Ser	Gly	Gly		
	130					135					140						
Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala		
145					150					155					160		
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val		
				165					170					175			
Gly	Thr	Ser	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys		
			180					185					190				

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
 195 200 205
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 210 215 220
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
 225 230 235 240
 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
 245 250 255
 His His His His His His
 260

<210> 29
 <211> 804
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(801)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide
 sequence of polypeptide 2 of BS2

<400> 29
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 gcc cag ccg gcg atg gcc atg gag gtc caa ctg gtg gag agc ggt gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct 144
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
 35 40 45
 ggc ttc gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct 192
 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
 50 55 60
 gga aaa ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg 240
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
 65 70 75 80
 att aac tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac 288
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
 85 90 95
 aac gcc aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa 336
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 100 105 110
 gac acc ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg 384
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp

115	120	125	
ttt gct tat tgg ggc caa ggg acc ccg gtc acc gtc tcc gga ggc ggt			432
Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly			
130	135	140	
gga tcc gac att gtg atg tca caa tct cca tcc tcc ctg gct gtg tca			480
Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser			
145	150	155	160
cca gga gag aag gtc act atg acc tgc aaa tcc agt cag agt ctg ttc			528
Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe			
	165	170	175
aac agt aga acc cga aag aac tac ttg ggt tgg tac cag cag aaa cca			576
Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro			
	180	185	190
ggg cag tct cct aaa ctt ctg atc tac tgg gca tct act cgg gaa tct			624
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser			
	195	200	205
ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act			672
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr			
	210	215	220
ctc acc atc aac agt gtg cag tct gaa gac ctg gca gtt tat tac tgc			720
Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys			
	225	230	235
act caa gtt tat tat ctg agc acg ttc ggt gct ggg acc aag ctg gag			768
Thr Gln Val Tyr Tyr Leu Ser Thr Phe Gly Ala Gly Thr Lys Leu Glu			
	245	250	255
ctg aaa cgg ctc gag cac cac cac cac cac tga			804
Leu Lys Arg Leu Glu His His His His His His			
	260	265	

<210> 30

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
sequence of polypeptide 2 of BS2

<400> 30

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

Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
 65 70 75 80
 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
 85 90 95
 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 100 105 110
 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
 115 120 125
 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
 130 135 140
 Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser
 145 150 155 160
 Pro Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe
 165 170 175
 Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
 180 185 190
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
 195 200 205
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 210 215 220
 Leu Thr Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys
 225 230 235 240
 Thr Gln Val Tyr Tyr Leu Ser Thr Phe Gly Ala Gly Thr Lys Leu Glu
 245 250 255
 Leu Lys Arg Leu Glu His His His His His His
 260 265

<210> 31
 <211> 807
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(804)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide
 sequence h679-scFv-L5

<400> 31
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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
 1 5 10 15
 gcc cag ccg gcg atg gcc atg gaa gtg cag ctg gtg gag tca ggg gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30

gac tta gtg aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct	144
Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser	
35 40 45	
gga ttc act ttc agt att tac acc atg tct tgg ctt cgc cag act ccg	192
Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro	
50 55 60	
gga aag ggg ctg gag tgg gtc gca acc ctg agt ggt gat ggt gat gac	240
Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp	
65 70 75 80	
atc tac tat cca gac agt gtg aag ggt cga ttc acc atc tcc aga gac	288
Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp	
85 90 95	
aat gcc aag aac agc cta tat ctg cag atg aac agt cta agg gct gag	336
Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu	
100 105 110	
gac acg gcc ttg tat tac tgt gca agg gtg cga ctt ggg gac tgg gac	384
Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp	
115 120 125	
ttc gat gtc tgg ggc caa ggg acc acg gtc tcc gtc tcc tca gga ggt	432
Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly	
130 135 140	
ggc gga tcc gac att gtg atg aca caa tct cca tcc tcc ctg gct gtg	480
Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val	
145 150 155 160	
tca ccc ggg gag agg gtc act ctg acc tgc aaa tcc agt cag agt ctg	528
Ser Pro Gly Glu Arg Val Thr Leu Thr Cys Lys Ser Ser Gln Ser Leu	
165 170 175	
ttc aac agt aga acc cga aag aac tac ttg ggt tgg tac cag cag aaa	576
Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys	
180 185 190	
cca ggg cag tct cct aaa ctt ctg atc tac tgg gca tct act cgg gaa	624
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu	
195 200 205	
tct ggg gtc cct gat cgc ttc tca ggc agt gga tcc gga aca gat ttc	672
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
act ctc acc atc aac agt ctg cag gct gaa gac gtg gca gtt tat tac	720
Thr Leu Thr Ile Asn Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr	
225 230 235 240	
tgc act caa gtt tat tat ctg tgc acg ttc ggt gct ggg acc aag ctg	768
Cys Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu	
245 250 255	
gag ctg aaa cgg ctc gag cac cac cac cac cac cac tga	807
Glu Leu Lys Arg Leu Glu His His His His His His	
260 265	

<210> 32
 <211> 268
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide
 sequence of h679-scFv-L5

<400> 32

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	1	5	10	15
Ala	Gln	Pro	Ala	Met	Ala	Met	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	20	25	30	
Asp	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	35	40	45	
Gly	Phe	Thr	Phe	Ser	Ile	Tyr	Thr	Met	Ser	Trp	Leu	Arg	Gln	Thr	Pro	50	55	60	
Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Thr	Leu	Ser	Gly	Asp	Gly	Asp	Asp	65	70	75	80
Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	85	90	95	
Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	100	105	110	
Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Leu	Gly	Asp	Trp	Asp	115	120	125	
Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ser	Val	Ser	Ser	Gly	Gly	130	135	140	
Gly	Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	145	150	155	160
Ser	Pro	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	165	170	175	
Phe	Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	180	185	190	
Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	195	200	205	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	210	215	220	
Thr	Leu	Thr	Ile	Asn	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	225	230	235	240
Cys	Thr	Gln	Val	Tyr	Tyr	Leu	Cys	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	245	250	255	
Glu	Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His	His	His	His	His	260	265		

<210> 33
 <211> 789
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(786)

<220>
 <223> Description of Artificial Sequence: Synthetic nucleotide sequence for polypeptide 1 of BS1.5H (h679XhMN14 bispecific diabody)

<400> 33
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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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gcc cag ccg gcg atg gcc atg gaa gtg cag ctg gtg gag tca ggg gga 96
 Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30

gac tta gtg aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct 144
 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 35 40 45

gga ttc act ttc agt att tac acc atg tct tgg ctt cgc cag act ccg 192
 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
 50 55 60

gga aag ggg ctg gag tgg gtc gca acc ctg agt ggt gat ggt gat gac 240
 Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
 65 70 75 80

atc tac tat cca gac agt gtg aag ggt cga ttc acc atc tcc aga gac 288
 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 85 90 95

aat gcc aag aac agc cta tat ctg cag atg aac agt cta agg gct gag 336
 Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 100 105 110

gac acg gcc ttg tat tac tgt gca agg gtg cga ctt ggg gac tgg gac 384
 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
 115 120 125

ttc gat gtc tgg ggc caa ggg acc acg gtc tcc gtc tcc tca gga ggt 432
 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly
 130 135 140

ggc gga tcc gac atc cag ctg acc cag agc cca agc agc ctg agc gcc 480
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
 145 150 155 160

agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag gat gtg 528
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
 165 170 175

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ggt act tct gta gct tgg tac cag cag aag cca ggt aag gct cca aag 576
Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
180 185 190

ctg ctg atc tac tgg aca tcc acc cgg cac act ggt gtg cca agc aga 624
Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
195 200 205

ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 672
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
210 215 220

ctc cag cca gag gac atc gcc acc tac tac tgc cag caa tat agc ctc 720
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
225 230 235

tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt ctc gag 768
Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
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<210> 34
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<213> Artificial Sequence

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sequence for polypeptide 1 of BS1.5H (h679XhMN14 bispecific
diabody)

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20 25 30

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35 40 45

Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
50 55 60

Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
65 70 75 80

Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
85 90 95

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
100 105 110

Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
115 120 125

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

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

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
                      165                      170                      175

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                      180                      185                      190

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
 195                      200                      205

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 210                      215                      220

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

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
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His His His His His His
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diabody)

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 1                      5                      10                      15

gcc cag ccg gcg atg gcc atg gag gtc caa ctg gtg gag agc ggt gga 96
Ala Gln Pro Ala Met Ala Met Glu Val Gln Leu Val Glu Ser Gly Gly
                20                      25                      30

ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct 144
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
                35                      40                      45

ggc ttc gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct 192
Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
 50                      55                      60

gga aaa ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg 240

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Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	His	Pro	Asp	Ser	Ser	Thr	
65					70					75					80	
att	aac	tat	gcg	ccg	tct	cta	aag	gat	aga	ttt	aca	ata	tcg	cga	gac	288
Ile	Asn	Tyr	Ala	Pro	Ser	Leu	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
				85				90					95			
aac	gcc	aag	aac	aca	ttg	ttc	ctg	caa	atg	gac	agc	ctg	aga	ccc	gaa	336
Asn	Ala	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	
			100				105					110				
gac	acc	ggg	gtc	tat	ttt	tgt	gca	agc	ctt	tac	ttc	ggc	ttc	ccc	tgg	384
Asp	Thr	Gly	Val	Tyr	Phe	Cys	Ala	Ser	Leu	Tyr	Phe	Gly	Phe	Pro	Trp	
		115					120					125				
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Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Gly	Gly	Gly	
	130					135					140					
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Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	Ser	
145					150				155						160	
ccc	ggg	gag	agg	gtc	act	ctg	acc	tgc	aaa	tcc	agt	cag	agt	ctg	ttc	528
Pro	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Phe	
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aac	agt	aga	acc	cga	aag	aac	tac	ttg	ggc	tgg	tac	cag	cag	aaa	cca	576
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Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
	210					215					220					
ctc	acc	atc	aac	agt	ctg	cag	gct	gaa	gac	gtg	gca	gtt	tat	tac	tgc	720
Leu	Thr	Ile	Asn	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	
225					230				235						240	
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Thr	Gln	Val	Tyr	Tyr	Leu	Cys	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	
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ctg	aaa	cgg	ctc	gag	cac	cac	cac	cac	cac	cac	tga					804
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<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide sequence for polypeptide 1 of BS1.5H (h679XhMN14 bispecific diabody)

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Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	His	Pro	Asp	Ser	Ser	Thr
65					70					75					80
Ile	Asn	Tyr	Ala	Pro	Ser	Leu	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp
				85					90					95	
Asn	Ala	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu
			100					105					110		
Asp	Thr	Gly	Val	Tyr	Phe	Cys	Ala	Ser	Leu	Tyr	Phe	Gly	Phe	Pro	Trp
		115					120					125			
Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	Ser
145					150					155					160
Pro	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Phe
				165					170					175	
Asn	Ser	Arg	Thr	Arg	Lys	Asn	Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro
			180					185					190		
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser
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Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
	210					215					220				
Leu	Thr	Ile	Asn	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys
225					230					235					240
Thr	Gln	Val	Tyr	Tyr	Leu	Cys	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu
				245					250					255	
Leu	Lys	Arg	Leu	Glu	His	His	His	His	His	His					
			260					265							

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<211> 40

<212> DNA

<213> Artificial Sequence

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<210> 38
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<210> 42
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<210> 43
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<212> DNA

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<210> 54

<211> 30

<212> DNA

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52392-36

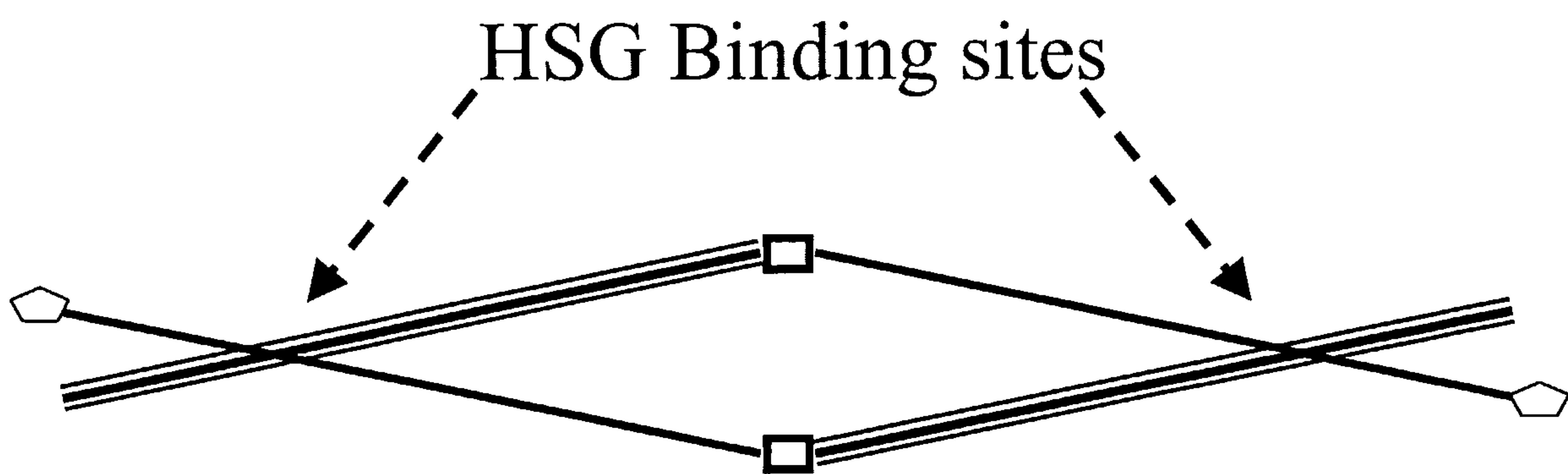
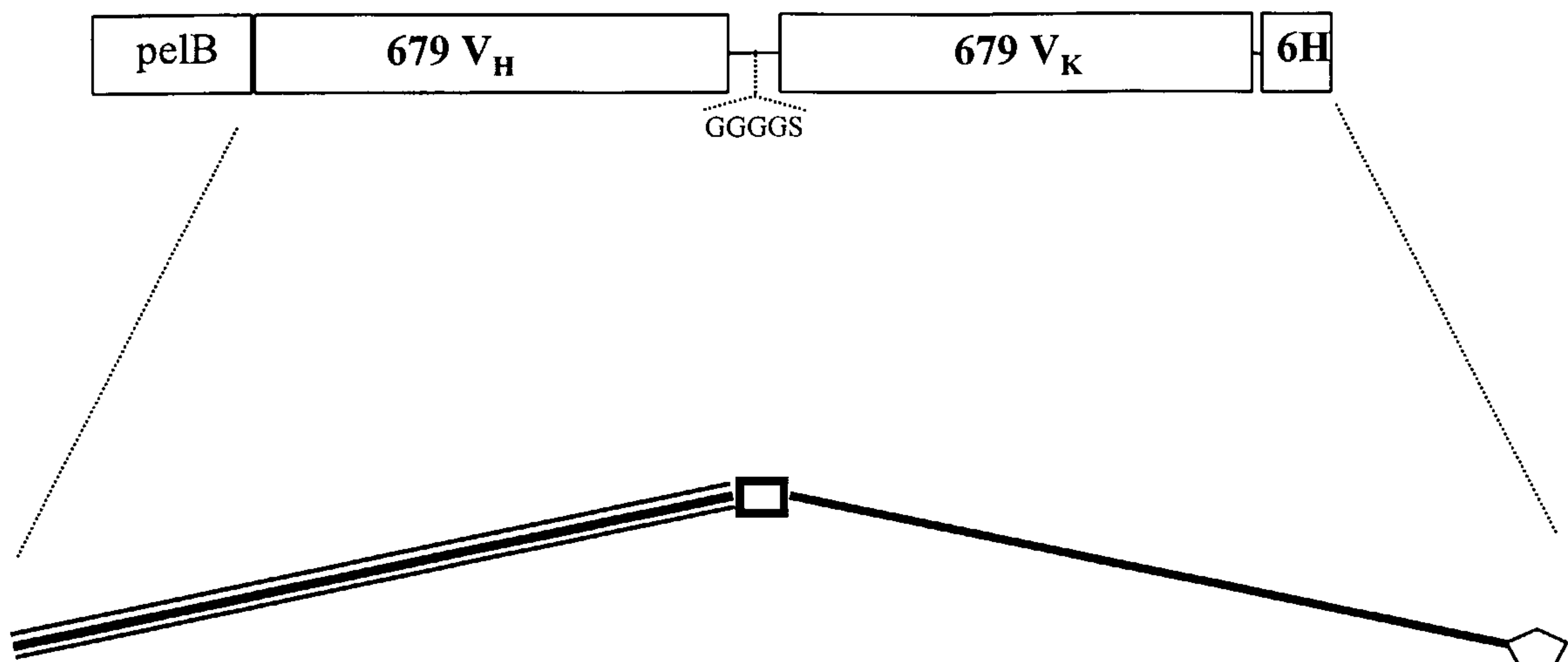
CLAIMS:

1. A humanized monoclonal antibody comprising the light chain variable region complementarity determining region (CDR) sequences CDR1 (KSSQSLFNSRRTKNYLG) CDR2 (WASTRES) and CDR3 (TQVYYLCT) and heavy chain CDR sequences CDR1 (IYTMS) CDR2 (TLSGDGDDIYYPDSVKG) and CDR3 (VRLGDWDFDV) and human antibody framework region (FR) and constant region sequences.
2. The humanized antibody of claim 1, comprising the VH polypeptide of h679 MAb, including residues 70-426 of SEQ ID NO:32 and the VK polypeptide of h679 MAb, including residues 442-780 of SEQ ID NO:32.
3. A fusion protein comprising a humanized monoclonal antibody or fragment thereof, wherein said antibody or fragment comprises the light chain variable region complementarity determining region (CDR) sequences CDR1 (KSSQSLFNSRRTKNYLG) CDR2 (WASTRES) and CDR3 (TQVYYLCT) and heavy chain CDR sequences CDR1 (IYTMS) CDR2 (TLSGDGDDIYYPDSVKG) and CDR3 (VRLGDWDFDV) and human antibody framework region (FR) sequences.
4. The fusion protein of claim 3, comprising the VH polypeptide of h679 MAb, including residues 70-426 of SEQ ID NO:32 and the VK polypeptide of h679 MAb, including residues 442-780 of SEQ ID NO:32.
5. A multivalent, multispecific binding protein comprising a histamine-succinyl-glycyl binding humanized monoclonal antibody or fragment thereof, wherein said antibody or fragment comprises the light chain variable region complementarity determining region (CDR) sequences CDR1 (KSSQSLFNSRRTKNYLG) CDR2 (WASTRES) and CDR3 (TQVYYLCT) and heavy chain CDR sequences CDR1 (IYTMS) CDR2 (TLSGDGDDIYYPDSVKG) and CDR3 (VRLGDWDFDV) and human antibody framework region (FR) sequences.
6. The multivalent, multispecific binding protein of claim 5, comprising the VH polypeptide of h679 MAb, including residues 70-426 of SEQ ID NO:32 and the VK polypeptide of h679 MAb, including residues 442-780 of SEQ ID NO:32.

52392-36

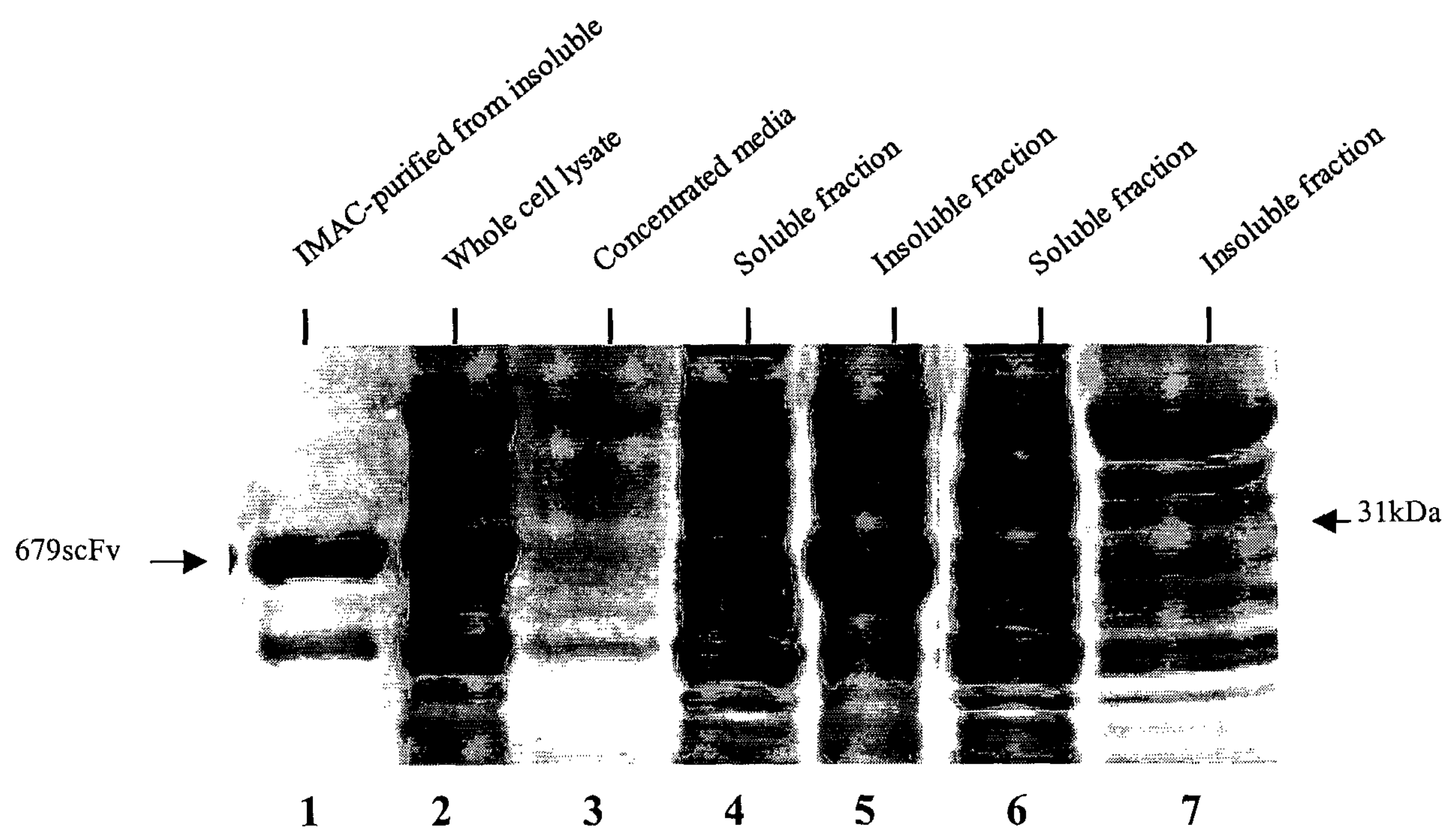
7. The multivalent, multispecific binding protein of claim 6, further comprising a carcinoembryonic antigen (CEA) binding site having an affinity towards CEA.
8. The multivalent binding protein of claim 7, comprising a VH polypeptide of hMN14, including residues 70-423 of SEQ ID NO: 18, and a VK polypeptide of hMN14, including residues 439-759 of SEQ ID NO: 18.
9. A kit comprising an antibody according to claim 1, a fusion protein according to claim 3, or a multivalent binding protein according to claim 5; and instructions for using the kit.
10. A pharmaceutical composition comprising an antibody according to claim 1, a fusion protein according to claim 3 or a multivalent binding protein according to claim 5, in a pharmaceutically acceptable excipient.
11. An isolated nucleic acid encoding an antibody according to claim 1, a fusion protein according to claim 3, or a multivalent binding protein according to claim 5.
12. An expression vector comprising a nucleic acid according to claim 11.
13. A host cell comprising an expression vector according to claim 12.

679scFv polypeptide

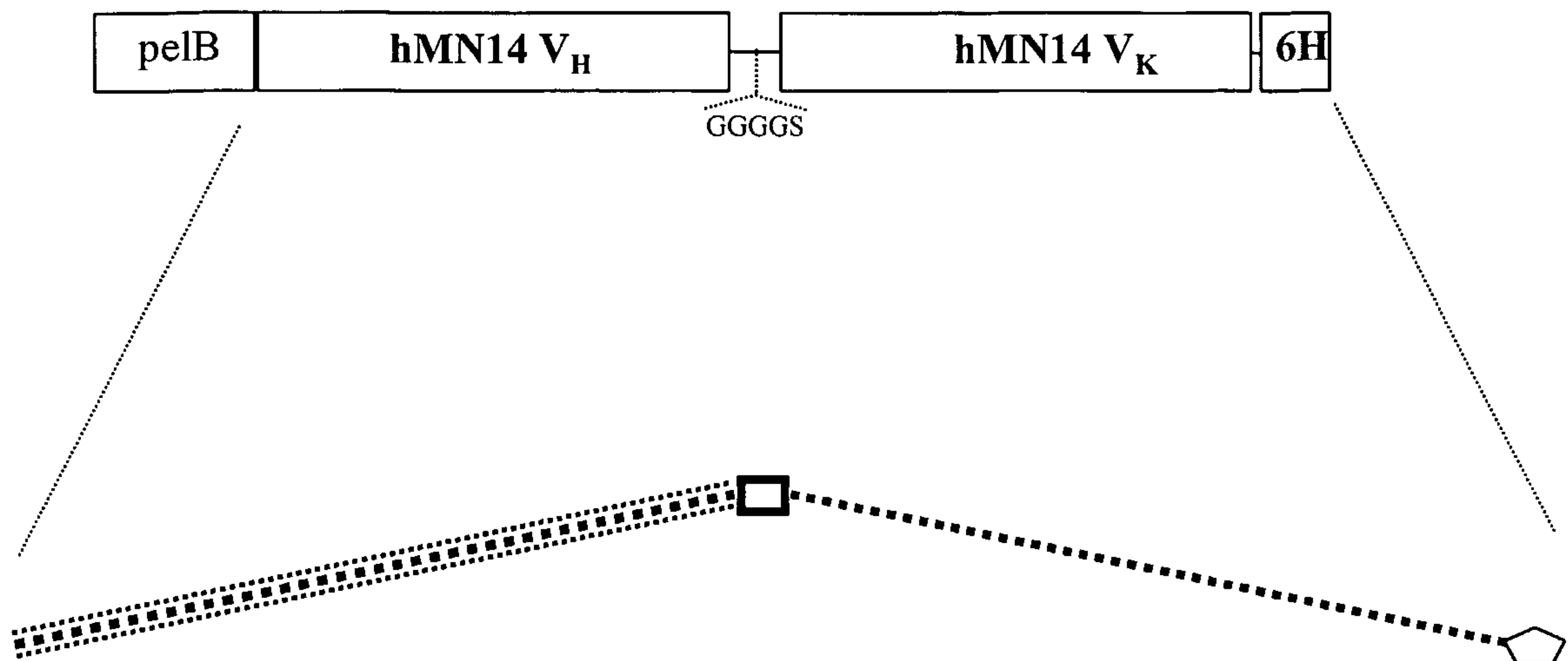


679 diabody

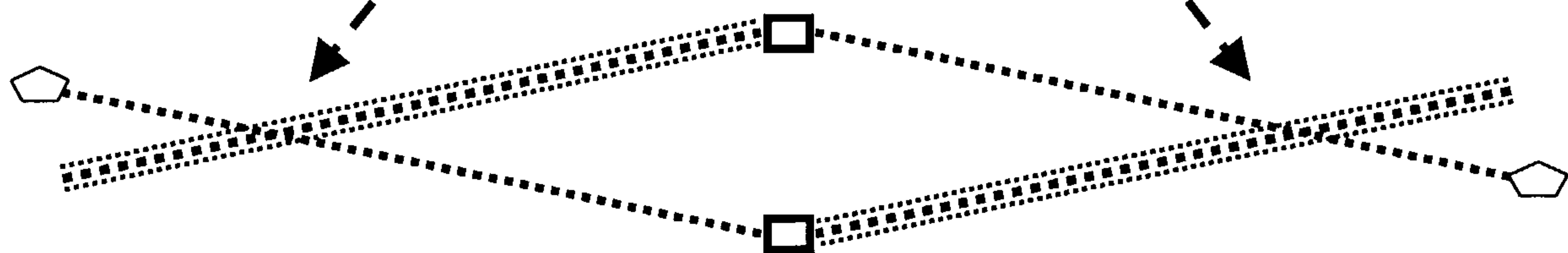
FIGURE 1

**FIGURE 2**

hMN14scFv polypeptide



CEA Binding sites



hMN14 diabody

FIGURE 3

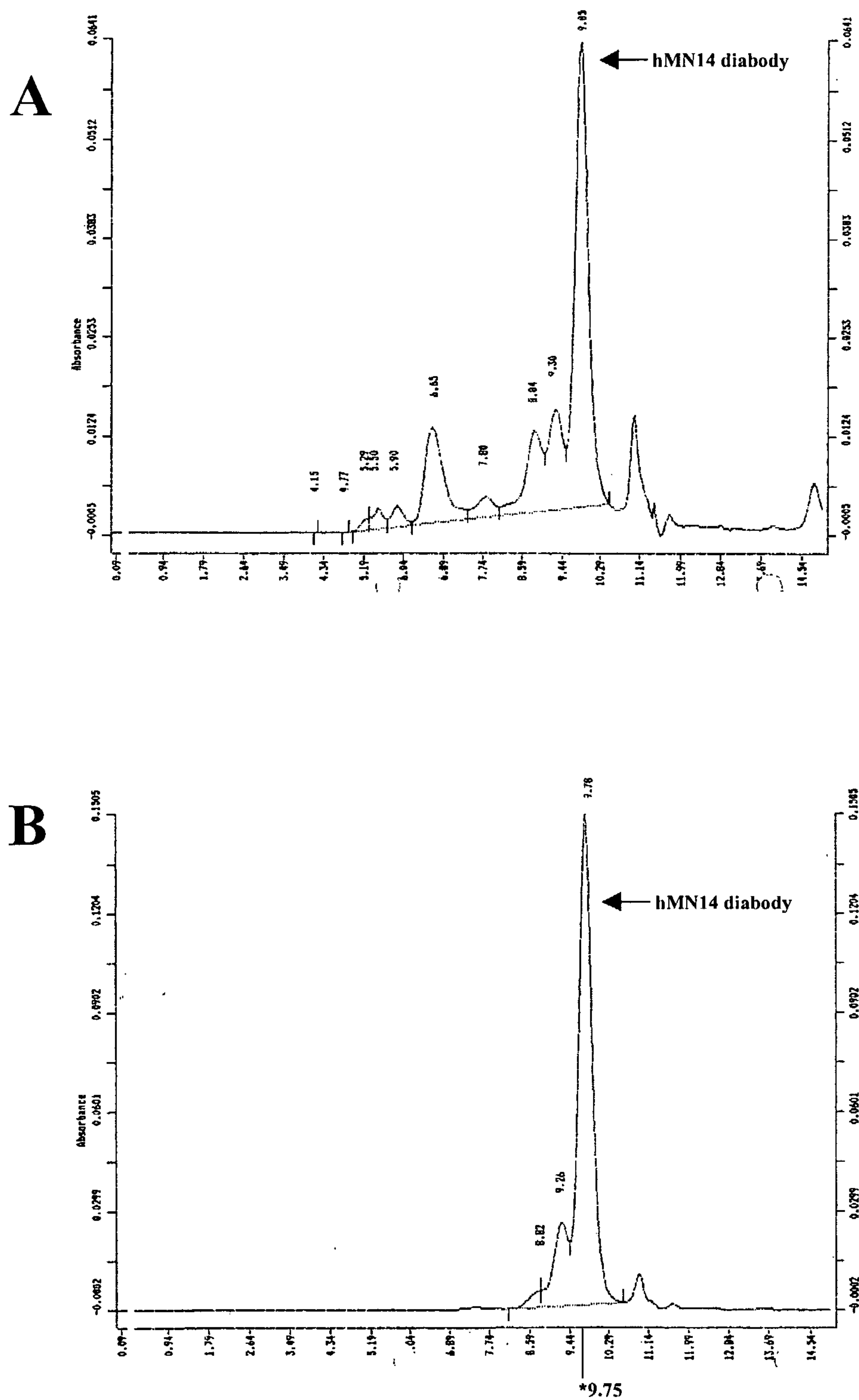


FIGURE 4

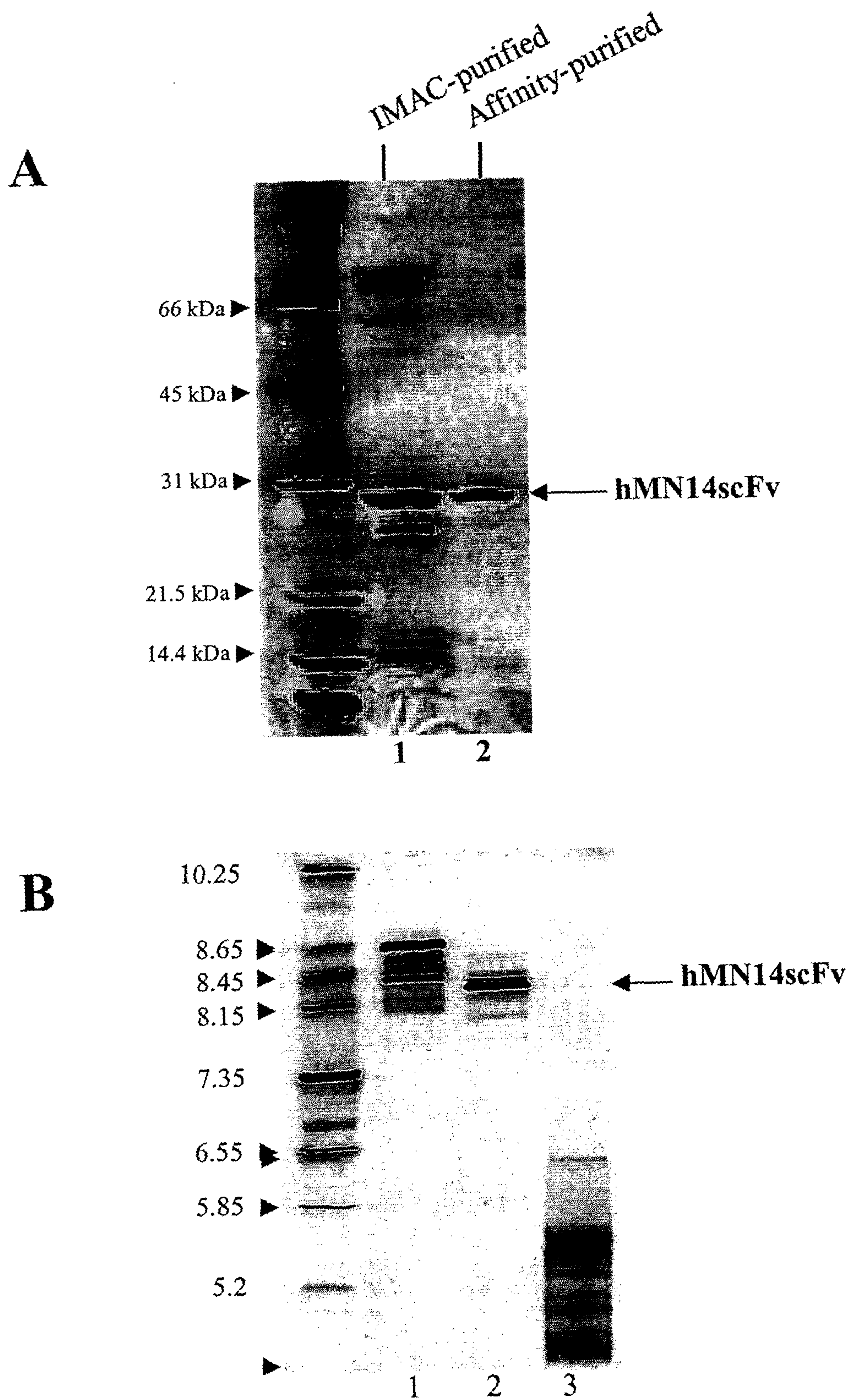
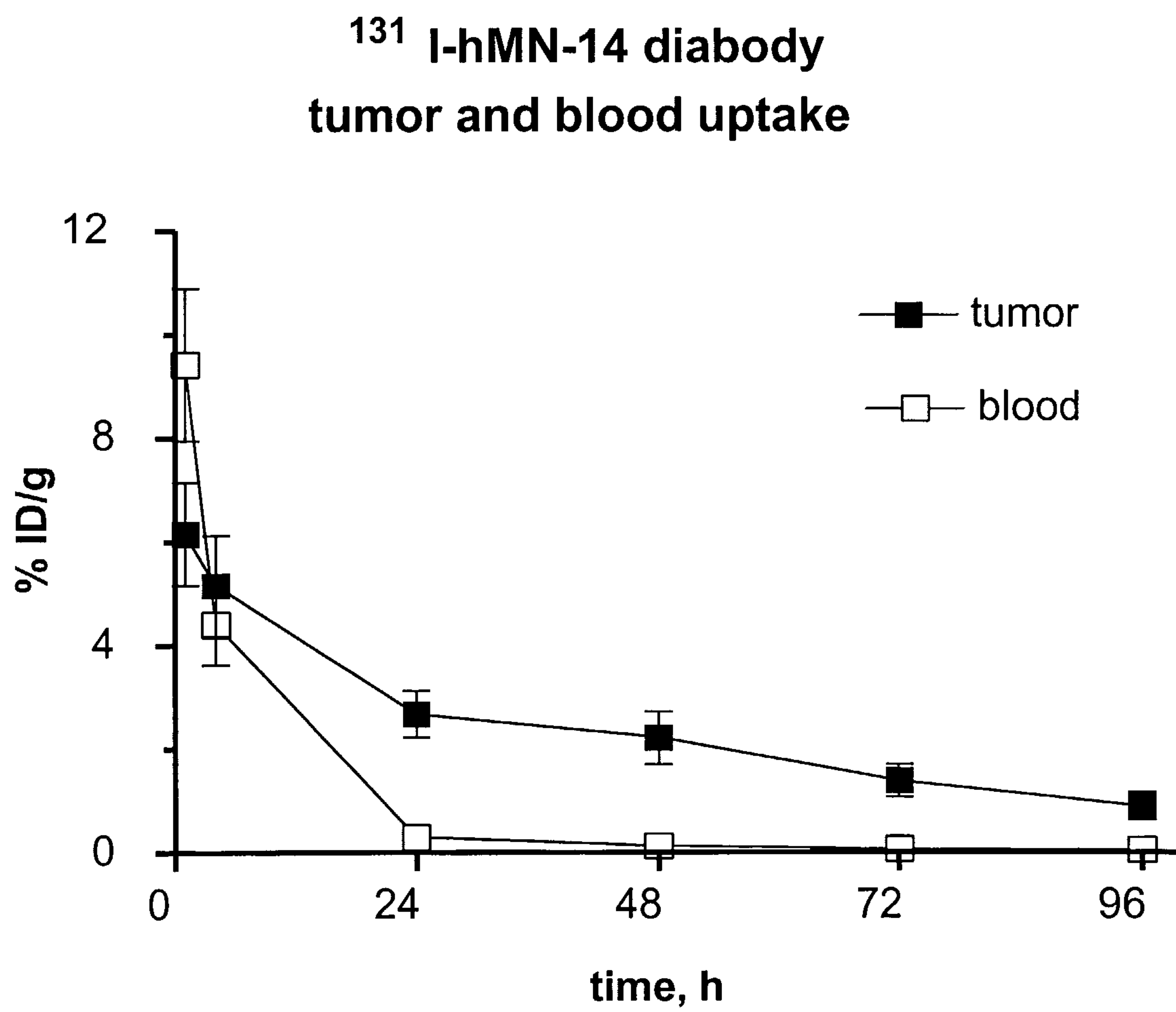
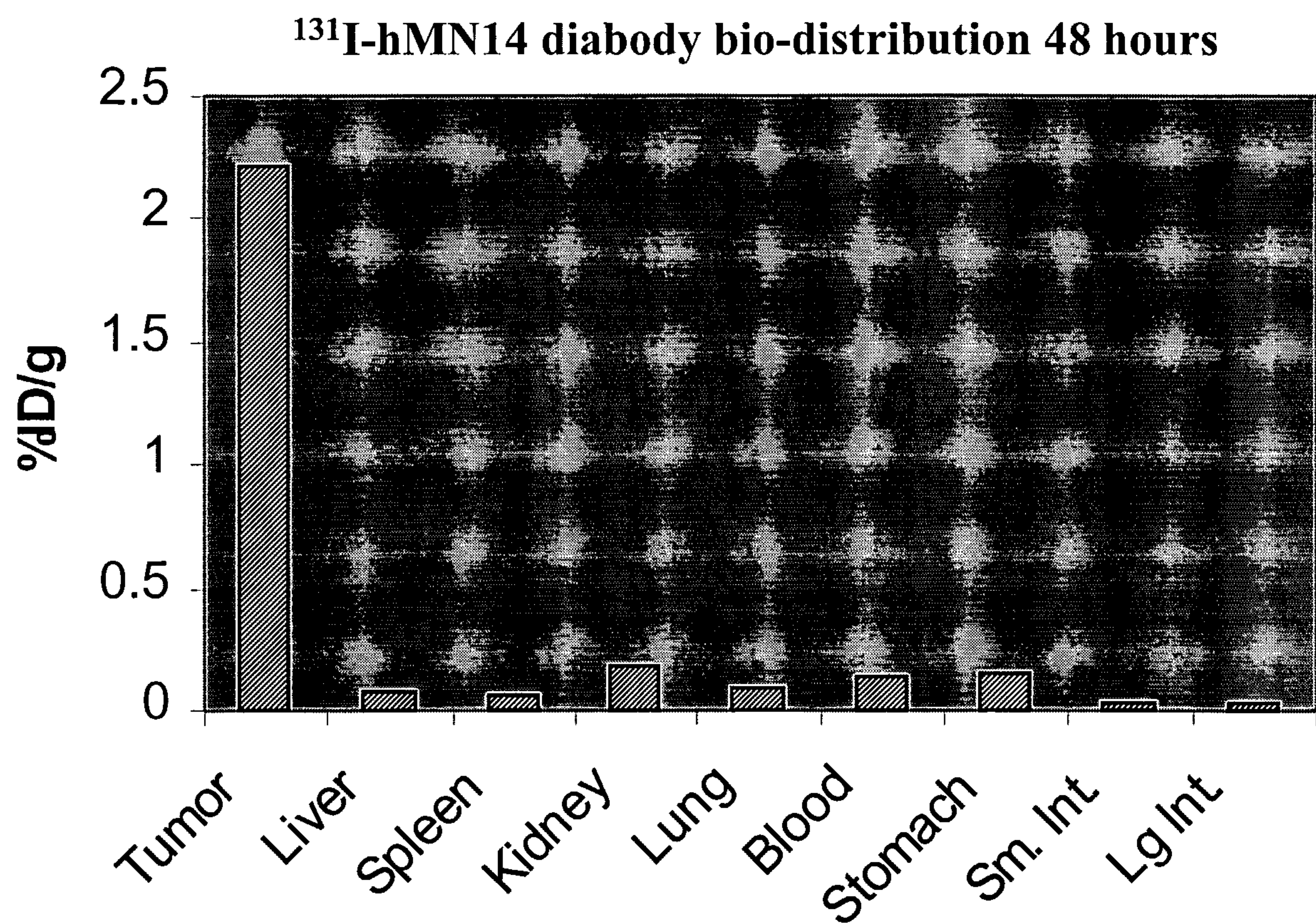


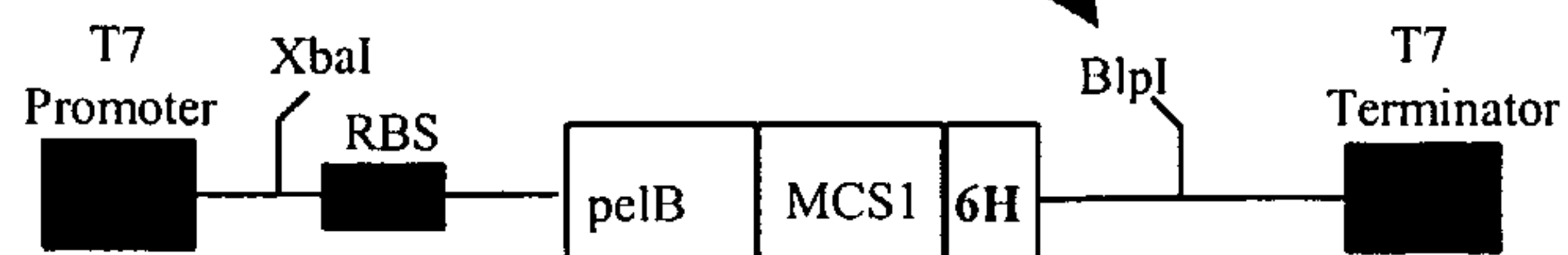
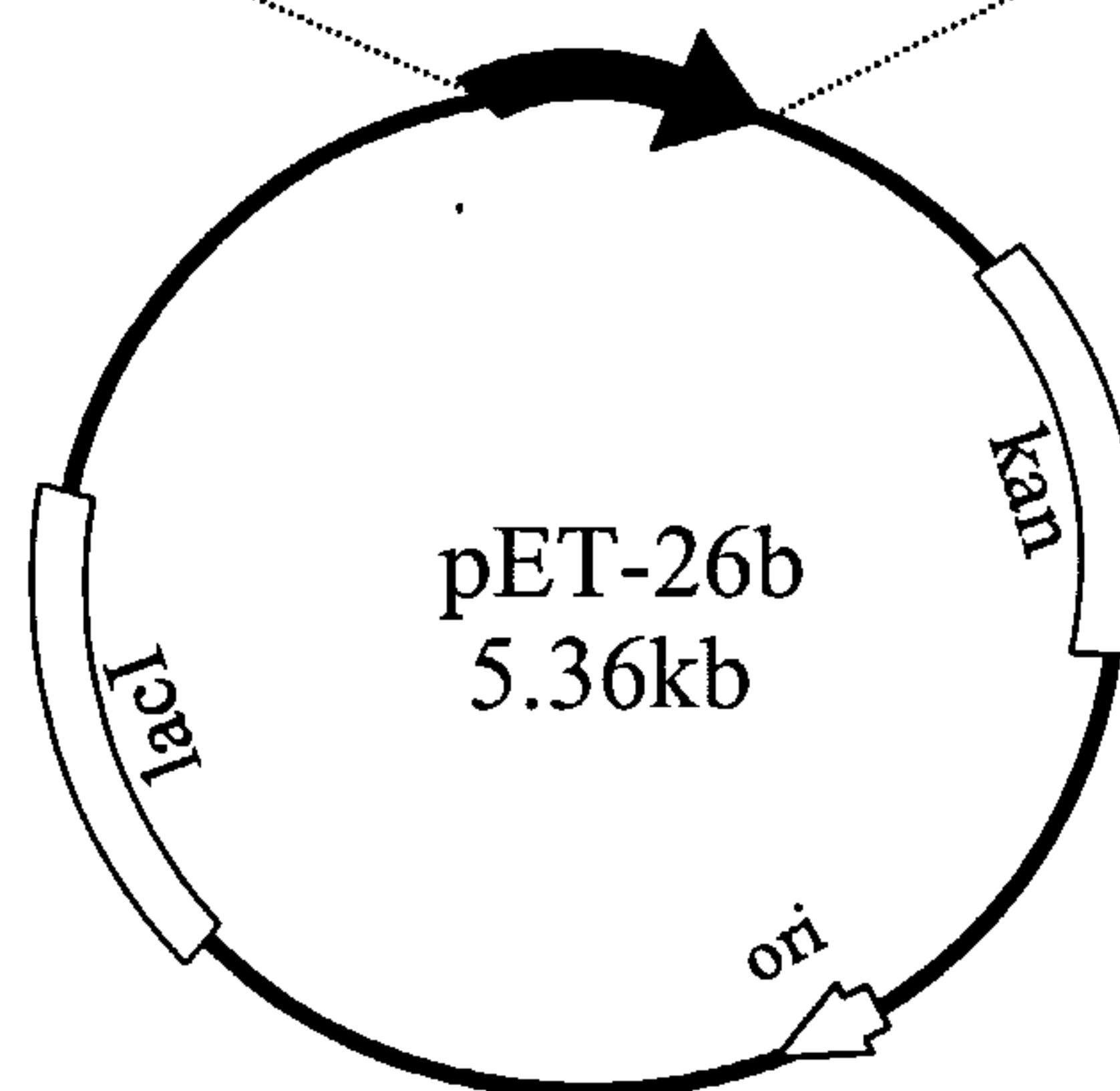
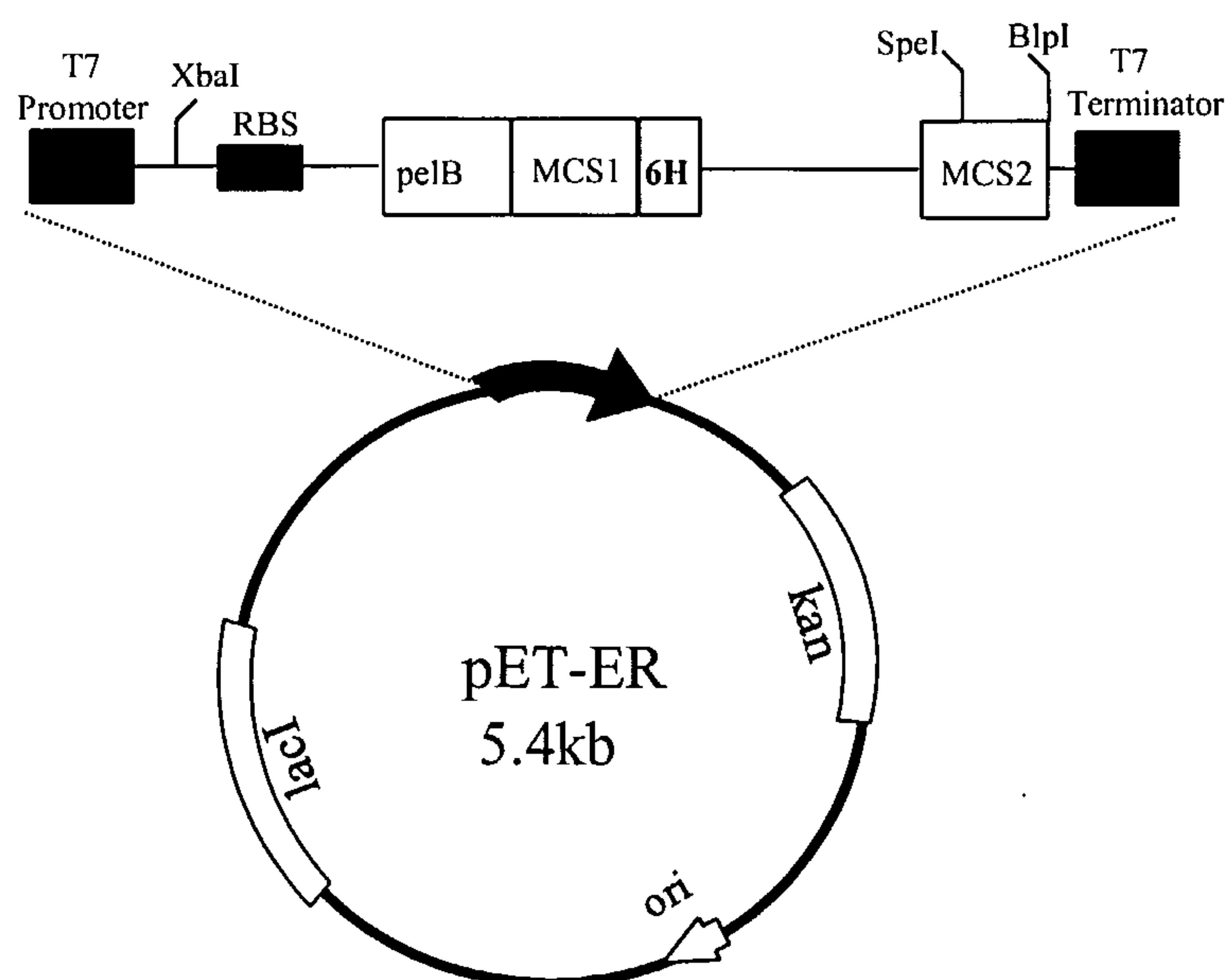
FIGURE 5

**FIGURE 6**

**FIGURE 7**

A

Age I Pst I Spe I Kpn I Sal I Stu I NheI NheI
 5' -TGACCGGTCTGCAGACTAGTGGTACCGTCGACAGGCCTGCTAGC-3'
 3' -GGCCAGACGTCTGATCACCATGGCAGCTGTCCGGACGATCGACT-5'

MCS2**B****C****FIGURE 8**

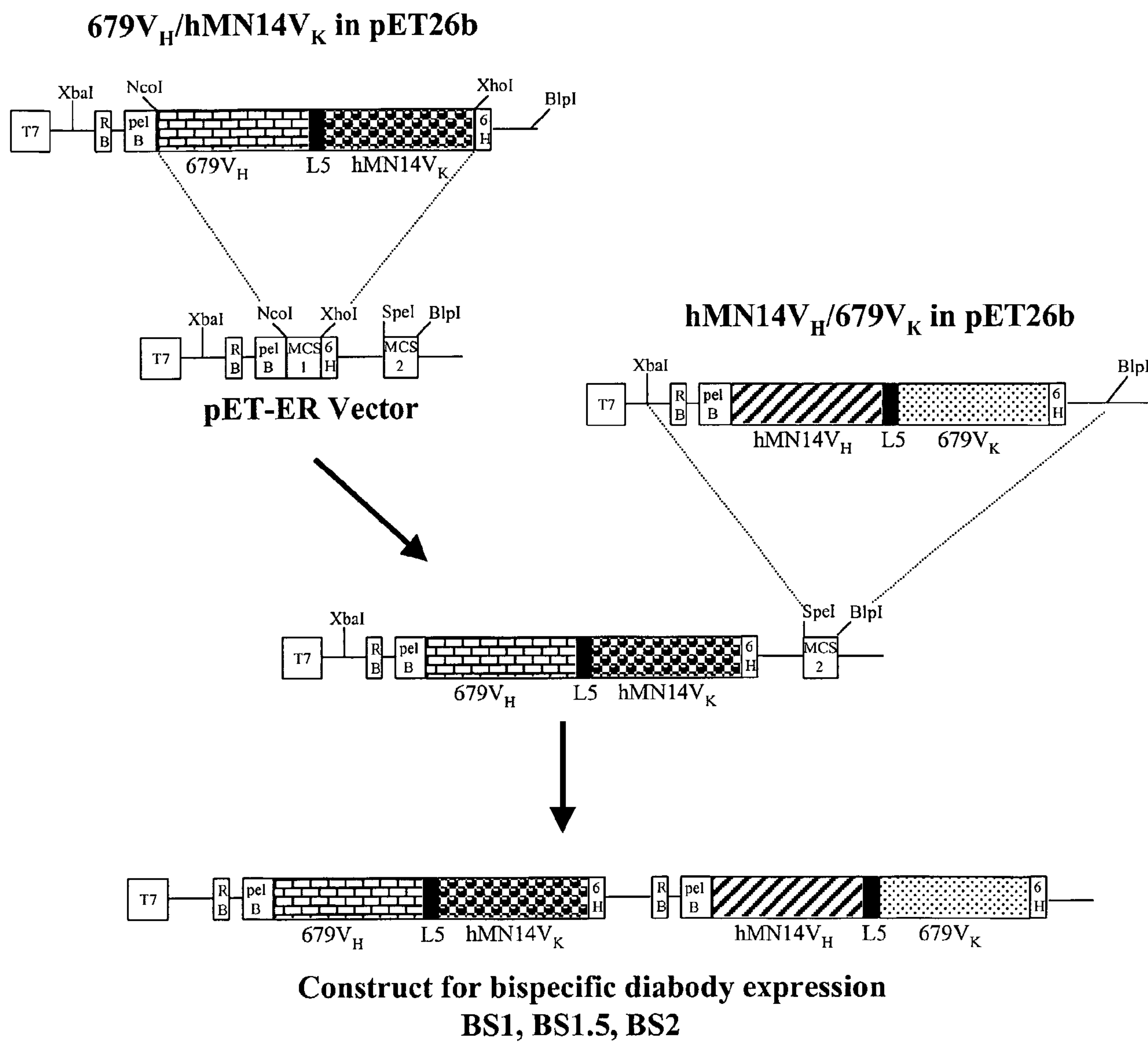


FIGURE 9

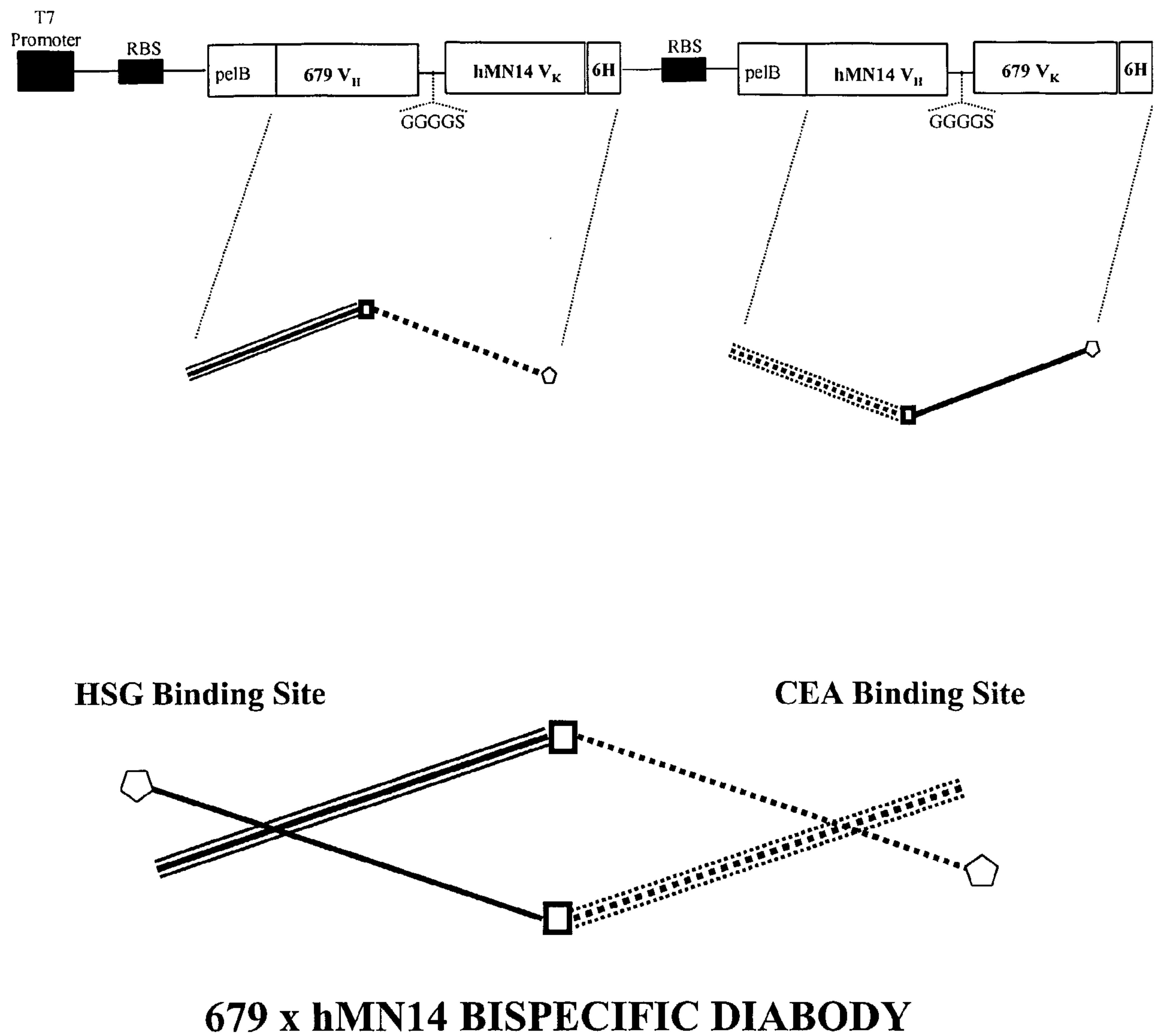


FIGURE 10

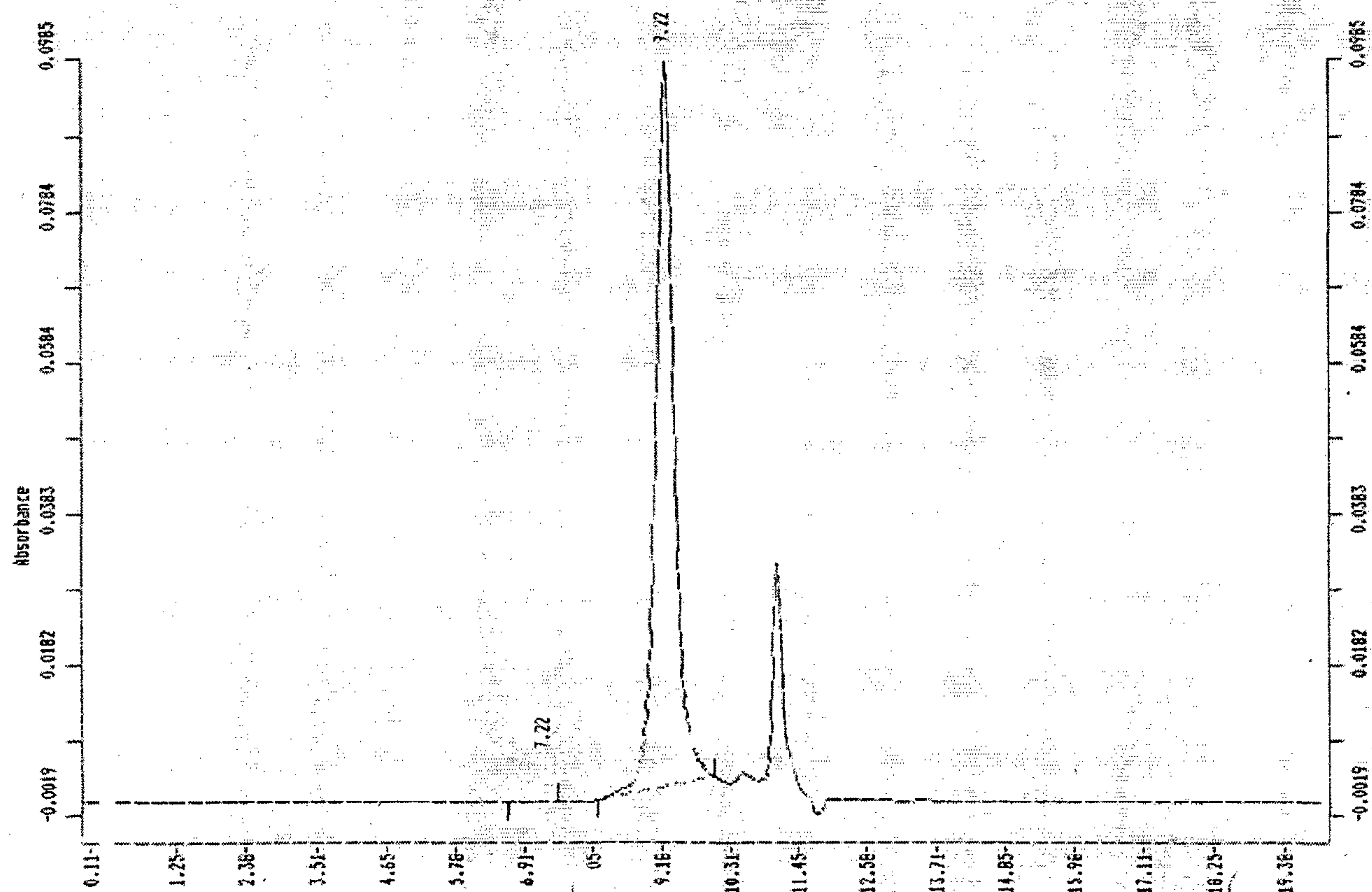


FIGURE 11

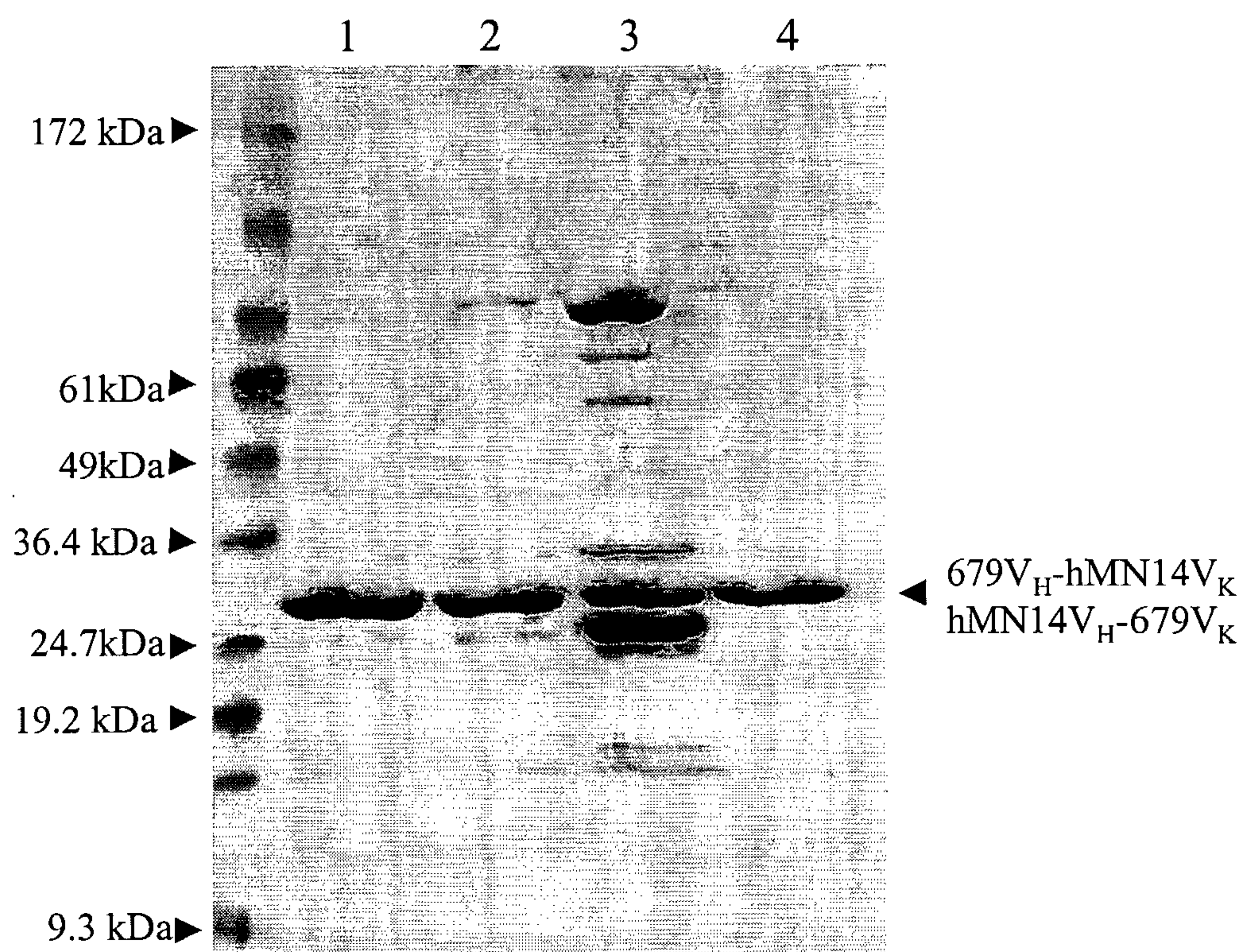
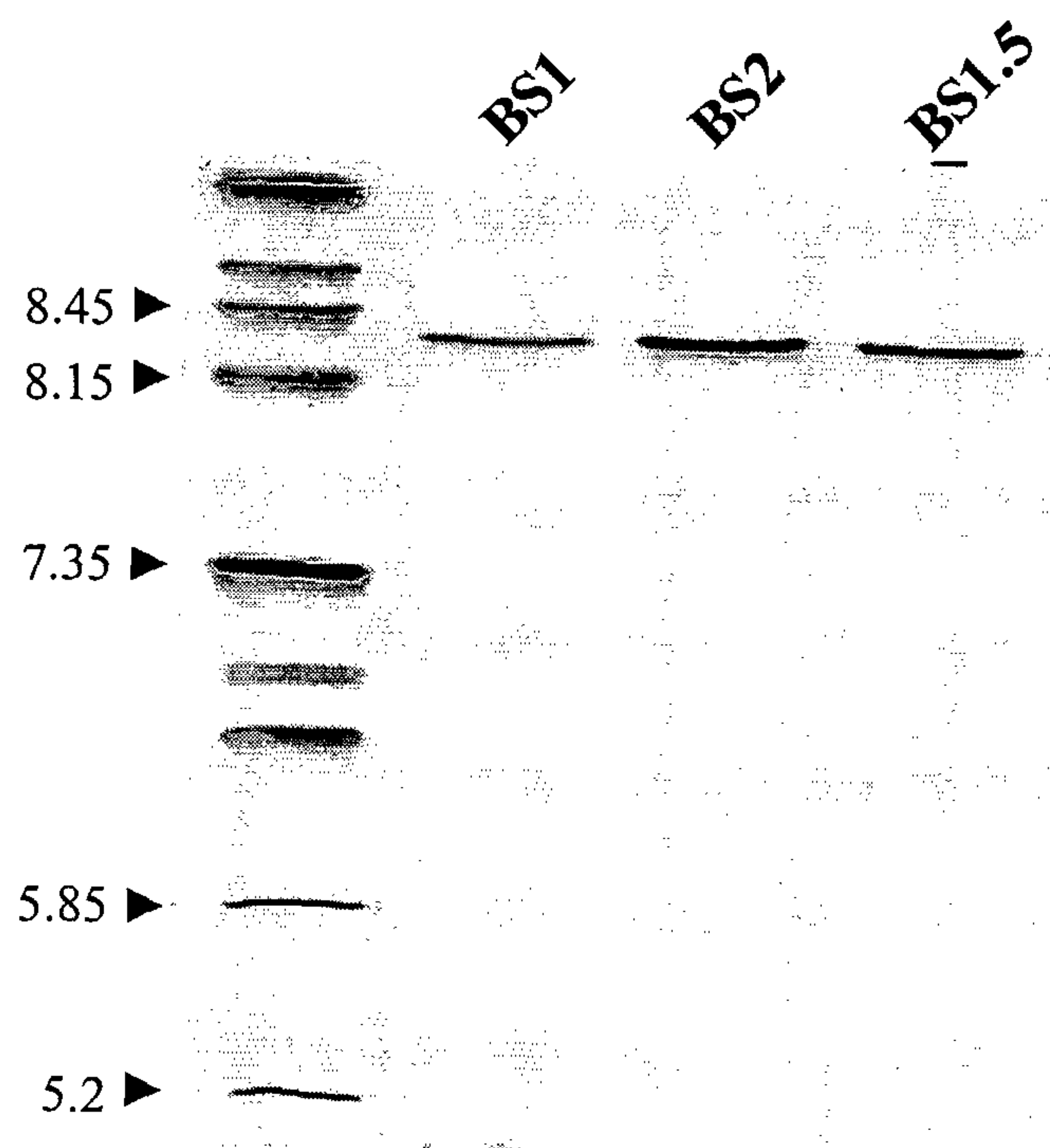


FIGURE 12

**FIGURE 13**

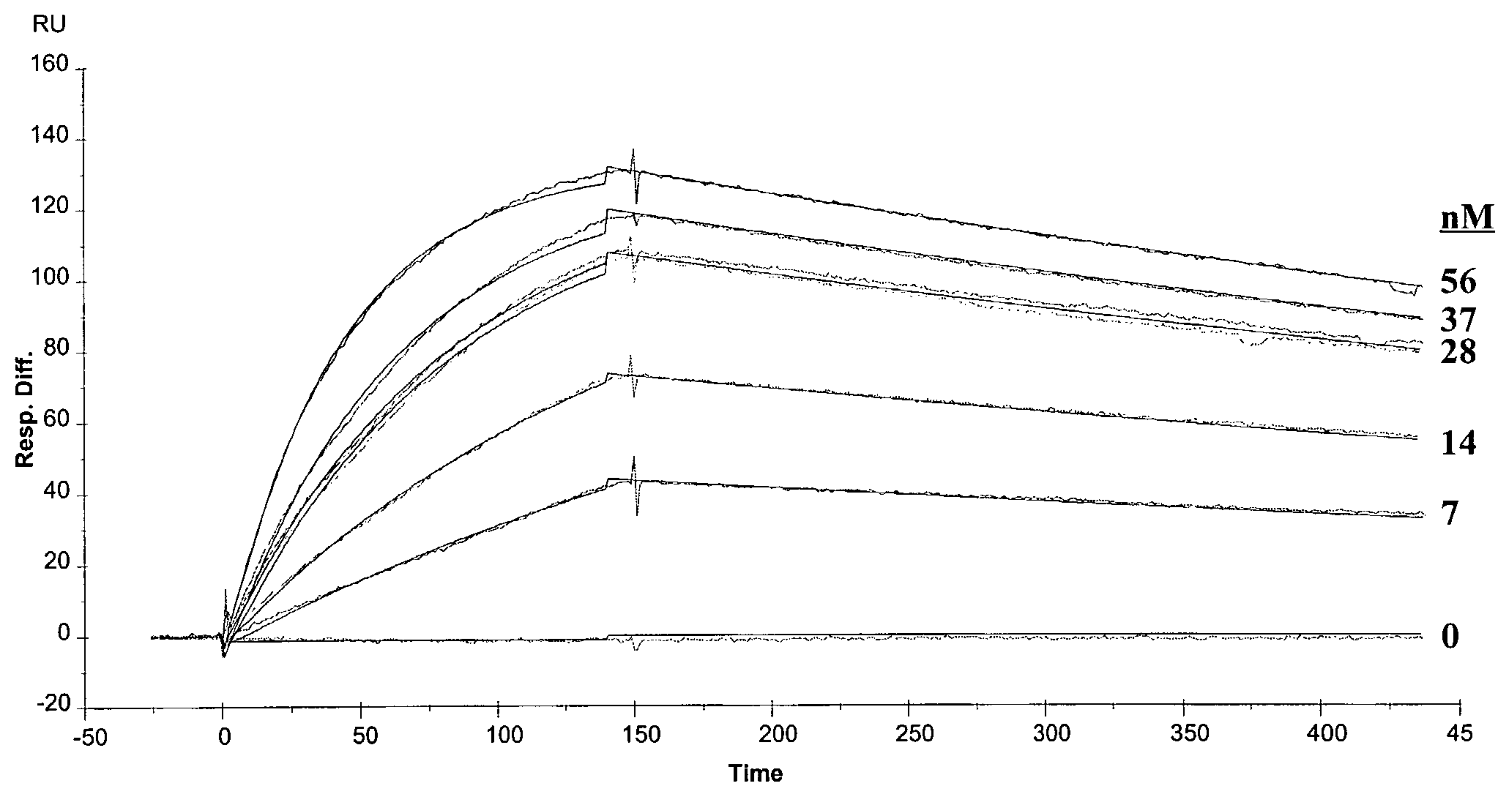
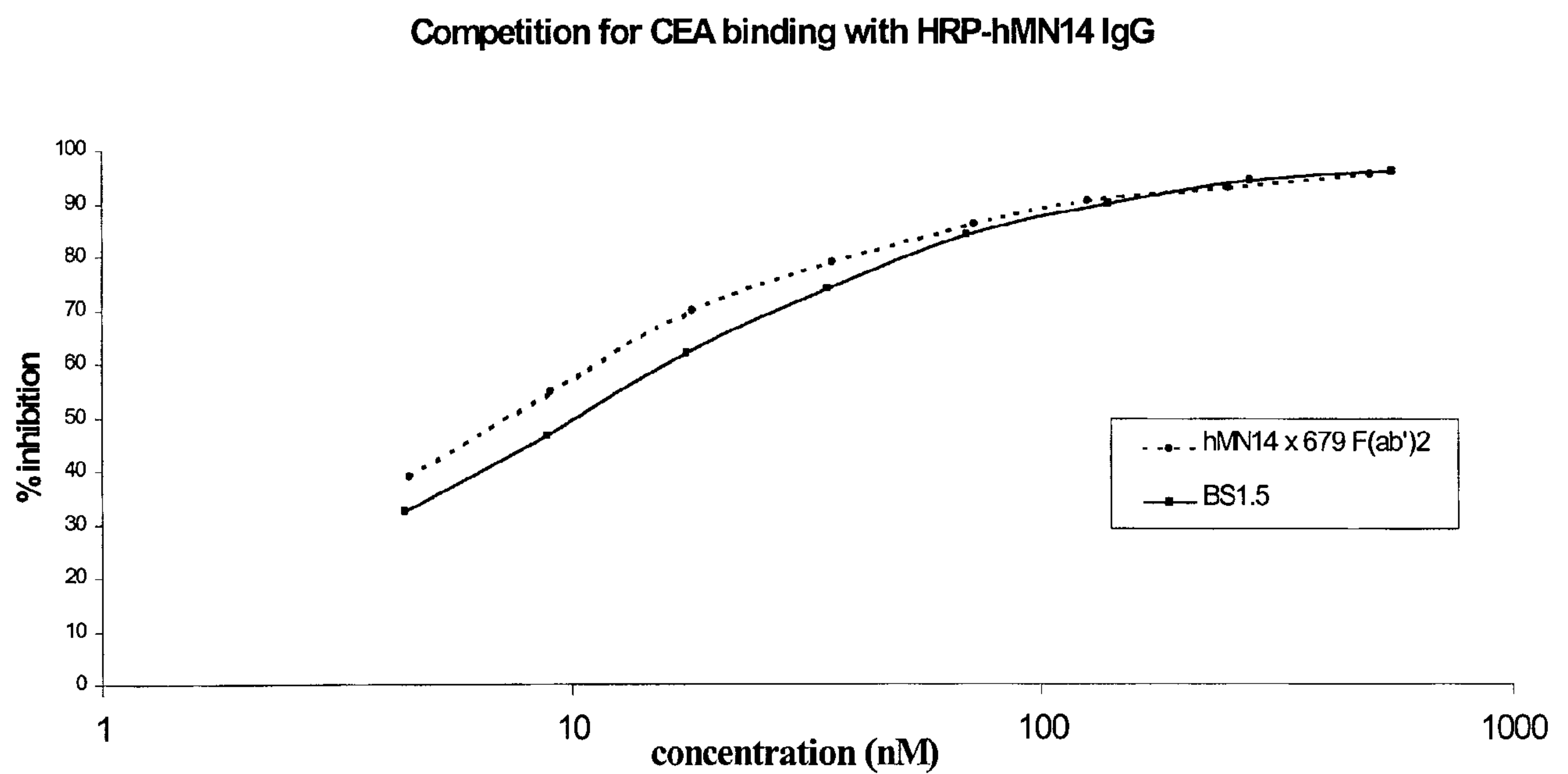


FIGURE 14



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

FIGURE 15

Simultaneous bi-specific binding of BS1.5

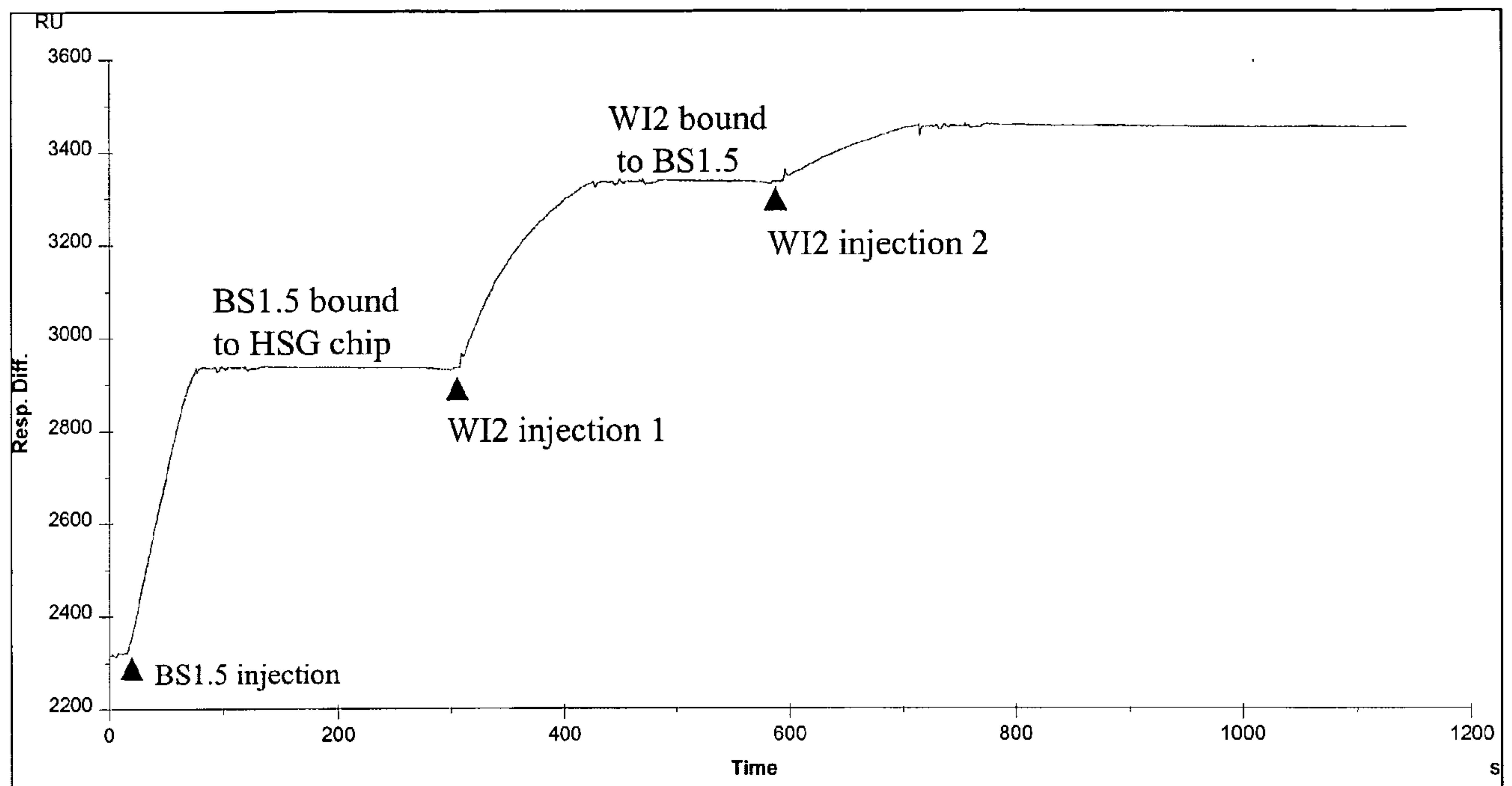
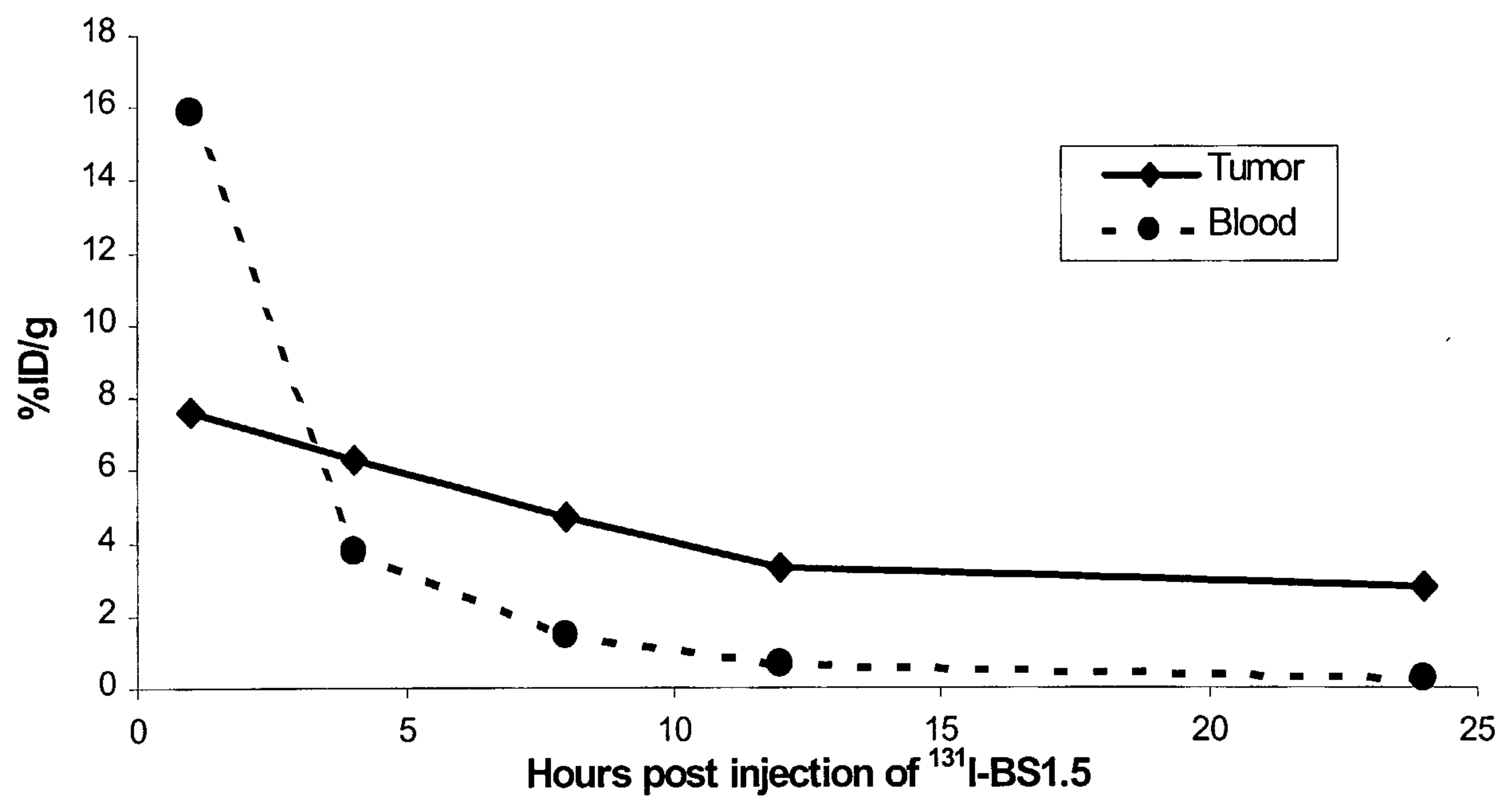
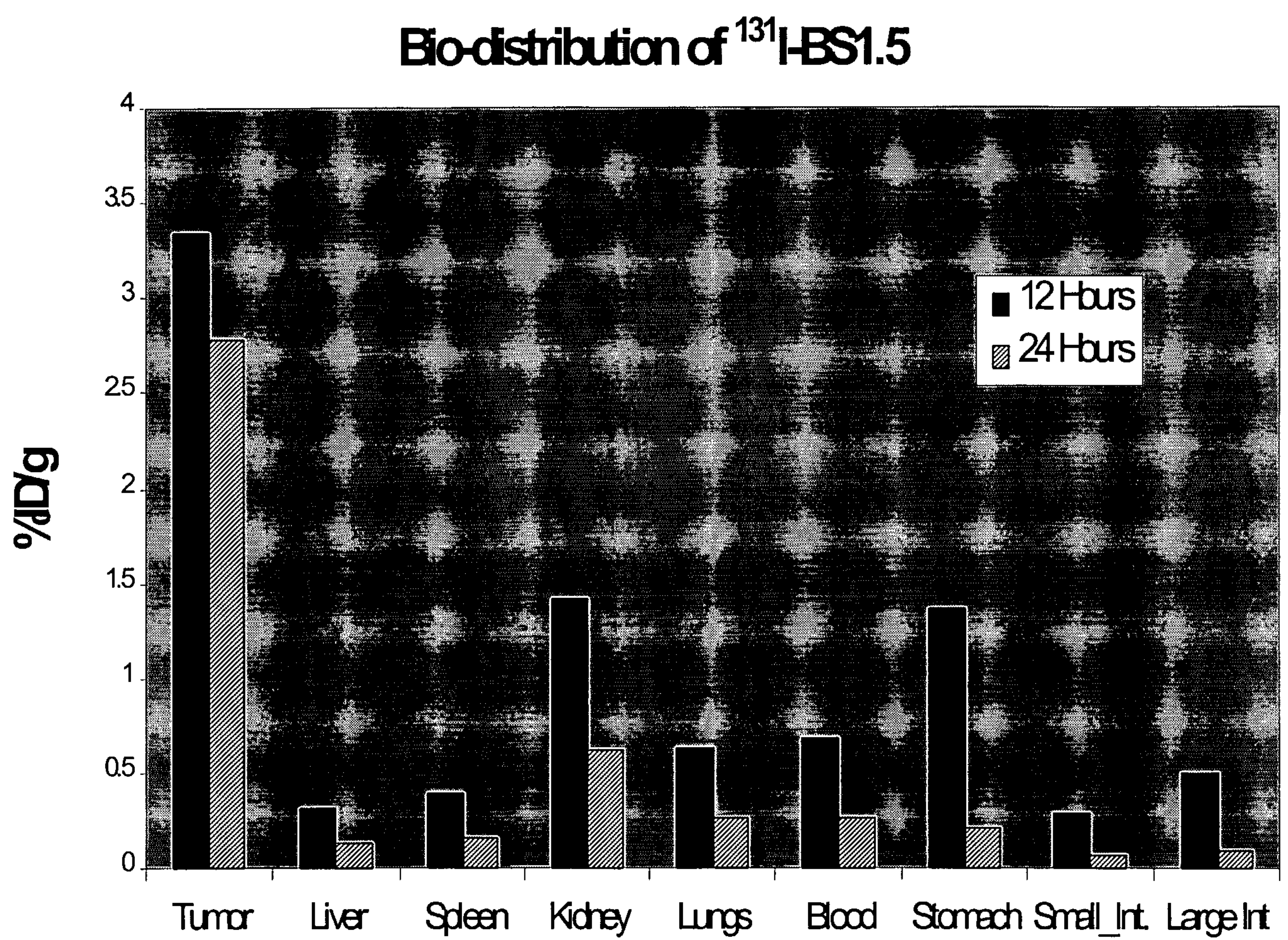
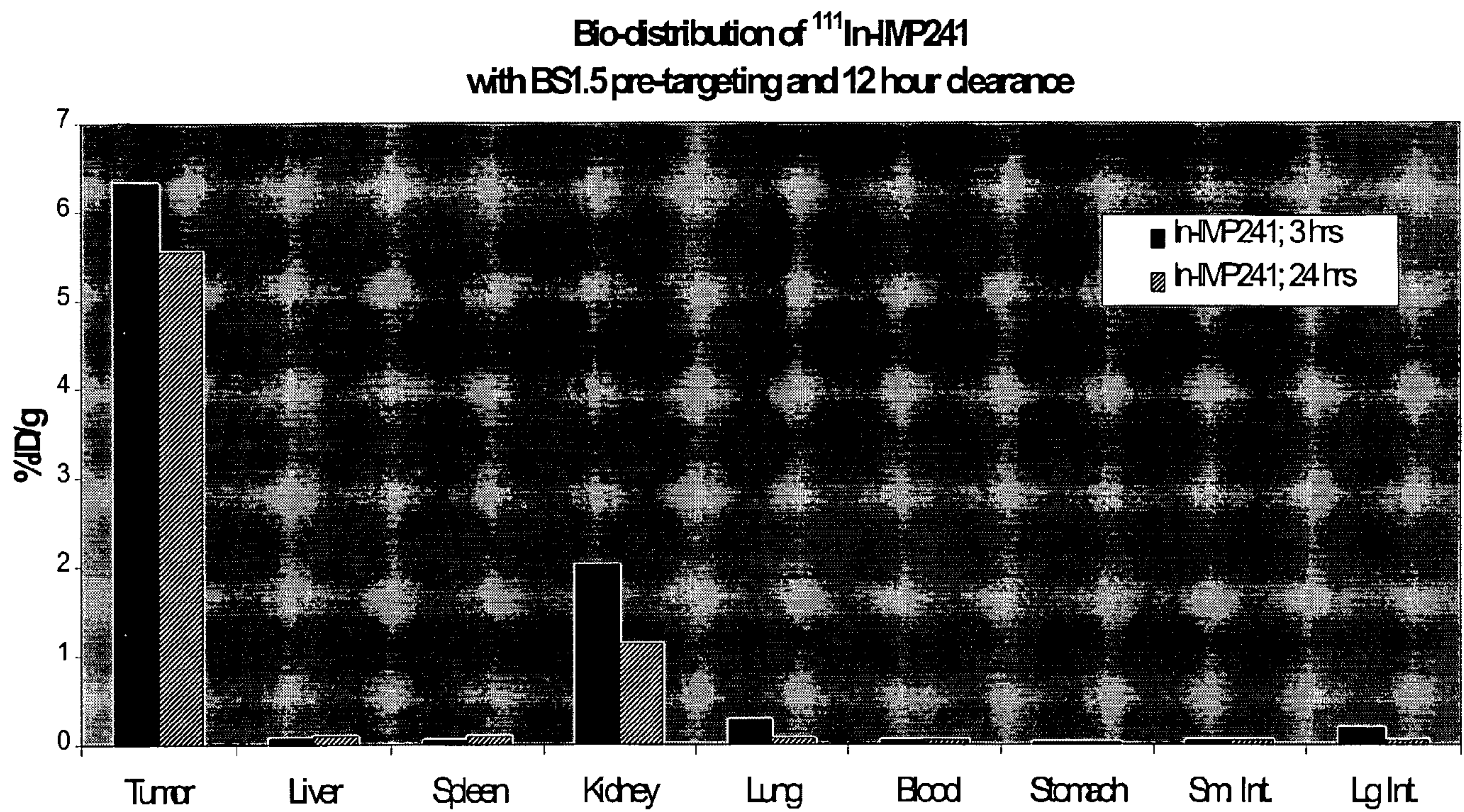


FIGURE 16

**FIGURE 17**

**FIGURE 18**

**FIGURE 19**

	V_HFR-1				CDR-H1	V_HFR-2			
m679VH	1	11	20	30	33	36	41	49	
	EVILVESGGDLVKPGGSLKLSCAASGFTFS				IYTMS	WLRQTPEKRLEWVA			
	▼						▼▼		
h679VH	EVQLVESGGDLVKPGGSLKLSCAASGFTFS				IYTMS	WLRQTPGKGLEWVA			
	CDR-H2				V_HFR-3				
m679VH	52A	61	65	66	71	81	82	abc	91
	TLSGDGDDIYYPDSVKG			RFTISRDN	AKNNLYLQMN	SLRSAD	TALYYCAR		
					▼		▼▼		
h679VH	TLSGDGDDIYYPDSVKG			RFTISRDN	AKNSLYLQMN	SLRAED	TALYYCAR		
	CDR-H3		V_HFR-4						
m679VH	95	100	103	113					
	VRLGDWDFDV	ab	WGQGTTVSVSS						
h679VH	VRLGDWDFDV		WGQGTTVSVSS						
	V_KFR-1				CDR-K1	V_KFR-2		CDR-K2	
679VK	1	11	21	24	27	34	41	49	53
	DIVMSQSPSSLAVSPGEKVTMTC			KSSQSLFNSRTRK	NYLG	WYQQKPGQSPKLLIY	WASTRES		
	▼		▼▼						
h679VK	DIVMTQSPSSLAVSPGERVT LTC			KSSQSLFNSRTRK	NYLG	WYQQKPGQSPKLLIY	WASTRES		
	V_KFR-3				CDR-K3	V_KFR-4			
m679VK	57	61	71	81	88	98	108		
	GVPDRFTGSGSGTDFTLTINSVQSEDLAVYYC			TQVYYLCT	FGAGTKLELKR				
	▼		▼▼▼						
h679VK	GVPDRFSGSGSGTDFTLTINSLQAEDVAVYYC			TQVYYLCT	FGAGTKLELKR				

Figure 20

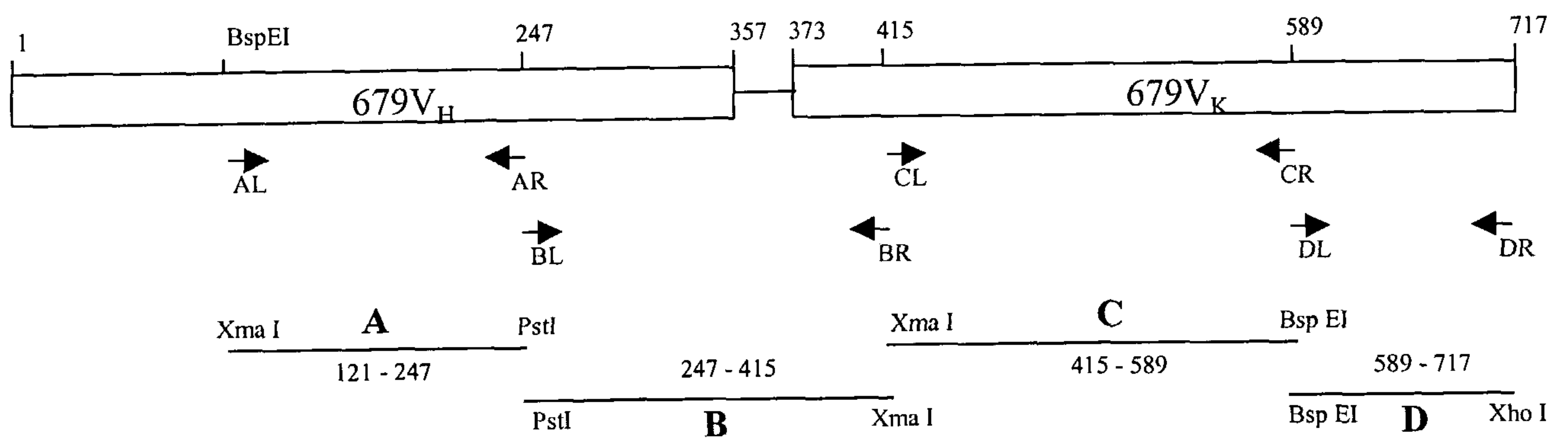


Figure 21

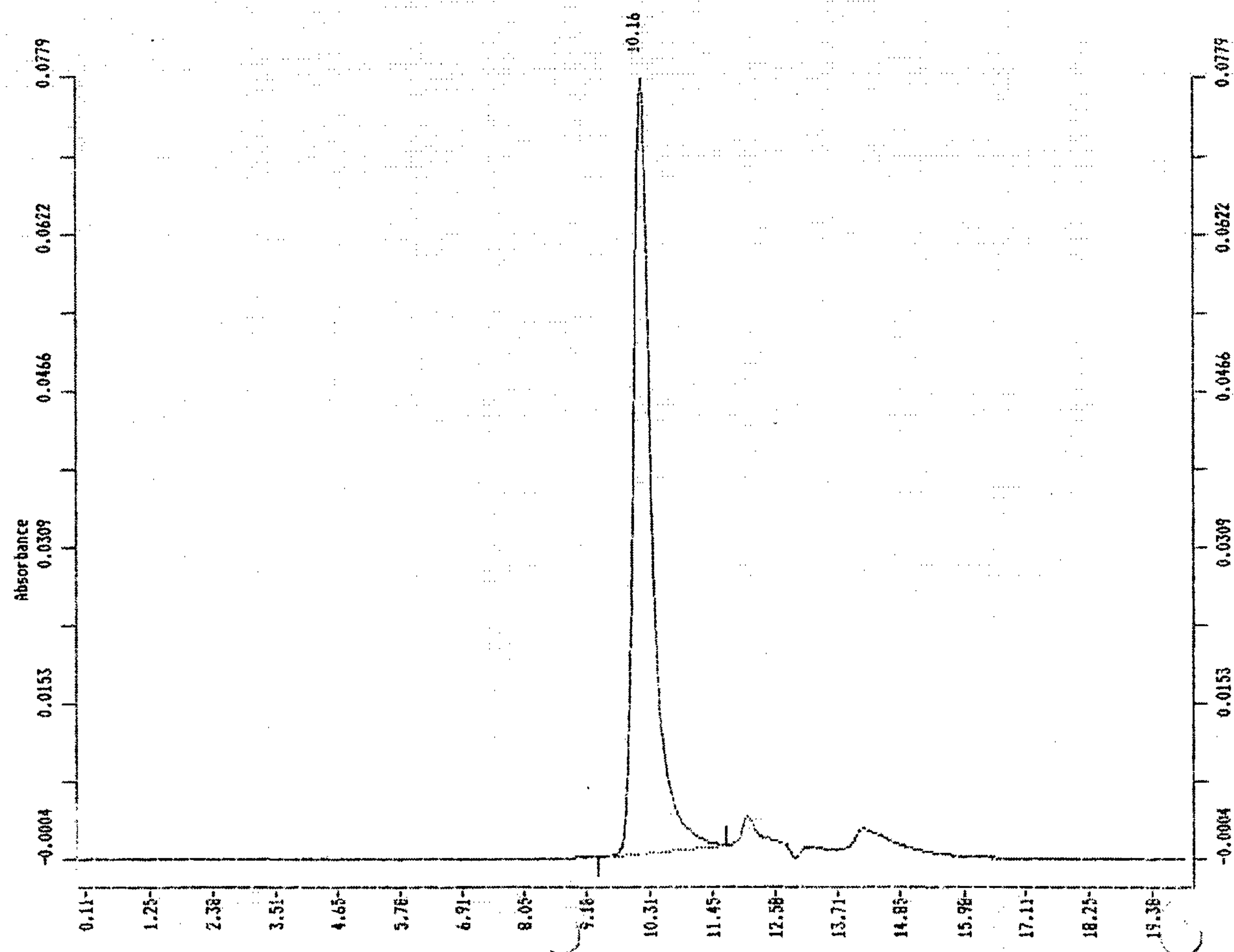
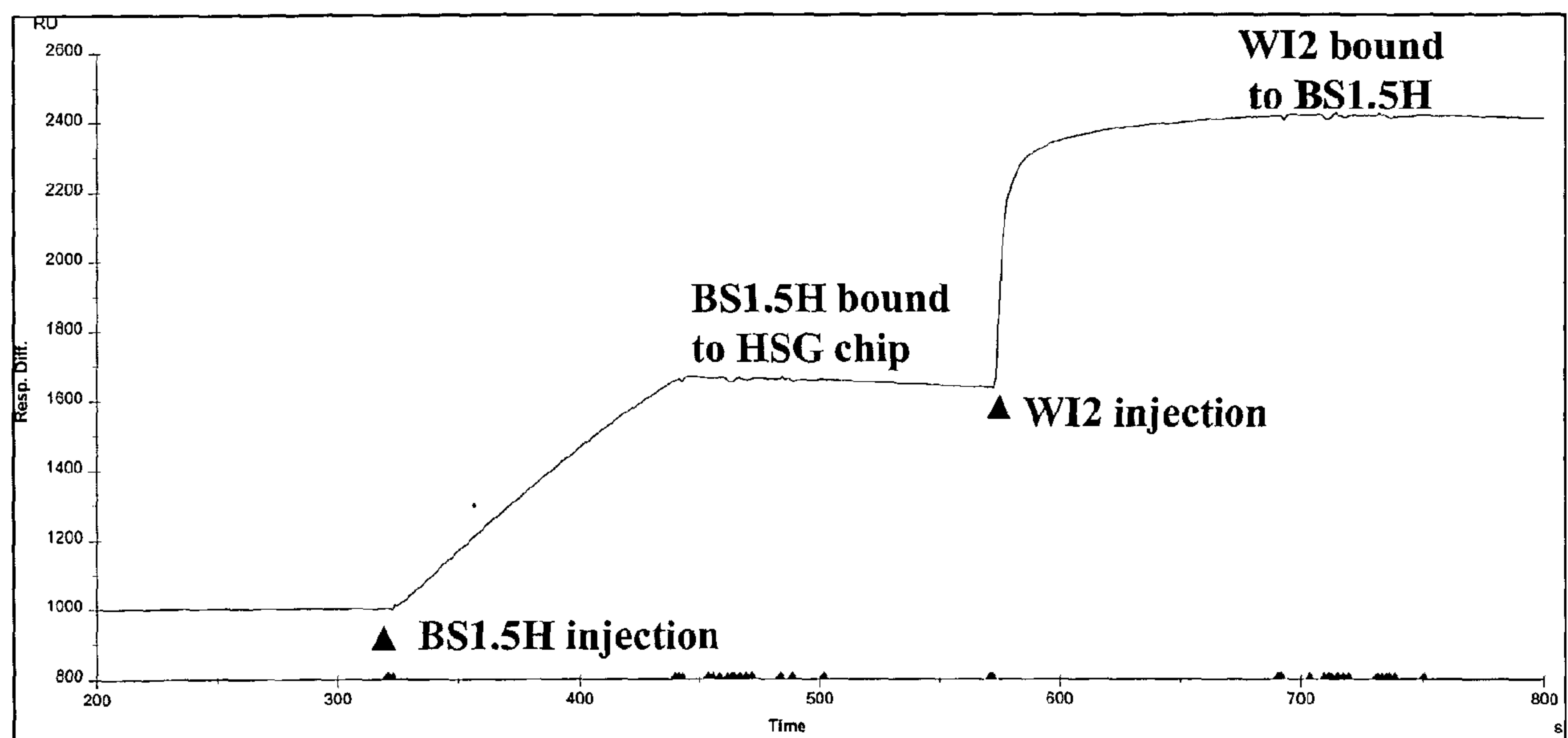
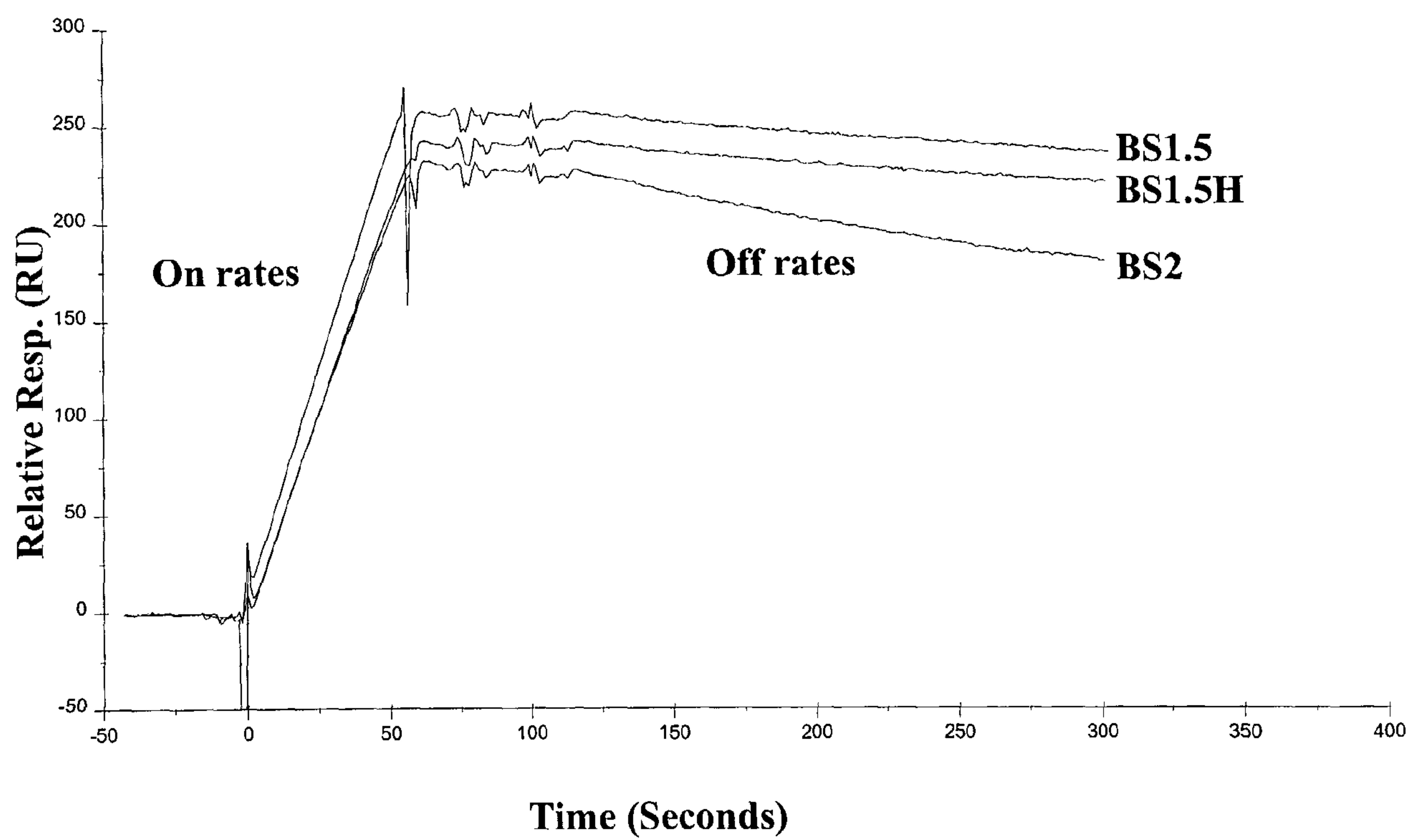


Figure 22

Simultaneous bi-specific binding of BS1.5H**Figure 23**

**Figure 24**

1 ATG AAA TAC CTG CTG CCG ACC GCT GCT 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 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 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 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 CAC TGA
 Glu Leu Lys Arg Leu Glu 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 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 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 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 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 CAC TGA
    Glu Leu Lys Arg Leu Glu 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 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 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 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 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 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 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 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 CAC TGA
    Glu Leu Lys Arg Leu Glu 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 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 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 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 His ---

```

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

Figure 29

```

1  ATG AAA TAC CTG CTG CCG ACC GCT 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 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 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 (679 x hMN14 bispecific diabody)

Figure 30

```

1  ATG AAA TAC CTG CTG CCG ACC GCT 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 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 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 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 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 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 ---

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

Figure 32

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1  ATG AAA TAC CTG CTG CCG ACC GCT 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 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 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 CAC TGA
   Leu Lys Arg Leu Glu His His His His His His ---

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**Nucleic acids and encoded amino acids for polypeptide #2 of BS1.5
(679 x hMN14 bispecific diabody)
Figure 33**

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1  ATG AAA TAC CTG CTG CCG ACC GCT 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 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 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 ---

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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 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 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 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 ---

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**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 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 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 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 TCA GGC AGT GGA TCC GGA ACA GAT TTC
Ser Gly Val Pro Asp Arg Phe Ser Gly 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 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

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1  ATG AAA TAC CTG CTG CCG ACC GCT 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  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 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 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 AAG1 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 ---

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**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 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 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 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 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 CAC TGA
   Leu Lys Arg Leu Glu His His His His His His ---

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

Figure 38