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(54) Title: METHOD FOR MAKING ANTIBODY FC-HETERODIMERIC MOLECULES USING ELECTROSTATIC STEERING EFFECTS

(57) Abstract: The invention relates to methods of making Fc-heterodimeric proteins or polypeptides. The invention also relates to the Fc-heterodimeric proteins or polypeptides themselves, including the individual polypeptide components that comprise the heterodimer. Nucleic acids encoding such polypeptides, expression vectors, and host cells. Moreover, the invention relates to pharmaceutical compositions comprising one of more Fc-heterodimeric proteins or polypeptides.



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METHOD FOR MAKING ANTIBODY FC-HETERODIMERIC MOLECULES USING ELECTROSTATIC STEERING EFFECTS

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BACKGROUND

Antibodies have become the modality of choice within the biopharma industry because they possess several characteristics that are attractive to those developing therapeutic molecules. Along with the ability to target specific structures or cells, antibodies make its target susceptible to Fc-receptor cell-mediated phagocytosis and killing (Raghavan and Bjorkman 1996). Further, the antibody's ability to interact with neonatal Fc-receptor (FcRn) in a pH dependent manner confers it with extended serum half-life (Ghetie and Ward 2000). This unique feature of antibodies allows extending the half-life of therapeutic protein or peptide in the serum by engineering Fc-fusion molecules.

Antibodies belong to the immunoglobulin class of proteins which includes IgG, IgA, IgE, IgM, and IgD. The most abundant immunoglobulin class in human serum is IgG whose schematic structure is shown in the Figure 1 (Deisenhofer 1981; Huber 1984; Roux 1999). The IgG structure has four chains, two light and two heavy chains; each light chain has two domains and each heavy chain has four domains. The antigen binding site is located in the Fab region (Fragment antigen binding) which contains a variable light (VL) and a variable heavy (VH) chain domain as well as constant light (LC) and constant heavy (CH1) chain domains. The CH2 and CH3 domain region of the heavy chain is called Fc (Fragment crystallizable). The IgG molecule can be considered as a heterotetramer having two heavy chains that are held together by disulfide bonds (-S-S-) at the hinge region and two light chains. The number of hinge disulfide bonds varies among the immunoglobulin subclasses (Papadea and Check 1989). The FcRn binding site is located in the Fc region of the antibody (Martin, West et al. 2001), and thus the extended serum half-life property of the antibody is retained in the Fc fragment. The Fc region alone can be thought of as a homodimer of heavy chains comprising CH2 and CH3 domains.

In certain instances, it is desirable to create a molecule that contains the Fc portion of an antibody but comprises a heterodimer. An important application of Fc heterodimeric molecules is the generation of bispecific antibodies (BsAbs). Bispecific antibodies refer to antibodies having specificities for at least two different antigens (Nolan and O'Kennedy 1990; de Leij, Molema et al. 1998; Carter 2001). Instead of having identical sequence in both the Fabs, bispecific antibodies bear different sequences in the two Fabs so that each arm of the Y-shaped molecule can bind to different antigens.

The use of bispecific antibodies for immunotherapy of cancer has been extensively reviewed in the literature (for example, see (Nolan and O'Kennedy 1990; de Leij, Molema et al. 1998; Carter

2001)). By having the ability to bind to two different epitopes or molecules, BsAbs provide means to both trigger an immune effector cell and bind a surface antigen on a tumor target cell. This helps to make use of the immune system to destroy cancer cells. Other applications of bispecific antibodies are extensively covered in U.S. Pat. Nos. 5,731,168 and 7,183,076.

5 The classical method of producing BsAbs by co-expressing two different IgGs in hybrid hybridomas leads to up to 10 possible combinations of heavy and light chains. This compromises the yield and imposes a purification challenge. Carter and co-workers engineered heavy chains for heterodimerization using a “knobs-into-holes” strategy (Ridgway, Presta et al. 1996; Atwell, Ridgway et al. 1997; Merchant, Zhu et al. 1998; Carter 2001). The knobs-into-holes concept was originally
10 proposed by Crick as a model for packing of amino acid side chains between adjacent α -helices (Crick 1952). Carter and co-workers created a knob at the CH3 domain interface of the first chain by replacing a smaller amino acid side chain with a larger one (for example, T366Y); and a hole in the juxtaposed position at the CH3 interface of the second chain was created by replacing a larger amino acid side chain with a smaller one (for example, Y407T). The basis for creating knob and hole in the
15 juxtaposed positions is that the knob and hole interaction will favor heterodimer formation, whereas the knob-knob and the hole-hole interaction will hinder homodimers formation due to the steric clash and deletion of favorable interactions, respectively. The knobs-into-holes mutations were also combined with inter-CH3 domain disulfide bond engineering to enhance heterodimer formation (Sowdhamini, Srinivasan et al. 1989; Atwell, Ridgway et al. 1997). In addition to these mutations,
20 the input DNA ratio was also varied to maximize the yield (Merchant, Zhu et al. 1998). The “knobs-into-holes” technique is disclosed in U.S. Pat. Nos. 5,731,168 and 7,183,076.

SUMMARY

25 This application describes a strategy for altering the interaction of antibody domains, e.g., altering a CH3 domain to reduce the ability of the domain to interact with itself, i.e., form homodimers. In particular, one or more residues that make up the CH3-CH3 interface is replaced with a charged amino acid such that the interaction becomes electrostatically unfavorable. In preferred embodiments, a positive-charged amino acid in the interface, such as a lysine, arginine, or histidine, is replaced with a negative charged amino acid, such as aspartic acid or glutamic acid. In
30 other embodiments, a negative-charged amino acid in the interface is replaced with a positive-charged amino acid. In certain embodiments, the amino acid is replaced with an unnatural amino acid having the desired charge characteristic.

35 Further described herein is a strategy for altering a pair of CH3 domains to reduce the ability of each domain to interact with itself but to increase the ability of the domains to interact with each other, i.e., form heterodimers. This can be achieved by replacing one or more residues that make up the CH3-CH3 interface in both CH3 domains with a charged amino acid such that homodimer formation is electrostatically unfavorable but heterodimerization is electrostatically favorable. In

certain embodiments, a charged amino acid in each CH3 domain is replaced with an amino acid with an opposite charge. For example, a positive-charged amino acid may be replaced with a negative charged amino acid in the first CH3 domain and a negative charged amino acid may be replaced with a positive-charged amino acid in the second CH3 domain. By reversing the charge of the amino acid, homodimer formation is reduced. When the replacements are coordinated properly, the reversed charges are electrostatically favorable, i.e., opposing charges in the interface, for heterodimerization formation.

In certain aspects, the invention provides a method of preparing a heterodimeric protein. The heterodimer may comprise a first CH3-containing polypeptide and a second CH3-containing polypeptide that meet together to form an interface engineered to promote heterodimer formation. The first CH3-containing polypeptide and second CH3-containing polypeptide are engineered to comprise one or more charged amino acids within the interface that are electrostatically unfavorable to homodimer formation but electrostatically favorable to heterodimer formation.

Such methods may include culturing a host cell comprising nucleic acids encoding the first and second CH3-containing polypeptides such that the polypeptides are co-expressed by the cell. In certain embodiments, the nucleic acids encoding the first and the second CH3-containing polypeptides are provided to the host cell at a ratio, for example 1:1, 1:2, 2:1, 1:3, 3:1, 1:4, 4:1, 1:5, 5:1, 1:6, 6:1, 1:7, 7:1, 1:8, 8:1, 1:9, 9:1, 1:10, 10:1. It is contemplated that altering the ratio of nucleic acids may increase the production of heterodimeric molecules versus homodimeric molecules.

The heterodimeric molecules may be purified from the host-cell culture using standard techniques. For example, when the heterodimeric protein comprises an Fc, the protein may be purified using a Protein A column. The purification techniques include but are not limited to chromatographic methods such as size exclusion, ion exchange and affinity-based chromatography and ultracentrifugation.

In certain embodiments, the CH3-containing polypeptide comprises an IgG Fc region, preferably derived from a wild-type human IgG Fc region. By "wild-type" human IgG Fc it is meant a sequence of amino acids that occurs naturally within the human population. Of course, just as the Fc sequence may vary slightly between individuals, one or more alterations may be made to a wild-type sequence and still remain within the scope of the invention. For example, the Fc region may contain additional alterations that are not related to the present invention, such as a mutation in a glycosylation site, inclusion of an unnatural amino acid, or a "knobs-into-holes" mutation.

In certain embodiments, the polypeptide containing the CH3 region is an IgG molecule and further contains a CH1 and CH2 domain. Exemplary human IgG sequences comprise the constant regions of IgG1 (e.g., SEQ ID NO:3; CH1 = amino acids 1-98, CH2 = amino acids 111-223, CH3 = 224-330), IgG2 (e.g., SEQ ID NO:4; CH1 = amino acids 1-94, CH2 = amino acids 111-219, CH3 = 220-326), IgG3 (e.g., SEQ ID NO:5; CH1 = amino acids 1-98, CH2 = amino acids 161-270, CH3 = 271-377), and IgG4 (e.g., SEQ ID NO:6; CH1 = amino acids 1-98, CH2 = amino acids 111-220, CH3

= 221-327). Those of skill in the art may differ in their understanding of the exact amino acids corresponding to the various domains of the IgG molecule. Thus, the N-terminus or C-terminus of the domains outlined above may extend or be shortened by 1, 2, 3, 4, 5, 6, 7, 8, 9, or even 10 amino acids. Also note that the numbering scheme used here to designate domains differ from the EU numbering
5 scheme of Kabat that is used in the rest of this patent application. For example, IgG1 "CH3=224-330" corresponds to "CH3=341-447" in EU numbering scheme.

The Fc region also may be comprised within the constant region of an IgA (e.g., SEQ ID NO:7), IgD (e.g., SEQ ID NO:8), IgE (e.g., SEQ ID NO:9), and IgM (e.g., SEQ ID NO:10) heavy chain.

10 The polypeptide containing the CH3 region may be an antibody heavy chain and the host cell may further express one or more antibody light chains. In embodiments wherein more than one heavy chain and light chains are co-expressed (e.g., bivalent antibody), each heavy chain may comprise a mutation in the CH1 region and each light chain may comprise a mutation in the constant region to preferentially bind to each other but not bind to the other light or heavy chain, respectively. In
15 preferred embodiments, such mutations involve altering the charge of one or more amino acids in the interface between the CH1 region and the constant region of a light chain.

Preferred embodiments of the invention include but are not limited to an antibody, a bispecific antibody, a monospecific monovalent antibody, a bispecific maxibody (maxibody refers to scFv-Fc), a monobody, a peptibody, a bispecific peptibody, a monovalent peptibody (a peptide fused
20 to one arm of a heterodimeric Fc molecule), and a receptor-Fc fusion protein. See FIG. 2.

Examples of mammalian host cells that may be used include but are not limited to CHO, 293, and myeloma cell lines. The host cell may also be yeast or a prokaryote, such as E. coli.

The heterodimeric proteins may be particularly useful in therapeutic compositions. In certain
25 embodiments, a heterodimeric protein may be formulated in a composition that includes one or more pharmaceutically acceptable buffer or excipient. Such therapeutic composition may be administered to a subject to treat a disease or may be given to prevent a disease or prevent the symptoms of a disease from progressing.

BRIEF DESCRIPTION OF THE DRAWINGS

30 Figure 1. Schematic diagram of IgG1 antibody with the domains indicated. The IgG1 antibody is a Y-shaped tetramer with two heavy chains (longer length) and two light chains (shorter length). The two heavy chains are linked together by disulfide bonds (-S-S-) at the hinge region. Fab – fragment antigen binding, Fc – fragment crystallizable, VL – variable light chain domain, VH – variable heavy chain domain, CL – constant (no sequence variation) light chain domain, CH1 –
35 constant heavy chain domain 1, CH2 – constant heavy chain domain 2, CH3 – constant heavy chain domain 3.

Figure 2. Figure depicts some of the embodiments that include Fc-heterodimeric molecules. These include bispecific antibodies (have specificity for two or more antigens) to receptor-Fc fusion molecules. Preferably, the Fc retains its ability to interact with the FcRn receptor, even without the Fab domains, leading to longer serum half-life for proteins/domains that are fused to the Fc heavy chains. scFv – single chain fragment variable, Pep. – peptibody, A and B stands for proteins or receptors or domains.

Figure 3. CH3 domain interface structure with residues involved in the domain-domain interaction shown. The interface residues were identified using a distance cutoff method. Structurally conserved and buried (solvent accessible surface area < 10%) residues are shown in the ball-and-stick model. Solvent exposed or structurally not conserved residues are shown in the stick representation. The analysis is based on the IgG1 crystal structure (PDB code: 1L6X) which is determined at high-resolution (1.65Å) (Idusogie, Presta et al. 2000).

Figure 4. Comparison of IgG subclass sequences from (a) human and (b) mouse. Only the heavy chain sequence corresponding to the CH3 domain is shown. The star (*) indicates residue positions involved in the CH3-CH3 domain interaction identified based on the IgG1 human Fc crystal structure (1L6X). Positions marked with rectangles are preferred residues for mutation to enhance heterodimer formation. It may be noted here that charged residues are highly conserved among the IgGs. (c) CH3 domain sequence comparison of other class of antibodies (IgA, IgE, IgD, and IgM). The interface residue positions (indicated by “*”) in (b) and (c) were identified based on sequence comparison with Hu IgG1 sequence that is also shown. In (a), the sequences derived from human IgG1, IgG2, IgG3, and IgG4 correspond to SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:14, respectively. In (b), the sequences derived from human IgG1, mouse IgG1, mouse IgG2a, mouse IgG2b, and mouse IgG3 correspond to SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, and SEQ ID NO:19, respectively. In (c), the sequences derived from human IgG1, human IgA, human IgE, human IgD, and human IgM correspond to SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24, respectively.

Figure 5. Crystal structure of CH3 domain homodimer with one domain shown in ribbon representation and the other domain shown in wire model. The Lys409 (Lys409' in the second domain) and Asp399 (Asp399' in the second) residues are shown in ball-and-stick model in order to illustrate each pair-wise interaction is represented twice in the structure. This is due to the two-fold symmetry present in the CH3-CH3 domain interaction. The figure was created using the 1L6X coordinates deposited in the PDB.

Figure 6. Schematics showing electrostatic interactions in the wild type and in the mutants designed as an example to enhance heterodimer formation and hinder homodimer formation. (a) In the case of WT, electrostatic interactions favor both heterodimer and homodimer formation giving them equal probability. (b) In the single mutant (K409E) case, one of the homodimer is discouraged by both the interactions and at the same time heterodimer is also discouraged by one of the interactions.

(c) In the double mutant case, both the electrostatic interactions favor heterodimer and disfavor homodimer formation. (d) Additional mutations involving charge change (for example, K360E) could also be used to enhance the electrostatic steering effects on the formation of heterodimer and homodimer.

5 Figure 7. This figure shows that electrostatic interactions could also be used to favor homodimers and disfavor heterodimer formation, when two different chains are co-expressed.

Figure 8. Figure (a) shows the schematic drawing of the constructs used in the Example. The first chain of the Fc has a maxibody (single chain fragment variable, scFv) covalently linked, and the second chain called dummy Fc does not have any domain or functionality attached to it. (b)
10 Illustration of expected relative mobility on the SDS-PAGE. Because the Fc chain attached to the maxibody has a higher molecular weight than the dummy Fc, homodimers and heterodimer have different mobility on the SDS-PAGE. The thickness of the band on the SDS-PAGE can be used as a measure of fraction of heterodimer and homodimer yield. The wild type is included as a control and to monitor relative improvement on the heterodimer yield due to various mutations.

15 Figure 9. SDS-PAGE analysis showing the effects of mutations on the D399'---K409 interaction pair.

Figure 10. SDS-PAGE analysis of charge residue mutations (listed in Table 6) in addition to D399'K --- K409D pair mutations. Wild type (first lane) and knobs-into-holes mutations (last lane) are also shown for comparison. 1:2 input DNA ratio of dummy Fc and M315 maxibody was used
20 here.

Figure 11. Western blot demonstrating certain combinations of mutant achieve high selectivity for heterodimer formation. Fc molecules were detected using goat-anti-human Fc HRP conjugated at 1:10,000.

25 DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

A total of 48 antibody crystal structures which had co-ordinates corresponding to the Fc region were identified from the Protein Data Bank (PDB) (Bernstein, Koetzle et al. 1977) using a structure based search algorithm (Ye and Godzik 2004). Examination of the identified Fc crystal structures revealed that the structure determined at highest resolution corresponds to the Fc fragment
30 of RITUXIMAB bound to a minimized version of the B-domain from protein A called Z34C (PDB code: 1L6X). The biological Fc homodimer structure for 1L6X was generated using the deposited Fc monomer co-ordinates and crystal symmetry. Two methods were used to identify the residues involved in the CH3-CH3 domain interaction: (i) contact as determined by distance limit criterion and (ii) solvent accessible surface area analysis.

35 According to the contact based method, interface residues are defined as residues whose side chain heavy atoms are positioned closer than a specified limit from the heavy atoms of any residues in

the second chain. Though 4.5Å distance limit is preferred, one could also use longer distance limit (for example, 5.5Å) in order to identify the interface residues (Bahar and Jernigan 1997).

The second method involves calculating solvent accessible surface area (ASA) of the CH3 domain residues in the presence and absence of the second chain (Lee and Richards 1971). The residues that show difference ($>1\text{\AA}^2$) in ASA between the two calculations are identified as interface residues. Both the methods identified similar set of interface residues. Further, they were consistent with the published work (Miller 1990).

Table 1 lists twenty four interface residues identified based on the contact criterion method, using the distance limit of 4.5Å. These residues were further examined for structural conservation. For this purpose, 48 Fc crystal structures identified from the PDB were superimposed and analyzed by calculating root mean square deviation for the side chain heavy atoms. The residue designations are based on the EU numbering scheme of Kabat, which also corresponds to the numbering in the Protein Data Bank (PDB).

Figure 3 shows the CH3 domain interface along with the structurally conserved, buried (% ASA ≤ 10), and exposed (% ASA > 10) positions (% ASA refers to ratio of observed ASA to the standard ASA of amino acids; (Lee and Richards 1971)). Conservation of interface residues among Human and Mouse IgG subclasses as well as among other Ig classes was also examined through sequence comparisons (Figure 4).

Table 1: List of CH3 domain interface residues in the first chain (A) and their contacting residues in the second chain (B)^a

<i>Interface Res. in Chain A</i>	<i>Contacting Residues in Chain B</i>
GLN A 347	LYS B 360'
TYR A 349	SER B 354' ASP B 356' GLU B 357' LYS B 360'
THR A 350	SER B 354' ARG B 355'
LEU A 351	LEU B 351' PRO B 352' PRO B 353' SER B 354' THR B 366'
SER A 354	TYR B 349' THR B 350' LEU B 351'
<i>ARG A 355^b</i>	THR B 350'
ASP A 356	TYR B 349' LYS B 439'
GLU A 357	TYR B 349' LYS B 370'
<i>LYS A 360^b</i>	GLN B 347' TYR B 349'
SER A 364	LEU B 368' LYS B 370'
THR A 366	LEU B 351' TYR B 407'
LEU A 368	SER B 364' LYS B 409'
LYS A 370	GLU B 357' SER B 364'
ASN A 390	SER B 400'
LYS A 392	LEU B 398' ASP B 399' SER B 400' PHE B 405'

THR A 394	THR B 394' VAL B 397' PHE B 405' TYR B 407'
PRO A 395	VAL B 397'
VAL A 397	THR B 393' THR B 394' PRO B 395'
ASP A 399	LYS B 392' LYS B 409'
SER A 400	ASN B 390' LYS B 392'
PHE A 405	LYS B 392' THR B 394' LYS B 409'
TYR A 407	THR B 366' THR B 394' TYR B 407' SER B 408' LYS B 409'
LYS A 409	LEU B 368' ASP B 399' PHE B 405' TYR B 407'
LYS A 439	ASP B 356'

^aPositions involving interaction between oppositely charged residues are indicated in bold. Due to the 2-fold symmetry present in the CH3-CH3 domain interaction, each pair-wise interaction is represented twice in the structure (for example, Asp A 356 --- Lys B 439' & Lys A 439 --- Asp B 356'; Figure 5)

5 ^bArg355 and Lys360 positions (shown in italics) could also be used for enhancing electrostatic steering effects though they are not involved in interaction with oppositely charged residues.

10 At neutral pH (=7.0), Asp and Glu residues are negatively charged and Lys, Arg and His are positively charged. These charged residues can be used to promote heterodimer formation and at the same time hinder homodimers. Attractive interaction takes place between opposite charges and repulsive interaction occurs between like charges. The method presented here makes use of the attractive and repulsive interactions for promoting heterodimer and hindering homodimer, respectively, by carrying out site directed mutagenesis of charged interface residues.

15 Examination of the identified CH3 domain interface residues (Table 1) reveals four unique charge residue pairs involved in the domain-domain interaction (Asp356---Lys439', Glu357---Lys370', Lys392---Asp399', Asp399---Lys409'; residue numbering in the second chain is indicated by prime '). These charge pairs are not necessarily involved in charge-charge interaction in the crystal structure used here (1L6X), since crystal structure is an end product in the protein folding reaction pathway and it represents structure in the crystalline state. It is assumed here that in order to have electrostatic steering effects it is sufficient if the residues are close in space as defined by the distance limit criterion (4.5Å). It must also be noted here that due to the 2-fold symmetry present in the CH3-CH3 domain interaction, each unique interaction will be represented twice in the structure (for example, Asp399---Lys409' & Lys409---Asp399'; Figure 5).

25 The four pairs were ranked according to the extent of solvent accessibility (ASA analysis) (Lee and Richards 1971). In Lys409---Asp399' case, both the residues were structurally conserved as well as buried. In other three pairs case, at least one of the partner is solvent exposed (%ASA > 10).

Therefore, for the Example herein, the Lys409---Asp399' pair was chosen for site directed mutagenesis. The strategy is schematically shown in Figure 6.

In the wild type, K409---D399' interaction favors both heterodimer and homodimer formation. A single mutation switching the charge polarity (K409E; positive to negative charge) in the first chain leads to unfavorable interactions for the formation of the first chain homodimer. The unfavorable interactions arise due to the repulsive interactions occurring between the same charges (negative---negative; D399---K409E & K409E---D399). A similar mutation switching the charge polarity (D399'K; negative to positive charge) in the second chain leads to unfavorable interactions (K409'---D399'K & D399'K---K409') for the second chain homodimer formation. But, at the same time, these two mutations (K409E & D399'K) lead to favorable interactions (K409E---D399'K & D399---K409') for the heterodimer formation.

The electrostatic steering effects on heterodimer formation and homodimer discouragement can be further enhanced by mutation of additional charge residues which may or may not be paired with an oppositely charged residue in the second chain, such as Arg355 and Lys360, as shown in Figure 6d. The mutations shown in Figure 6 are for the purpose of illustration only. Table 2 lists many possible mutations involving charge change, and the mutations can be combined to enhance the electrostatic effects.

Table 2a: List of some possible pair-wise charge residue mutations to enhance heterodimer formation^a

Position in the First Chain	Mutation in the First Chain	Interacting Position in the Second Chain	Corresponding Mutation in the Second Chain
Lys409	Asp or Glu	Asp399'	Lys or Arg ^b
Lys392	Asp or Glu	Asp399'	Lys or Arg ^b
Lys439	Asp or Glu	Asp356'	Lys or Arg ^b
Lys370	Asp or Glu	Glu357'	Lys or Arg ^b
Asp399	Lys or Arg ^b	Lys409'	Asp or Glu
Asp399	Lys or Arg ^b	Lys392'	Asp or Glu
Asp356	Lys or Arg ^b	Lys439'	Asp or Glu
Glu357	Lys or Arg ^b	Lys370'	Asp or Glu

^aCombinations of the above pair-wise charge residue mutations could also be used. For example Lys409 --- Asp399' interaction pair mutations could be combined with Lys439 --- Asp356' pair mutations.

^bHistidine (His) could also be added to this list of positively charged residues, however, increase in side chain volume and pH dependency should be taken into account in the design.

Table 2b: Additional single charge residue mutations to enhance electrostatic steering effects^a

Position in Chain 1	Mutation	Position in Chain 2	Mutation
Arg355	Asp or Glu	Arg355'	Asp or Glu
Lys360	Asp or Glu	Lys360'	Asp or Glu

^aThese single residue mutations could be combined with the Table 2a pair-wise mutations to enhance the heterodimer formation (Figure 6d).

5

Each positively charged residue (Lys and Arg) can be mutated to two negatively charged residues (Asp or Glu) and *vice versa*, and as a result the method described here provides numerous combinations. It must be stated here that different combinations will have diverse effect on the quaternary (homodimer/heterodimer) structure formation depending on surrounding residues at the mutation site and role of water molecules. The amino acid Histidine (His) is positively charged at neutral pH and therefore mutation to His is also contemplated. However, mutating negatively charged residues (Asp or Glu) to His will lead to increase in side chain volume which may cause steric issues. Further, Histidine proton donor- and acceptor-form depends on the localized environment. These issues should be taken into consideration during the design strategy.

10

15

Because the interface residues are highly conserved in Human and Mouse IgG subclasses, electrostatic steering effects can be applied to Human or Mouse IgG1, IgG2, IgG3, or IgG4. This strategy can also be extended to modifying uncharged residues to charged residues at the CH3 domain interface. A similar strategy involving charge residue mutations can also be used to enhance homodimers and hinder heterodimer formation when two different heavy chains are co-expressed (Figure 7).

20

25

In order to assess the stability of the charge residue mutants, EGAD software was used to estimate the CH3-CH3 domain binding free energy. By optimizing parameters used in the calculation, Pokala and Handel could predict the effects of nearly 400 mutations on protein-protein complex formation within 1.0kcal/mol error (Pokala and Handel 2005). EGAD was used to roughly compare the binding free energy of various mutations made at the CH3 domain interface.

30

Table 3 lists computed binding free energy ($\Delta\Delta G$) for the interface charge residue mutants. The binding free energy of a mutant is defined as $\Delta\Delta G_{mut} = \mu (\Delta G_{mut} - \Delta G_{wt})$. Where, μ ($=0.1$, in general) is the scaling factor used to normalize the predicted changes in binding affinity to have a slope of 1 when comparing with the experimental energies (Pokala and Handel 2005). The free energy of dissociation (ΔG) is defined as the energy difference between the complex (ΔG_{bound}) and free states (ΔG_{free}). The comparison shows that charged residue mutations affect the stability to a much lesser extent compared to the knobs-into-holes mutations. For comparison, melting temperatures reported for the wild type and knobs-into-holes mutants are given. The melting temperatures were measured by Carter and coworkers using only the CH3 domain construct (Atwell,

Ridgway et al. 1997). For the knobs-into-holes mutants, decrease in enthalpy was also observed in the differential scanning calorimetry experiments.

5 Table 3: CH3-CH3 domain binding free energy for various mutants designed to enhance heterodimer formation, calculated using the EGAD program (Pokala and Handel 2005)^a

Protein	Description	ΔG (in kcal/mol)	$\Delta\Delta G_{mut}$ (in kcal/mol)	Melting Temp. T_m (in °C)
WT	Wild Type	-30.69	0	80.4
T366W-Y407'A	Knob-Hole	-24.60	6.09	65.4
T366W-T366'S-L368'A-Y407'V	Knob-Hole	-28.57	2.12	69.4
K409E-D399'K	Charge-Charge	-29.56	1.13	ND
K409E-D399'R	Charge-Charge	-29.47	1.22	ND
K409D-D399'K	Charge-Charge	-28.16	2.53	ND
K409D-D399'R	Charge-Charge	-27.69	3.00	ND
K392E-D399'R	Charge-Charge	-29.27	1.42	ND
K392E-D399'K	Charge-Charge	-29.87	0.82	ND
K392D-D399'R	Charge-Charge	-28.82	1.87	ND
K392D-D399'K	Charge-Charge	-29.42	1.27	ND

^aNot all possible charge-charge pairs were considered for the binding free energy calculation. Wild type is listed for comparison. ΔG is defined as energy difference between the complex and free states. The binding free energy of a mutant ($\Delta\Delta G_{mut}$) is defined as difference between the mutant (ΔG_{mut}) and wild type (ΔG_{WT}) free energies.

10 Figure 2 depicts several embodiments comprising Fc heterodimeric molecules, from bispecific antibodies to heterodimeric receptor complexes. The two heavy chains of heterodimeric Fc molecules can be fused with proteins and/or domains that have different functionalities. For example, fusing Fabs that bind to different antigens will lead to bispecific antibodies (BsAbs). Fusing two different single-chain Fv (scFv; variable light and heavy chains joined by a flexible peptide linker) domains will lead to bispecific maxibodies. Further, domains or proteins that interact for functional reasons can also be fused with heterodimeric Fc for the purpose of developing functional assays or for therapeutic uses. For instance, in the hematopoietic receptor family gp130 is known to interact with other receptors such as Leukemia Inhibitory Factor Receptor (LIFR). The extra cellular domain (ECD) of gp130 can be fused to the first heavy chain of Fc and the ECD of LIFR can be fused to the second Fc heavy chain, which will lead to formation of gp130-LIFR complex that is likely to mimic the biological state. Since FcRn binding site is located in the Fc region, Fc fusion molecules are likely to have extended serum half-life - a feature that distinguishes Fc heterodimeric molecules from

20

other heterodimeric molecules such as leucine zipper fusion proteins (Liu, Caderas et al. 2001). It is not essential to have different functionalities attached to the two heavy chains of the Fc heterodimer. A monobody can also be created (Figure 2).

In certain embodiments, e.g., when producing bispecific antibodies, multiple different light chains may be co-expressed with the multiple different heavy chains. To increase the fidelity of each light chain binding to the proper heavy chain thereby maintaining specificity of the antibody “arm,” the CH1 domains of one or more of the heavy chains and the constant region of one or more of the light chains can be engineered to favor dimerization. Preferably, this is accomplished using an electrostatic steering technique similar to that described above for the CH3 domains

The interaction of the kappa light chain sequence corresponding to the Protein Data Bank (PDB) deposition code 1N0X (SEQ ID NO:25) and the lambda light chain corresponding to (PDB) deposition code 7FAB (SEQ ID NO:26) with the heavy chain sequence corresponding to the CH1 domain of IgG1 (SEQ ID NO:27) was analyzed. The lambda light chain-Heavy chain contacts within the interface are shown in Table 4.

Table 4: List of lambda light chain interface residues and their contacting residues in the heavy chain^a

<i>Interface Res. in Lambda Light Chain</i>	<i>Contacting Residues in the Heavy Chain</i>
THR L 112	ALA H 141
PHE L 114	LEU H 128 ALA H 129 ALA H 141 LEU H 142 GLY H 143 VAL H 185
SER L 117	PHE H 126 PRO H 127
GLU L 119	VAL H 125 PHE H 126 PRO H 127 LYS H 213
GLU L 120	PHE H 126
LYS L 125	LYS H 147 ASP H 148
THR L 127	LEU H 145 LYS H 147
VAL L 129	LEU H 128 LEU H 145 SER H 183
LEU L 131	PHE H 170 SER H 183 VAL H 185
SER L 133	HIS H 168 PHE H 170
GLU L 156	VAL H 173 LEU H 174 GLN H 175 SER H 176
THR L 158	PRO H 171 ALA H 172 VAL H 173
SER L 161	PRO H 171
GLN L 163	HIS H 168
ALA L 169	HIS H 168 PHE H 170
SER L 171	PHE H 170 PRO H 171
TYR L 173	LEU H 145 VAL H 173 SER H 181 LEU H 182 SER H 183

^aContacting residues were identified using 4.5Å distance limit criterion. The light and heavy chain numbering scheme corresponds to that in the deposited co-ordinates file (PDB code:7FAB).

The kappa light chain-heavy chain contacts within the interface are shown in Table 5.

5

Table 5: List of kappa light chain interface residues and their contacting residues in the heavy chain^a

<i>Interface Res. in Kappa Light Chain</i>	<i>Contacting Residues in the Heavy Chain</i>
PHE 116	THR H 139 ALA H 140 ALA H 141
PHE 118	LEU H 128 ALA H 129 PRO H 130 ALA H 141 LEU H 142
SER 121	PHE H 126 PRO H 127
ASP 122	LYS H 218
GLU 123	VAL H 125 PHE H 126 LYS H 213
GLN 124	PHE H 126 LEU H 145 LYS H 147
SER 131	LEU H 145 LYS H 147
VAL 133	LEU H 128
LEU 135	ALA H 141 PHE H 170 VAL H 185
ASN 137	HIS H 168 THR H 187
ASN 138	HIS H 168
GLN 160	VAL H 173 LEU H 174 GLN H 175
SER 162	PHE H 170 PRO H 171 VAL H 173
THR 164	THR H 169 PHE H 170 PRO H 171
SER 174	HIS H 168 PHE H 170
SER 176	PHE H 170 SER H 183

^aContacting residues were identified using 4.5Å distance limit criterion. The light chain numbering scheme corresponds to that in the deposited co-ordinates file (PDB code:1N0X). The heavy chain numbering scheme corresponds to that in the Table 4.

10

In certain embodiments, Lys125 of the lambda chain is mutated to a negatively charged amino acid and a corresponding mutation is made in a heavy chain at Asp148, changing the residue to a positively charged amino acid. Alternatively, or in addition, Glu119 of the lambda chain is mutated to a positively charged amino acid a corresponding mutation is made in a heavy chain at Lys213, changing the residue to a negatively charged amino acid.

15

The analysis of the light chain-heavy chain interaction revealed positions in which charge pairs could be introduced into the sequence to enhance binding of a specific light and heavy chain pair. These positions include Thr112 of lambda and Ala141 of the heavy chain, Glu156 of lambda

and Ser176 of the heavy chain, and Ser171 of lambda and Ser183 of the heavy chain and other positions shown in Table 4 and 5 in bold face.

EXAMPLES

5 **Example 1**

This example demonstrates that CH3 domains can be engineered to favor heterodimerization while disfavoring homodimerization using electrostatic steering effects. A maxibody – dummy Fc construct as shown in Figure 8(a) was made having charge residue mutations at the CH3 domain interface. The formation of homodimer and heterodimer yield was assessed through SDS
 10 polyacrylamide gel electrophoresis. Because the maxibody has a higher molecular weight compared to dummy Fc, the heterodimer (maxibody-dummy Fc) and homodimers (maxibody-maxibody & dummy Fc-dummy Fc) have different mobility on the SDS-PAGE facilitating the identification of the various pairings (FIG. 8(b)).

A rat anti-mouse NKG2D antibody, designated M315, was generated through conventional
 15 hybridoma fusions and the DNA sequences encoding the variable heavy chain (VH) and variable light chain (VL) were used to construct M315scFv-Fc using previously described method (Gilliland, Norris, et al. 1996).

The sequence of M315 scFv-Fc (SEQ ID NO:1) and huIgG1Fc (SEQ ID NO:2) were cloned
 20 into the pTT5 mammalian expression vector and the two constructs were used to co-transfect 293-6E cells to assess the formation Fc/scFv-Fc heterodimer relative to Fc homodimer and scFv-Fc homodimer.

SEQ ID NO: 1

M315scFv-huFc

HMAEVQLQQSGAELVKPGSSVKISCKASGYTFANNFMHWIKQQPGNGLEW
 25 IGWIYPGDGDEYNQKFSGKATLTADKSSSTAYMQLNSLTSEDSAVYFCI
 RLTEGTTYWGQGVMTVSSGGGGSGGGGSQFVLTQPNSVSTNLGS
 TVKLSCKRSTGNIGSNYVNWYQQHEGRSPTTMIYRDDKRPDGVDPDRFSGS
 IDGSSNSALLTINNVQTEDEADYFCQSYSRGVSPVFGGGTKLTVLAAAE**P**
KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
 30 **HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK**
EYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCL
LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

35 SEQ ID NO: 2

huIgG1-Fc

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK

EYKCKVSNKALPAPLEKLTISKAKG@PREPOVYTLPPSREEMTKNOVSLTC
 LVKGFYPSDIAVEWESNGOPENNYKLTTPPVLDSDGSEELYSKLTVDKSRW
 QOGNVFSCSVMHEALTHNHYTOKSLSTLSPGK

(Shading corresponds to the Fc region)

5 The charge residue pairs in the CH3 region identified through computational analysis were changed to amino acid of opposite charge polarity on either human IgG1Fc (dummy) or M315 scFv-Fc (mx) constructs. The mutations, which are listed in Table 6, were generated using the QuikChange® mutagenesis kit from Stratagene and verified by DNA sequencing. The mutations are denoted by wild type residue followed by the position using the Kabat numbering system (Kabat et al., *Sequences of Proteins of Immunological Interest*, National Institutes of Health, Bethesda, Md., ed, 10 5, [1991]), which is consistent with the crystal structure (PDB code: 1L6X) numbering scheme, and then the replacement residue in single letter code. The Fc sequence used in these two constructs was derived from human IgG1 non-(a) allotype, which has a Glu at position 356 and a Met at position 358. The CH3 sequences from the crystal structure are from a different IgG1 allotype, which has an Asp at 15 position 356 and a Leu at position 368.

TABLE 6: List of charge residue mutations

huIgG1Fc (dummy)	M315 scFv-Fc(mx)
Fc-WT	M315 scFv-Fc(WT)
K409D	D399'K
K409E	D399'R
K409D&K360D	D399'K&E356'K
K409D&K370D	D399'K&E357'K
K409D&K392D	D399'K&E356'K&E357'K
K409D&K439D	

20 DNA was transfected into human embryonic kidney cell line 293-6E using Lipofectamine™ 2000 reagent (Invitrogen). The cell culture supernatant was harvested 3-4 days after transfection and analyzed on SDS-PAGE Gels under non-reduced condition. The gel was then transferred to nitrocellulose membrane and subject to western analysis using peroxidase-conjugated goat anti-human IgG antibody (Jackson ImmunoResearch Laboratories) and results are shown in Fig 10.

25 Co-transfection of expression vector for M315 scFv-Fc (mx) together with dummy Fc resulted in the formation of scFv-Fc/Fc heterodimer as well as scFv-Fc homodimer and Fc homodimer. The ratio of scFv-Fc/Fc heterodimer to scfv-Fc homodimer and Fc homodimer is close to 1:1:1 when the wild type CH3 sequence is used.

The introduction of one charge pair mutation K409D on dummy Fc and D399'K on M315 maxibody significantly increased the ratio of scFv-Fc/Fc heterodimer relative to scFv-Fc homodimer as well as Fc homodimer. Similar enhancement of heterodimer formation was also observed for other

mutant variants such as K409D/D399'R, K409E/D399'K and K409E/D399'R (Fig.9), further underscore the importance of charge polarity complementation for the formation of Fc heterodimers. (The wild type M315 scFv-Fc construct used in this study has an extra tag at the carboxyl terminal of Fc, so it migrates slower on the SDS-PAGE gel.)

5 When additional mutations were introduced at charge residues that are located near K409 such as K360 and K392, a further increase of heterodimer formation was observed (Fig. 10). For example, the combination K409D;K392D on dummy Fc with D399'K on M315 maxibody showed increased ratio of heterodimer to homodimers, likely due to the disruption of Fc homodimer. A 25KD band correspond to the size of Fc monomer was detected on all transfections using K409D;K392D
10 dummy Fc (data not shown). Adding another mutation such as D356'K or D357'K on top of D399'K variant of M315 maxibody showed additional improvement. The combination of K409D;K392D on dummy Fc with D399'K;D356'K on M315 maxibody resulted almost exclusive formation of heterodimer. Other combinations such as K409D;K392D/D399'K;D357'K and
15 K409D;K370D/D399'K;D357'K also offered significant improvement over the K409D/D399'K variant.

Table 7: Quantification of percentage of homodimer and heterodimer yields for the SDS-PAGE shown in Figure 10.^a

Dummy Fc	M315 scFv-Fc	M315 scFv-Fc Homodimer	M315 scFv-Fc – Dummy Fc Heterodimer	Dummy Fc Homodimer
WT	WT	25.5	32.4	42.1
K409D;K360D	D399'K	16.8	55.1	28.1
K409D;K392D	D399'K	23.1	76.9	ND
K409D;K392D	D399'K;E356'K	ND	100	ND
K409D;K392D	D399'K;E357'K	ND	79.1	20.9
K409D;K439D	D399'K;E356'K	ND	92.3	7.7
K409D;K370D	D399'K;E357'K	ND	85.2	14.8
T366S;L368A;Y407V (Knob)	T366'W (Hole)	13.3	86.7	ND

5 ^a ND stands for Not Detectable in the density based analysis.

Example 2

This example demonstrates that CH3 domains containing certain triple charge-pair mutations were unable to form homodimers when expressed alone but were capable of forming heterodimers when co-expressed. Mutants were made and cells transfected as described in Example 1. When the constructs were co-transfected, a 1:1 ratio of plasmids were used. The results are shown in Figure 11. Heterodimer and homodimers were detected by Western blot using goat-anti-human Fc HRP

conjugated antibody. Interestingly, Fc-containing molecules having triple mutations wherein positive-charged residues were changed to negative-charged residues (K409D,K392D,K370D or K409D,K392D,K439D) were unable to be detected when expressed alone. Similarly, Fc-containing molecules having triple mutations wherein negative-charged residues were changed to positive-charged residues (D399K,E356K,E357K) were unable to be detected when expressed alone. When co-expressed with an Fc-containing molecule having mutations of opposite charge polarity, however, heterodimers only were detected.

Throughout this invention application, it is to be understood that use of a term in the singular may imply, where appropriate, use of respective term in the plural, and *vice versa*.

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CLAIMS

1. A method of preparing a heterodimeric protein comprising a first CH₃-containing polypeptide and a second CH₃-containing polypeptide that meet together to form an interface engineered to promote heterodimer formation, wherein said first CH₃-containing polypeptide and said second CH₃-containing polypeptide comprise one or more charged amino acids within the interface that are electrostatically unfavorable to homodimer formation but electrostatically favorable to heterodimer formation, the method comprising the steps of:
 - (a) culturing a host cell comprising a nucleic acid encoding the first CH₃-containing polypeptide and a nucleic acid comprising the second CH₃-containing polypeptide, wherein the cultured host cell expresses the first and second CH₃-containing polypeptides; and
 - (b) recovering the heterodimeric protein from the host cell culture.
2. The method of claim 1, wherein the heterodimeric protein comprises an Fc region.
3. The method of claim 2, wherein the Fc region comprises an IgG Fc region.
4. The method of claim 3, wherein the IgG Fc region comprises a human IgG Fc region.
5. The method of claim 4, wherein the human IgG region comprises an IgG1 Fc region.
6. The method of claim 4, wherein the IgG region comprises an IgG2 Fc region.
7. The method of claim 4, wherein the IgG region comprises an IgG3 Fc region.
8. The method of claim 4, wherein the IgG region comprises an IgG4 Fc region.
9. The method of claim 2, wherein the Fc region comprises an IgA, IgE, IgD, or IgM Fc region.
10. The method of claim 4, wherein the first CH₃-containing polypeptide or the second CH₃-containing polypeptide comprises a polypeptide sequence differing from wild-type human IgG such that one or more positive-charged amino acids in a wild-type human IgG sequence are replaced with one or more negative-charged amino acids.
11. The method of claim 10, wherein the positive-charged amino acid is selected from the group consisting of lysine, histidine, and arginine.

12. The method of claim 10, wherein the negative-charged amino acid is selected from the group consisting of aspartic acid and glutamic acid.
13. The method of claim 10, wherein the first CH₃-containing polypeptide or the second CH₃-containing polypeptide comprises a polypeptide sequence differing from wild-type human IgG such that one or more negative-charged amino acids in a wild-type human IgG sequence is replaced with one or more positive-charged amino acids.
14. The method of claim 13, wherein the positive-charged amino acid is selected from the group consisting of lysine, histidine, and arginine.
15. The method of claim 13, wherein the negative-charged amino acid is selected from the group consisting of aspartic acid and glutamic acid.
16. The method of claim 5, wherein the IgG1 Fc comprises a first CH₃-containing polypeptide or second CH₃-containing polypeptide having a polypeptide sequence differing from wild-type human IgG1 such that one or more positive-charged amino acids in a wild-type human IgG1 sequence are replaced with one or more negative-charged amino acids.
17. The method of claim 16, wherein the first CH₃-containing polypeptide comprises a replacement of a lysine with a negative-charged amino acid.
18. The method of claim 17, wherein the lysine is selected from the group consisting of Lys409, Lys392, Lys439, and Lys370.
19. The method of claim 5, wherein the IgG1 Fc comprises a first CH₃-containing polypeptide or second CH₃-containing polypeptide having a polypeptide sequence differing from wild-type human IgG1 such that one or more negative-charged amino acids in a wild-type human IgG1 sequence are replaced with one or more positive-charged amino acids.
20. The method of claim 19, wherein the first CH₃-containing polypeptide comprises a replacement of an aspartic acid with a positive-charged amino acid.
21. The method of claim 20, wherein the aspartic acid is selected from the group consisting of Asp399 and Asp356.

22. The method of claim 19, wherein the first CH₃-containing polypeptide comprises a replacement of a glutamic acid with a positive-charged amino acid.
23. The method of claim 22, wherein the glutamic acid is Glu357.
24. The method of claim 18, wherein the first CH₃-containing polypeptide comprises a replacement of Lys409 with a negative-charged amino acid and the second CH₃-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
25. The method of claim 18, wherein the first CH₃-containing polypeptide comprises a replacement of Lys392 with a negative-charged amino acid and the second CH₃-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
26. The method of claim 18, wherein the first CH₃-containing polypeptide comprises a replacement of Lys439 with a negative-charged amino acid and the second CH₃-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
27. The method of claim 18, wherein the first CH₃-containing polypeptide comprises a replacement of Lys370 with a negative-charged amino acid and the second CH₃-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
28. The method of claim 20, wherein the first CH₃-containing polypeptide comprises a replacement of Asp399 with a positive-charged amino acid and the second CH₃-containing polypeptide comprises a replacement of Lys409, Lys439, Lys370, or Lys392 with a negative-charged amino acid.
29. The method of claim 20, wherein the first CH₃-containing polypeptide comprises a replacement of Asp356 with a positive-charged amino acid and the second CH₃-containing polypeptide comprises a replacement of Lys409, Lys439, Lys370, or Lys392 with a negative-charged amino acid.
30. The method of claim 23, wherein the first CH₃-containing polypeptide comprises a replacement of Glu357 with a positive-charged amino acid and the second CH₃-containing

- polypeptide comprises a replacement of Lys409, Lys439, Lys370, or Lys392 with a negative-charged amino acid.
31. The method of claim 1, wherein the first CH3-containing polypeptide is an antibody heavy chain.
 32. The method of claim 1, wherein the second CH3-containing polypeptide is an antibody heavy chain.
 33. The method of claim 1, wherein the host cell expresses one or more antibody light chains.
 34. The method of claim 1, wherein the heterodimeric protein is selected from the group consisting of an antibody, a bispecific antibody, a monospecific monovalent antibody, a bispecific maxibody, a monobody, a peptibody, a bispecific peptibody, a monovalent peptibody, and a receptor fusion protein.
 35. A host cell comprising a nucleic acid encoding a first CH3-containing polypeptide and a nucleic acid comprising a second CH3-containing polypeptide, wherein the first CH3-containing polypeptide and the second CH3-containing polypeptide meet together to form an interface engineered to promote heterodimer formation, and wherein said first CH3-containing polypeptide and said second CH3-containing polypeptide comprise one or more charged amino acids within the interface that are electrostatically unfavorable to homodimer formation but electrostatically favorable to heterodimer formation.
 36. A composition comprising a nucleic acid encoding a first CH3-containing polypeptide and a nucleic acid comprising a second CH3-containing polypeptide, wherein the first CH3-containing polypeptide and the second CH3-containing polypeptide meet together to form an interface engineered to promote heterodimer formation, and wherein said first CH3-containing polypeptide and said second CH3-containing polypeptide comprise one or more charged amino acids within the interface that are electrostatically unfavorable to homodimer formation but electrostatically favorable to heterodimer formation.
 37. A heterodimeric protein comprising a first CH3-containing polypeptide and a second CH3-containing polypeptide that meet together to form an interface engineered to promote heterodimer formation, wherein said first CH3-containing polypeptide and said second CH3-containing polypeptide comprise one or more charged amino acids within the interface that

- are electrostatically unfavorable to homodimer formation but electrostatically favorable to heterodimer formation.
38. The heterodimeric protein of claim 37, wherein the heterodimeric protein comprises an Fc region.
 39. The heterodimeric protein of claim 38, wherein the Fc region comprises an IgG Fc region.
 40. The heterodimeric protein of claim 39, wherein the IgG Fc region comprises a human IgG Fc region.
 41. The heterodimeric protein of claim 40, wherein the human IgG region comprises an IgG1 Fc region.
 42. The heterodimeric protein of claim 40, wherein the IgG region comprises an IgG2 Fc region.
 43. The heterodimeric protein of claim 40, wherein the IgG region comprises an IgG3 Fc region.
 44. The heterodimeric protein of claim 40, wherein the IgG region comprises an IgG4 Fc region.
 45. The heterodimeric protein of claim 38, wherein the Fc region comprises an IgA, IgE, IgD, or IgM Fc region.
 46. The heterodimeric protein of claim 40, wherein the first CH3-containing polypeptide or the second CH3-containing polypeptide comprises a polypeptide sequence differing from wild-type human IgG such that one or more positive-charged amino acids in a wild-type human IgG sequence are replaced with one or more negative-charged amino acids.
 47. The heterodimeric protein of claim 46, wherein the positive-charged amino acid is selected from the group consisting of lysine, histidine, and arginine.
 48. The heterodimeric protein of claim 46, wherein the negative-charged amino acid is selected from the group consisting of aspartic acid and glutamic acid.
 49. The heterodimeric protein of claim 46, wherein the first CH3-containing polypeptide or the second CH3-containing polypeptide comprises a polypeptide sequence differing from wild-

- type human IgG such that one or more negative-charged amino acids in a wild-type human IgG sequence is replaced with one or more positive-charged amino acids.
50. The heterodimeric protein of claim 49, wherein the positive-charged amino acid is selected from the group consisting of lysine, histidine, and arginine.
 51. The heterodimeric protein of claim 49, wherein the negative-charged amino acid is selected from the group consisting of aspartic acid and glutamic acid.
 52. The heterodimeric protein of claim 41, wherein the IgG1 Fc comprises a first CH3-containing polypeptide or second CH3-containing polypeptide having a polypeptide sequence differing from wild-type human IgG1 such that one or more positive-charged amino acids in a wild-type human IgG1 sequence are replaced with one or more negative-charged amino acids.
 53. The heterodimeric protein of claim 52, wherein the first CH3-containing polypeptide comprises a replacement of a lysine with a negative-charged amino acid.
 54. The heterodimeric protein of claim 53, wherein the lysine is selected from the group consisting of Lys409, Lys392, Lys439, and Lys370.
 55. The heterodimeric protein of claim 41, wherein the IgG1 Fc comprises a first CH3-containing polypeptide or second CH3-containing polypeptide having a polypeptide sequence differing from wild-type human IgG1 such that one or more negative-charged amino acids in a wild-type human IgG1 sequence are replaced with one or more positive-charged amino acids.
 56. The heterodimeric protein of claim 55, wherein the first CH3-containing polypeptide comprises a replacement of an aspartic acid with a positive-charged amino acid.
 57. The heterodimeric protein of claim 56, wherein the aspartic acid is selected from the group consisting of Asp399 and Asp356.
 58. The heterodimeric protein of claim 55, wherein the first CH3-containing polypeptide comprises a replacement of a glutamic acid with a positive-charged amino acid.
 59. The heterodimeric protein of claim 58, wherein the glutamic acid is Glu357.

60. The heterodimeric protein of claim 54, wherein the first CH3-containing polypeptide comprises a replacement of Lys409 with a negative-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
61. The heterodimeric protein of claim 54, wherein the first CH3-containing polypeptide comprises a replacement of Lys392 with a negative-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
62. The heterodimeric protein of claim 54, wherein the first CH3-containing polypeptide comprises a replacement of Lys439 with a negative-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
63. The heterodimeric protein of claim 54, wherein the first CH3-containing polypeptide comprises a replacement of Lys370 with a negative-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Asp399, Asp356, or Glu357 with a positive-charged amino acid.
64. The heterodimeric protein of claim 57, wherein the first CH3-containing polypeptide comprises a replacement of Asp399 with a positive-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Lys409, Lys439, Lys370, or Lys392 with a negative-charged amino acid.
65. The heterodimeric protein of claim 57, wherein the first CH3-containing polypeptide comprises a replacement of Asp356 with a positive-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Lys409, Lys439, Lys370, or Lys392 with a negative-charged amino acid.
66. The heterodimeric protein of claim 59, wherein the first CH3-containing polypeptide comprises a replacement of Glu357 with a positive-charged amino acid and the second CH3-containing polypeptide comprises a replacement of Lys409, Lys439, Lys370, or Lys392 with a negative-charged amino acid.
67. The heterodimeric protein of claim 37, wherein the first CH3-containing polypeptide is an antibody heavy chain.

68. The heterodimeric protein of claim 37, wherein the second CH3-containing polypeptide is an antibody heavy chain.
69. The heterodimeric protein of claim 37, wherein the heterodimeric protein further comprises one or more antibody light chains.
70. The heterodimeric protein of claim 37, wherein the heterodimeric protein is selected from the group consisting of an antibody, a bispecific antibody, a monospecific monovalent antibody, a bispecific maxibody, a monobody, a peptibody, a bispecific peptibody, a monovalent peptibody, and a receptor fusion protein.
71. A polypeptide comprising a CH3 region of an antibody, wherein the CH3 region comprises a polypeptide sequence differing from a wild-type CH3 region such that one or more positive-charged amino acids in wild-type CH3 are replaced with one or more negative-charged amino acids, wherein the polypeptide has decreased ability to form homodimers compared to a polypeptide comprising a wild-type CH3 region.
72. A polypeptide comprising a CH3 region of an antibody, wherein the CH3 region comprises a polypeptide sequence differing from a wild-type CH3 region such that one or more negative-charged amino acids in wild-type CH3 are replaced with one or more positive-charged amino acids, wherein the polypeptide has decreased ability to form homodimers compared to a polypeptide comprising a wild-type CH3 region.
73. The polypeptide of claim 71, further comprising a CH2 region.
74. The polypeptide of claim 72, further comprising a CH2 region.
75. The polypeptide of claim 73, wherein the polypeptide comprises an antibody heavy chain.
76. The polypeptide of claim 74, wherein the polypeptide comprises an antibody heavy chain.
77. An antibody comprising the polypeptide of claim 75.
78. An antibody comprising the polypeptide of claim 76.
79. An isolated nucleic acid encoding a polypeptide of any of claims 71-76.

80. An expression vector comprising the isolated nucleic acid of claim 79 operably linked to a promoter.
81. A host cell containing the expression vector of claim 80.
82. A pharmaceutical composition comprising a polypeptide of any of claim 71-76.

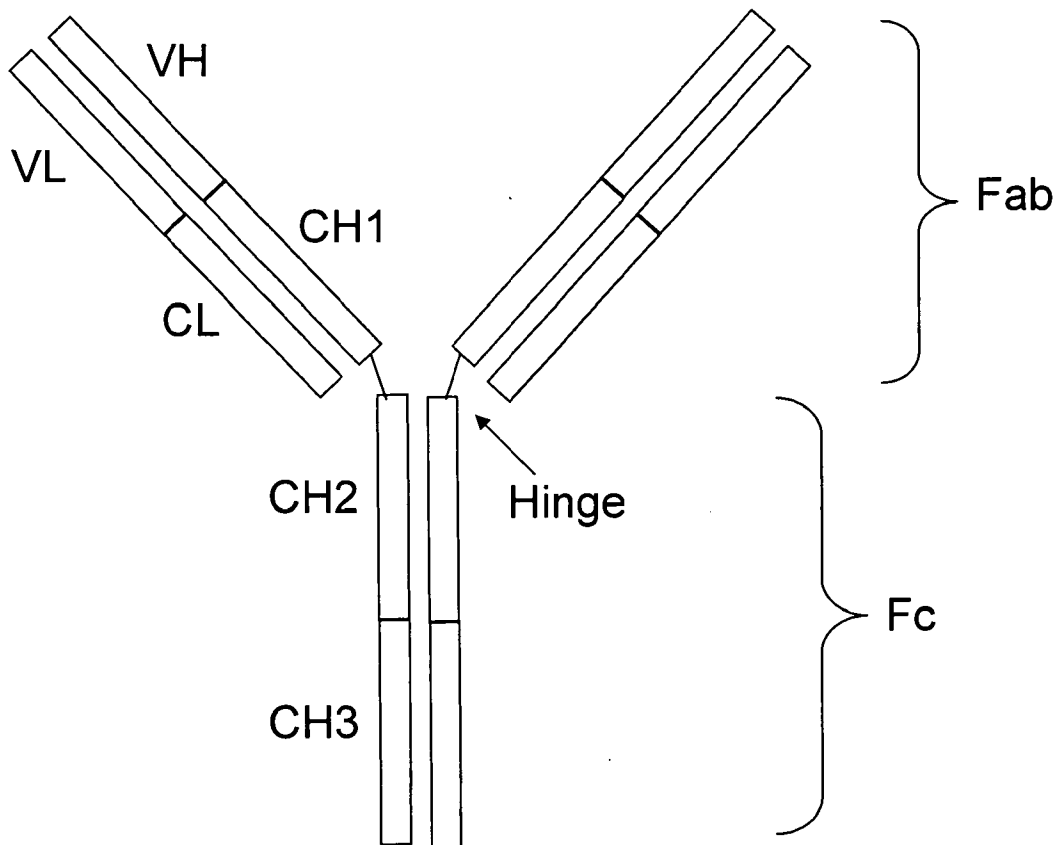


Figure 1

Replacement Sheet
1/12

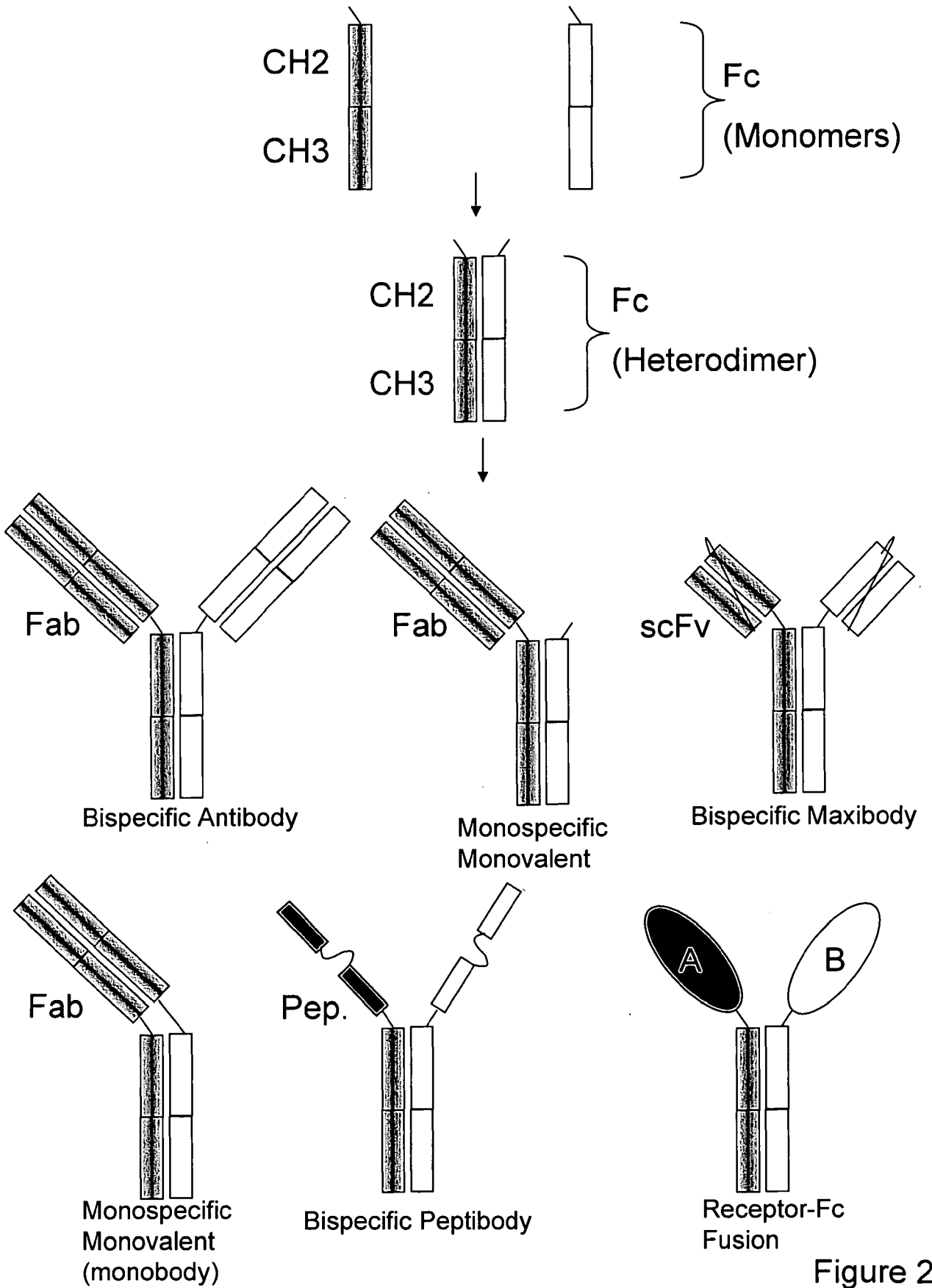


Figure 2

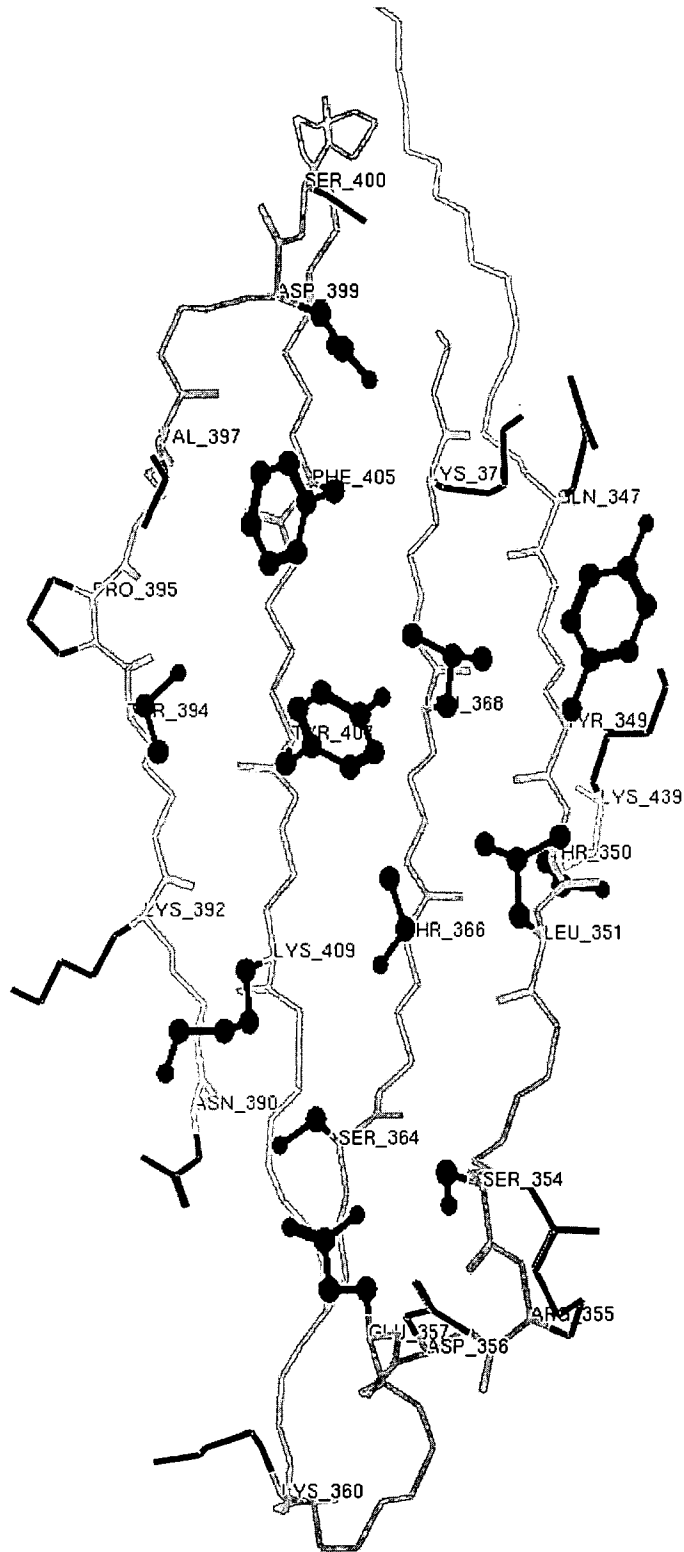


Figure 3

Replacement Sheet
3/12

(a)

IGG1_HUMAN AKGQPREPQVYTLPPSRDELTAKNQVSLTCLVKGFYPSDIAEVESNGQPENNYKTTTPPVL 390
 IGG2_HUMAN TKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAEVESNGQPENNYKTTTPPML
 IGG3_HUMAN TKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAEVESNGQPENNYKTTTPPML
 IGG4_HUMAN AKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAEVESNGQPENNYKTTTPPVL * * * * *

IGG1_HUMAN
 IGG2_HUMAN
 IGG3_HUMAN
 IGG4_HUMAN

DSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKLSLSLSPGK 440
 DSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKLSLSLSPGK
 DSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKLSLSLSPGK
 DSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKLSLSLSPGK *

(b)

IGG1_MOUSE TKGRPKAPQVYTIPTPKKEMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPI 390
 IGG2A_MOUSE PKGSVRAPQVYVLPPEPEEMTKKQVTLTCMVTDPMEDIYVEWTNNGKTELNKNTPEVL
 IGG2B_MOUSE IKGLVRAPQVYTLPPPAEQLSRKDVSLTCLVVGFPDGSVEWTSNGHTEENYKDTAPVL
 IGG3_MOUSE PKGRAQTPOVYTIPTPKKEMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPIL * * * * *

IGG1_MOUSE
 IGG2A_MOUSE
 IGG2B_MOUSE
 IGG3_MOUSE

NTNGSYFVYSKLVNQKSNWEAGNTFTCSVLHEGLHNHHTKLSLSHS 390
 DSDGSYFMYSKLVRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRT
 DSDGSYFIYSKLVNMTSKWEKTD SFCNVRHEGLKNYLLKTI SRS
 DSDGTYFLYSKLVTDSDSWLQGEIFTCSVVHEALHNHHTKLSLSRS *

IGG1_MOUSE
 IGG2A_MOUSE
 IGG2B_MOUSE
 IGG3_MOUSE

Figure 4

(c)

IGA_HUMAN -SGNT-FRPEVHLLPPSEELALNELVTLTCLARGFSPKDVLRWLQGSQELPREKYLITW
 IGE_HUMAN TSGPR-AAPEVYAFATPEWPGSRDK-RTLACLIQNFMPEDISVQWLHNEVQLPDRHSTT
 IGD_HUMAN REPAA-QAPVKLSINLLASSDPPPEAASWLLCEVSGFSPNILLMWLEDQREVNTSGFAPA
 IGM_HUMAN PKGVALHRPDVYLLPPAREQLNLRRESATITCLVTGFSPADVVFQWMQRGQPLSPEKYVTS
 *

IGA_HUMAN ASRQEPSQGTTFAVTSILRVAEDWKKGDTFSCMVGHEAL-PLAFTQKTIDRLAGK
 IGE_HUMAN QPRKT---KSGFFVFSRLEVTRAWEQKDEFICRAVHEAASPQTVQRAVSVNPGK
 IGD_HUMAN RPPPQP--GSTTFWAWSVLRVPAPPSPQPATYTCVVSHEDSRLLNASRSLEVS YVT
 IGM_HUMAN APMPEP-QAPGRYFAHSILTVSEEEWNTGETYTCVVAHEAL-PNRVTERTVDKSTGK
 *

Replacement Sheet
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Figure 4

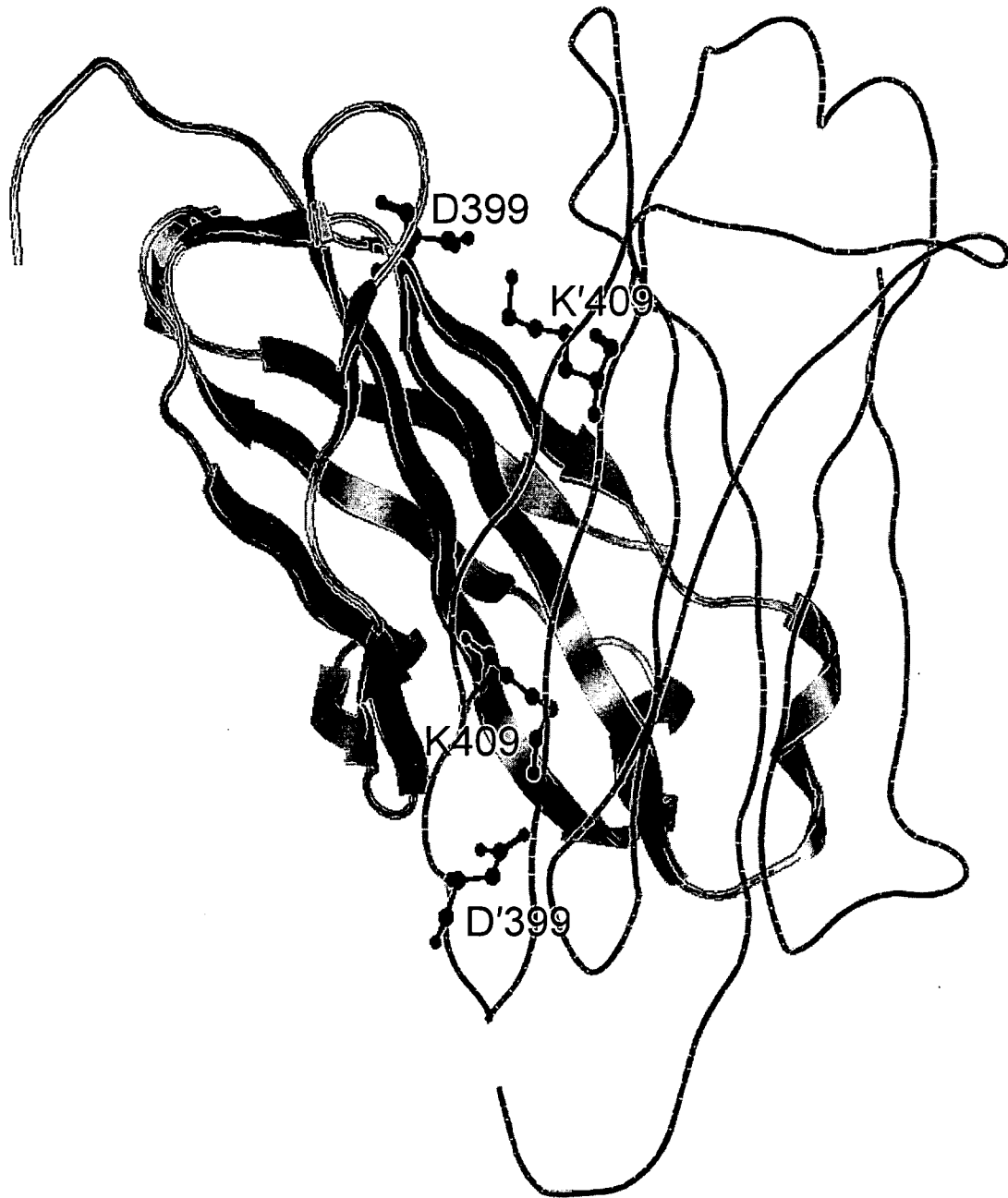


Figure 5

Replacement Sheet
6/12

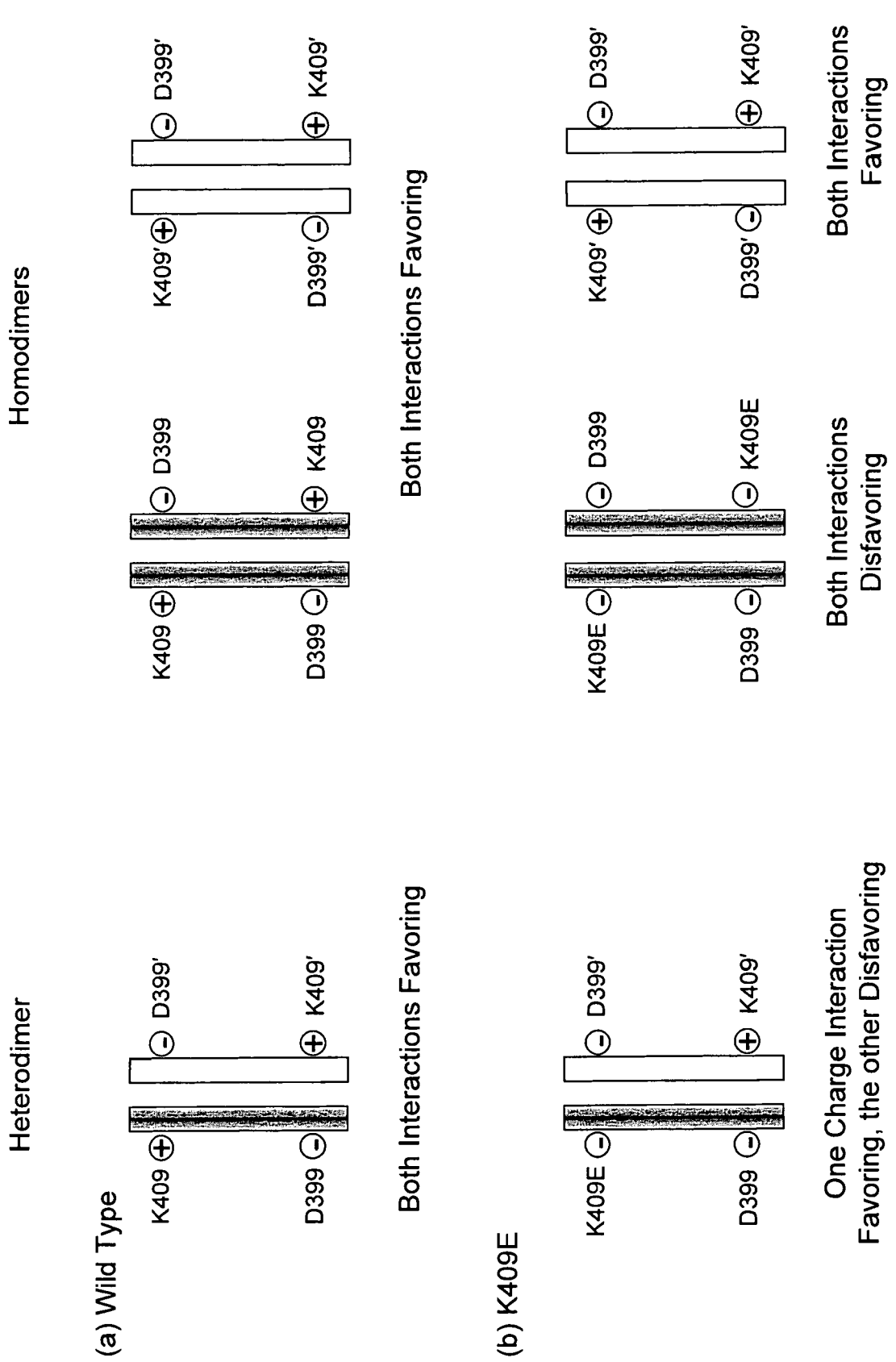
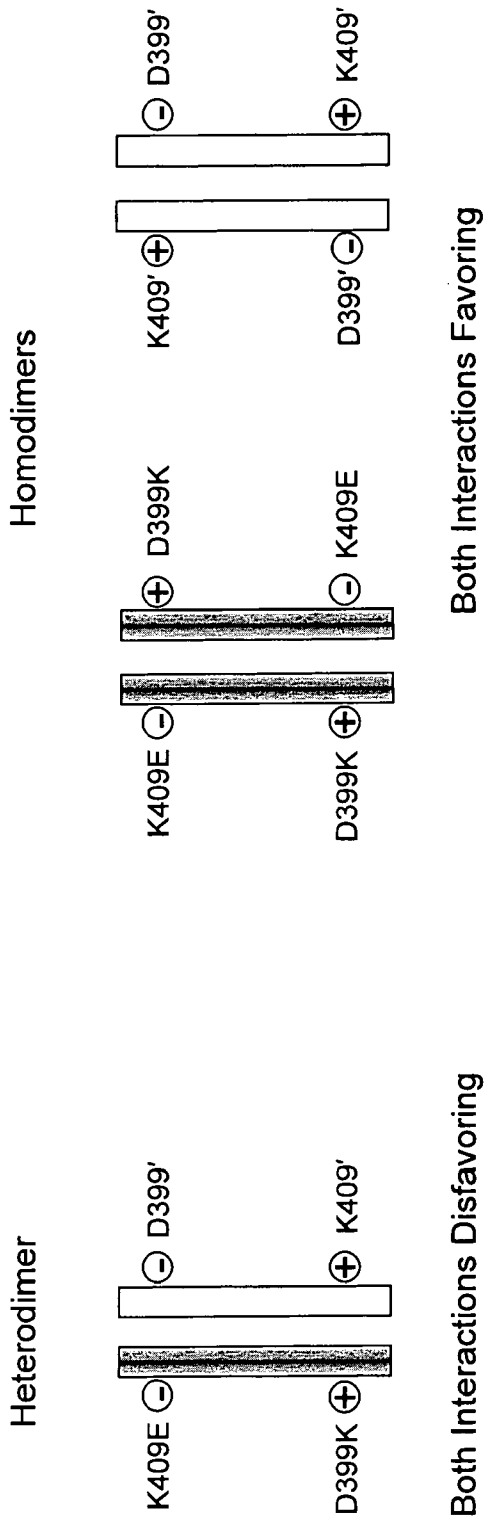


Figure 6



K409E & D399K Mutations as An Example for Promoting Homodimers

Figure 7

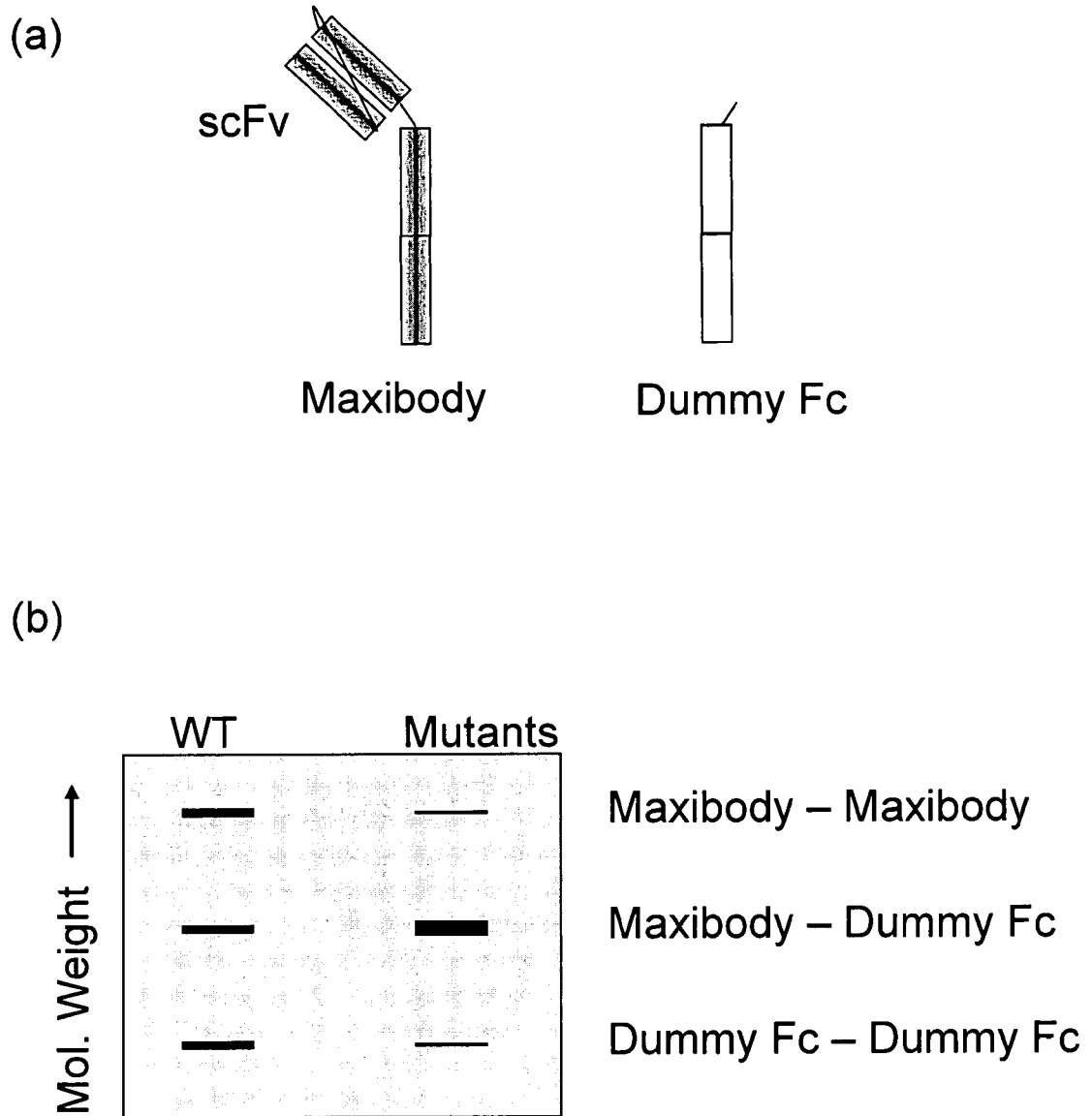


Figure 8

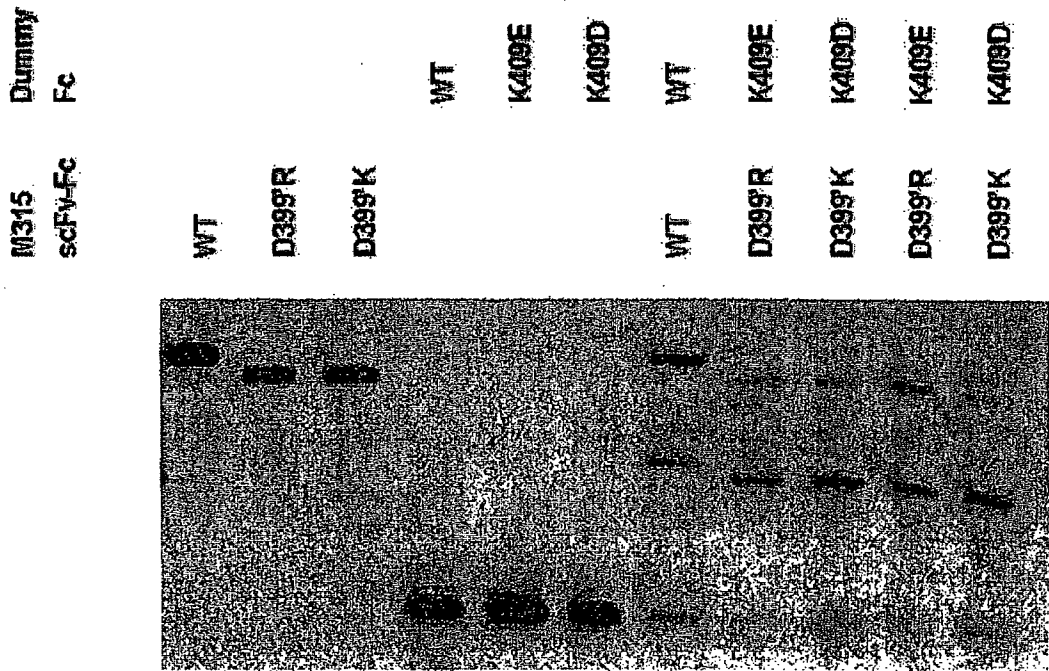


Figure 9

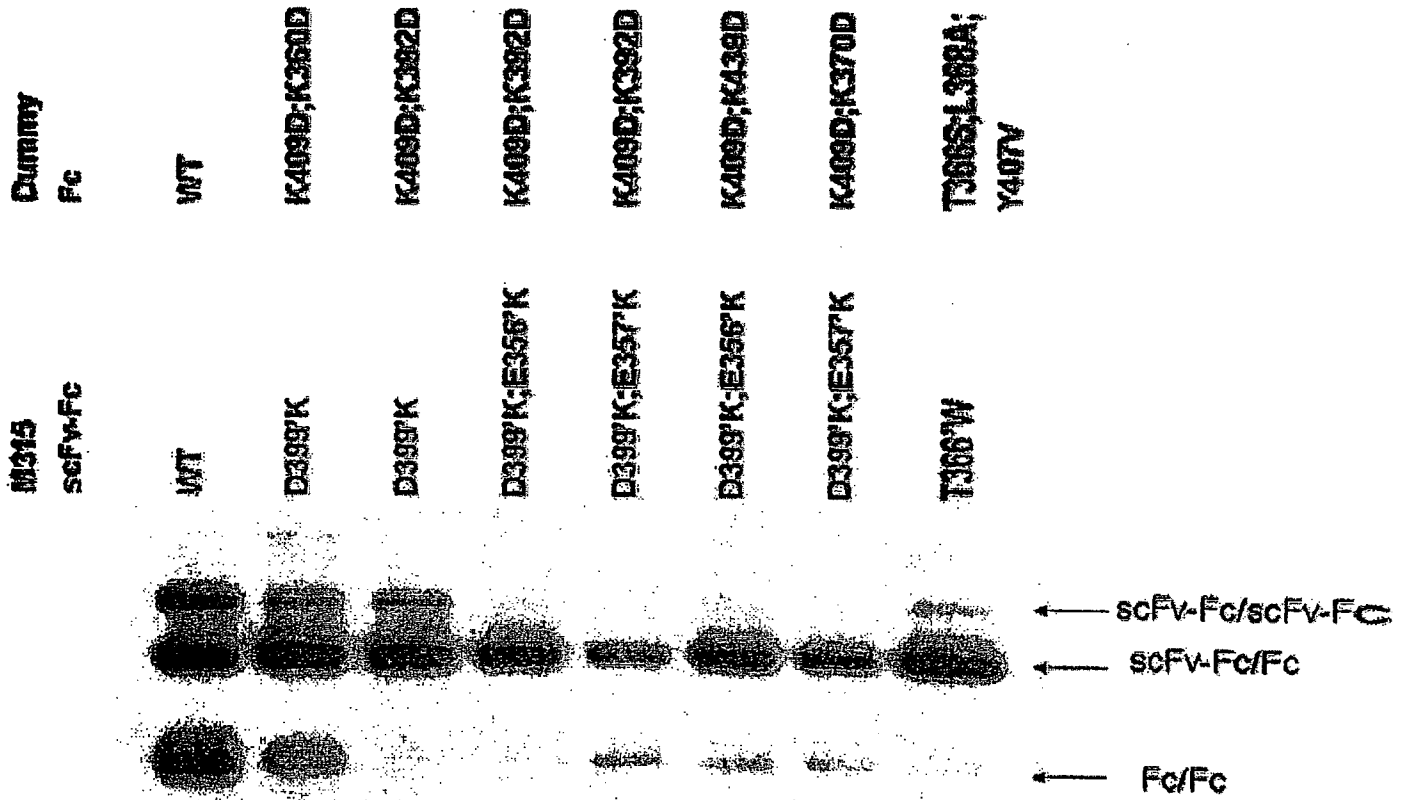


Figure 10

M31&scFv	-	WT	WT	-	D399K E356K	D399K E356K	-	D399K E356K E357K	D399K E356K E357K	D399K E356K E357K
Fc	-	WT	WT	-	D399K E356K	D399K E356K E357K	-	D399K E356K E357K	D399K E356K E357K	D399K E356K E357K
dummyFc	WT	-	WT	K409D K392D	-	K409D K392D K370D	K409D K392D K439D	K409D K392D K439D	K409D K392D K439D	K409D K392D K439D

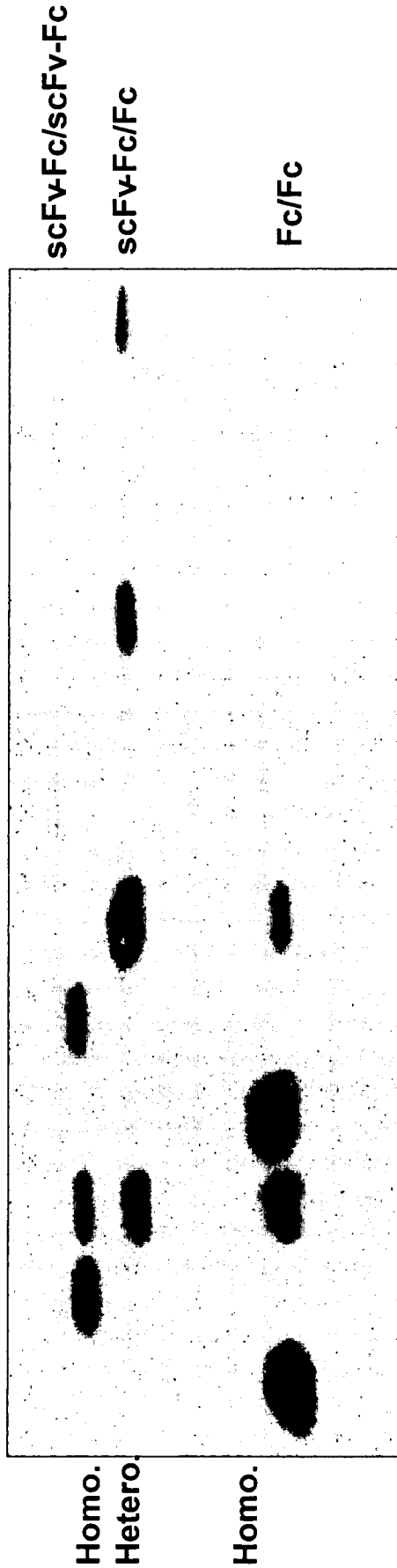


Figure 11

INTERNATIONAL SEARCH REPORT

International application No PCT/US2009/000071

A. CLASSIFICATION OF SUBJECT MATTER
 INV. C07K16/46

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
 EPO-Internal, WPI Data, CHEM ABS Data, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SINHA NEETI ET AL: "ELECTROSTATICS IN PROTEIN BINDING AND FUNCTION" CURRENT PROTEIN AND PEPTIDE SCIENCE, BENTHAM SCIENCE PULBISHERS, NL, vol. 3, no. 6, 1 December 2002 (2002-12-01), pages 601-614, XP008077600 ISSN: 1389-2037 the whole document	1-82
X	WO 2007/110205 A (MERCK PATENT GMBH [DE]; DAVIS JONATHAN H [US]; HUSTON JAMES STAFFORD []) 4 October 2007 (2007-10-04) the whole document	35-82

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents :

A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
E earlier document but published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
O document referring to an oral disclosure, use, exhibition or other means	*Z* document member of the same patent family
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 20 May 2009	Date of mailing of the international search report 28/05/2009
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Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Meyer, Wolfram
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2009/000071

Box No. 1 Nucleotide and/or amino acid sequence(s) (Continuation of item 1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:
 - a. type of material
 - a sequence listing
 - table(s) related to the sequence listing
 - b. format of material
 - on paper
 - in electronic form
 - c. time of filing/furnishing
 - contained in the international application as filed
 - filed together with the international application in electronic form
 - furnished subsequently to this Authority for the purpose of search
2. In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

 International application No
 PCT/US2009/000071

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	RIDGWAY ET AL: "'KNOBS-INTO-HOLES' ENGINEERING OF ANTIBODY CH3 DOMAINS FOR HEAVY CHAIN HETERODIMERIZATION" PROTEIN ENGINEERING, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 9, no. 7, 1 January 1996 (1996-01-01), pages 617-621, XP002084766 ISSN: 0269-2139 cited in the application the whole document	1-82
Y	NOHAILE M J ET AL: "Altering dimerization specificity by changes in surface electrostatics" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, DC.; US, vol. 98, no. 6, 13 March 2001 (2001-03-13), pages 3109-3114, XP002412033 ISSN: 0027-8424 the whole document	1-82
Y	ZHU ET AL: "REMODELLING DOMAIN INTERFACES TO ENHANCE HETERODIMER FORMATION" PROTEIN SCIENCE, CAMBRIDGE UNIVERSITY PRESS, CAMBRIDGE, GB, vol. 6, no. 4, 1 April 1997 (1997-04-01), pages 781-788, XP002084764 ISSN: 0961-8368 page 786	1-82

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2009/000071

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2007110205 A	04-10-2007	AR 060070 A1	21-05-2008
		AU 2007229698 A1	04-10-2007
		CA 2646965 A1	04-10-2007
		EP 1999154 A2	10-12-2008
		US 2007287170 A1	13-12-2007
