SEQUENCE SYMMETRIC MODIFIED IGG4 BISPECIFIC ANTIBODIES

The present invention relates to a bispecific IgG4 antibody having an altered arrangement of disulphide bonds compared to a wild type antibody and a method to produce the improved antibody. In a further aspect the present disclosure provides an efficient method for preparing bispecific antibodies.

The biopharmaceutical industry encompassing recombinant proteins, monoclonal antibodies (mAbs) and nucleic acid-based drugs is growing rapidly. Antibody engineering has resulted in the design and production of antibody fragments or alternative formats. Preferred molecular format along with other aspects such as production yield, protein quality and storage stability are taken into consideration when selecting an antibody-based protein as a therapeutic agent.

The basic structure of all immunoglobulin (Ig) molecules comprises two identical heavy chains (HCs) and two identical light chains (LCs) which are coupled by disulphide bonds. Each LC consists of a variable (V_L) and constant domain (C_L). Based on the HC, five main Ig classes are recognized: IgG, IgA, IgD, IgE and IgM. For IgG, the HC consists of one variable domain (V_H) and three constant domains (C_H1-3). The C_H2 and C_H3 domains form the Fc part of the molecule that is responsible for stimulating effector function and is linked to the Fab fragment (V_HV_L and C_HC_L) by a hinge region which confers flexibility to the IgG molecule. Two antigen recognition sites are located at the ends of the V_L and V_H domains. IgG is further subdivided into 4 different isotypes: IgG1, IgG2, IgG3 and IgG4.

Fc-mediated effector functions i.e. antibody dependent cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC) are isotype dependent. Each isotype has evolved to perform a specific function within the body. The IgG1 isotype is currently the most widely used as a therapeutic due to its extended half-life, enhanced ADCC activation and complement activation. Other isotypes are employed as therapeutic agents as appropriate to the target and desired effect. For instance, when target antigens are simply to be neutralized and effector functions are less important, alternative isotypes such as IgG2 and IgG4 can be used. Alternatively, IgG with re-engineered Fc/effector function may be considered.

IgG2 also has minimal associated effector function but is prone to dimerisation which is not fully understood.

IgG4 remains a useful isotype because of its relative lack of effector function induction. However, IgG4 also has some inherent practical difficulties namely its shorter serum half-life and its ability to undergo "Fab-arm exchange" (also referred to as dynamic heavy chain exchange or heavy chain exchange), wherein the heavy chain and its attached light chain of one

antibody is exchanged with the heavy chain and its attached light chain of another antibody to form another whole antibody composed of two heavy chains and two attached light chains (van der Neut Kolfschoten et al., 2007 Science 317, 1554-1557).

In vivo, Fab-arm exchange results in bispecific antibodies that, due to their different variable domains, can co-engage distinct target antigens. This produces a large percentage of circulating IgG4 which have been observed to be bispecific, but functionally monovalent. (Schuurman,J., Van Ree,R., Perdok,G.J., Van Doorn,H.R., Tan,K.Y., Aalberse,R.C., 1999. Normal human immunoglobulin G4 can be bispecific: it has two different antigen-combining sites. Immunology 97, 693-698).

In vitro, when IgG4 antibodies are analysed by non-reducing SDS-PAGE, they have been observed to form so called 'half-molecules' each comprising a single covalently associated heavy-light chain pair caused by the absence of inter heavy chain disulphide bonds typically due to the formation of intra heavy chain disulphide bonds within the hinge region. The heavy chain of a "half-molecule" may non-covalently associate with its heavy chain paired partner, the association being maintained by CH3:CH3 domain interactions. In solution such 'half-molecules' are actually observed using methods such as size exclusion chromatography to be full sized, that is approximately 150kDa but on non-reducing SDS-PAGE are comprised of 75kDa LC:HC pairings (so-called "half-molecule").

A Ser to Pro mutation at position 241 (numbered according to the Kabat numbering system) in the hinge reduces the appearance of these 'half molecules' by non-reducing, SDS-PAGE (Angal,S. et al., 1993. A single amino acid substitution abolishes the heterogeneity of chimeric mouse/human (IgG4) antibody as observed during SDS-PAGE analysis Mol Immunol 30, 105-108). In addition, this point mutation does not influence the compact structure of IgG4 thereby allowing IgG4 to retain its reduced ability to activate complement.

Following the discovery of the S241P mutation, further mutations to IgG4 have been investigated in order to understand the inter-heavy chain interaction in IgG4 antibodies, reduce IgG4 effector function and enhance structural stability. In Schuurman et al. (Schuurman,J et al., 2001. The inter-heavy chain disulphide bonds of IgG4 are in equilibrium with intra-heavy chain disulphide bonds. Molecular Immunology 38, 1-8), the observed instability of inter-heavy chain disulphide bonds of IgG4 was investigated using IgG4 mutants. In mutant M1 Cys 131 (numbered according to EU numbering system or Cys 127 according to Kabat numbering system), which is involved in the inter-heavy-light chain (C_L-C_{H1}) disulphide bond, was replaced by serine and it was found that this mutant resulted in the formation of dimers of light chains and dimers of heavy chains. In mutant M2 cysteine 226 (226 numbered according to EU

numbering system or 239 according to Kabat numbering system), which is involved in an inter-heavy chain disulphide bond in the hinge, was replaced by serine and it was found that this mutant had a more stable inter-heavy chain linkage compared to IgG4 and prevents the formation of an intra-heavy chain disulphide bond.

Mutations in the C_H2 and C_H3 domains of IgG4 antibodies have also been investigated in order to reduce the formation of aggregates of IgG4 antibodies. US 2008/0063635 Takahashi et al. has investigated a mutant of IgG4 in which arginine at position 409 (409 numbered according to EU numbering system or 440 numbered according to the Kabat numbering system) in the CH3 domain is substituted with lysine, threonine, methionine or leucine in order to inhibit aggregate formation at low pH. Further mutations at L235, D265, D270, K322, P329 and P331 (L235, D265, D270, K322, P329 and P331 numbered according to EU numbering system or L248, D278, D283, K341, P348 and P350 numbered according to the Kabat numbering system) are also taught in order to attenuate CDC activity. WO2008/145142 Van de Winkel et al. discloses stable IgG4 antibodies that have a reduced ability to undergo Fab-arm exchange by substitution of the arginine residue at position 409, the Phe residue at position 405 or the Lys at position 370 (R409, F405 and K370 numbered according to EU numbering system or R440, F436 and K393 numbered according to the Kabat numbering system) even in the absence of the S228P (S228 numbered according to EU numbering system or S241 according to the Kabat numbering system) mutation in the hinge region.

The present invention provides new mutant antibodies which have advantageous properties including improved biophysical properties compared to wild-type antibodies, in particular wild-type IgG4 antibodies and fragments. In particular it has been surprisingly found that a change of the location of the cysteine residue in the heavy chain of an IgG4 antibody which forms a disulphide bond with a cysteine in the light chain provides an IgG4 antibody having improved stability compared to a wild-type IgG4 antibody. It has also been found that the mutant IgG4 antibodies are capable of forming bispecific antibodies having advantageous Fab-arm exchange properties.

In vitro the exchange of the Fab-arms can be promoted by employing high concentrations of antibodies and/or employing chemical stimulants such as glutathione to generate a bispecific format that is stable and suitable for use as a therapeutic agent. This has application in the field pharmaceutical biological products because bispecific entities can be difficult to express as a single construct.

Summary of the Invention

In one aspect, the present invention provides a symmetric bispecific antibody of the class IgG4 comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, wherein in each heavy chain:

a. the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is substituted with another amino acid; and
b. one or more of the amino acids positioned in the upper hinge region is substituted with cysteine,

wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

In one embodiment the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is the cysteine at position 127, numbered according to the Kabat numbering system, for example as shown in Figure 1b.

In one embodiment the inter-chain cysteine at position 127, numbered according to the Kabat numbering system, in the C_H1 domain is substituted with another amino acid in one or both heavy chains.

The one or more amino acids positioned in the upper hinge region which are substituted with cysteine may be selected from 226, 227, 228, 229, 230, 237 and 238, numbered according to the Kabat numbering system, as shown in Figure 1b (underlined amino acids in upper hinge region). In one embodiment the one or more amino acids positioned in the upper hinge region which are substituted with cysteine are one or more of the amino acids at positions selected from 227, 228, 229 and 230, numbered according to the Kabat numbering system, as shown in Figures 1b and 2a.

In one embodiment a mutation to cysteine at position 229 reduces Fab-arm exchange.

In one embodiment a mutation to cysteine at position 230 in combination with a mutation at position 241 to a non-polar amino acid, for example selected from proline, alanine, glycine, isoleucine, phenylalanine, tryptophan and valine, is employed.

In one embodiment Fab-arm may be increased employing a mutation to a polar residue, for example selected rom arginine, aspartic acid, glutamic acid, histidine, lysine, threonine and tyrosine, such as threonine.

In one embodiment there is provide a mutation at position 241 to a non-polar amino acid, for example selected from proline, alanine, glycine, isoleucine, phenylalanine, tryptophan and valine, is employed.

In a further aspect, the present invention also provides a symmetric bispecific antibody of the class IgG4 comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, wherein in each heavy chain:

a. the cysteine at position 127, numbered according to the Kabat numbering system, is substituted with another amino acid; and
b. the cysteine at position 239 or the cysteine at position 242, numbered according to the Kabat numbering system, are substituted with another amino acid,

wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

The antibodies provided by the present invention have no effector function and may show advantageous properties compared to a wild-type IgG4 antibody, for example improved stability, such as improved thermal stability.

Whilst not wishing to be bound by theory it is hypothesized that the modified hinge in the antibodies according to the present disclosure relieves internal strain inherent in the IgG4 molecule and thereby promotes improved stability.

The natural processes of heavy chain exchange can be promoted in IgG4 antibodies to facilitate the preparation of bispecific IgG4 antibodies according to the present disclosure, for example *in vitro* by employing high concentrations of antibodies and/or employing a chemical stimulant of exchange such as glutathione.

The antibodies of the present disclosure may be beneficial in that they have improved stability over wild-type IgG4 molecules and/or improved heavy chain exchange. The antibodies of the present invention may demonstrate reduced heavy chain exchange compared to wild-type IgG4, which provides a bispecific antibody which demonstrates little or no exchange with wild-type IgG4 *in vivo* due to its reduced propensity to exchange compared to IgG4 and also due to the relatively low concentration of a bispecific antibody *in vivo* compared to natural circulating IgG4 antibodies.

Whilst not wishing to be bound by theory it is thought that the exchange between similar type constructs as those described according to the present invention is more favorable than exchange between a construct of the present disclosure and a wild-type IgG4.

The bispecific antibodies of the present invention may demonstrate reduced heavy change exchange at concentrations greater than *in vivo* concentrations, for example concentrations of 0.5mM or less compared to IgG4 wild type. Whilst the bispecific antibodies of the invention demonstrate reduced heavy chain exchange compared to wild type IgG4, they do demonstrate a degree of heavy chain exchange, compared to IgG1 wt and IgG4 S241P,

which is sufficient to create the bispecific antibody from two antibodies having different antigen specificities *in vitro*. The symmetry in the constant region of the constructs herein advantageously minimizes the internal strain of the antibody and therefore aids stability.

Accordingly, the present invention also provides method of generating a symmetric bispecific antibody comprising the step of mixing a first IgG4 antibody with a second IgG4 antibody *ex vivo*, under conditions conducive to heavy chain exchange, wherein the antigen specificity of variable regions in the first the antibody are different to antigen specificity of the variable regions in the second antibody.

The method of the present disclosure allows the efficient preparation of bispecific symmetrical antibodies employing only routine techniques and stimulation of naturally occurring processes.

Brief Description of the Figures

Figure 1a shows the human C_H1 and hinge sequences of IgG1 wild type and IgG4 wild type, wherein the hinge residues are underlined, and the kappa light chain constant sequence.

Figure 1b shows:

the human kappa light chain constant sequence indicating the cysteine (underlined) that forms the inter-chain C_L-C_H1 disulphide bond;

the human IgG 1, 2, 3 and 4 heavy chain N-terminal C_H1 residues and hinge region sequences wherein the cysteine position (in upper hinge for IgG1 and in N-terminal C_H1 for IgG 2, 3 and 4) is indicated (underlined) which forms the inter-chain C_L-C_H1 disulphide bond;

the human IgD heavy chain N-terminal C_H1 residues and part of the hinge region sequences wherein the cysteine position in the N-terminal C_H1 sequence is indicated (underlined) which forms the inter-chain C_L-C_H1 disulphide bond;

the human IgM heavy chain N-terminal C_H1, C-terminal C_H1 residues and selected N-terminal C_H2 residues wherein the cysteine position in the N-terminal C_H1 is indicated (underlined) which forms the inter-chain C_L-C_H1 disulphide bond; and

the residues in the upper hinge of IgG3 and IgG4, the hinge of IgD and in the C-terminal C_H1 and the C_H2 of IgM where underlined residues indicate positions where one or more residues may be substituted with cysteine in the antibodies of the present invention.

Figure 2a shows the C_H1 cysteine residue (C127) which forms the inter-chain disulphide bond with a cysteine in the light chain and the upper and core hinge residues of IgG1 wild type, IgG4 wild type and the positions where mutations have been introduced in the IgG4 antibodies of the present invention.

Figure 2b shows the C_H1 cysteine residue (C127) which forms the inter-chain disulphide bond with a cysteine in the light chain and the hinge residues of IgG3 wild type and the positions where one or more residues are substituted with cysteine in the IgG3 antibodies of the present invention.

Figure 2c shows the C_H1 cysteine residue (C127) which forms the inter-chain disulphide bond with a cysteine in the light chain and selected C_H1 and C_H2 residues of IgM wild type and the positions where one or more residues are substituted with cysteine in the IgM antibodies of the present invention.

Figure 2d shows the C_H1 cysteine residue (C128) which forms the inter-chain disulphide bond with a cysteine in the light chain and the hinge residues of IgD wild type and the positions where one or more residues are substituted with cysteine in the IgD antibodies of the present invention.

Figure 3a shows the mutations introduced in IgG4 antibodies according to the present invention.

Figure 3b shows the positions of the residues in the mutated heavy chain of the IgG4 antibodies shown in Figure 3a and the predicted disulphide bond that can form with a cysteine in either the light chain (LC) or with another mutated heavy chain (HC). Where the cysteine may bond with a cysteine in the LC or HC, the underlined chain is the predicted predominant disulphide bond arrangement.

Figure 4a shows the mutations introduced in IgG4 antibodies according to the present invention.

Figure 4b shows the positions of the cysteine residues in the IgG4 antibodies shown in Figure 4a and predicted disulphide bond that can form with a cysteine in either the light chain (LC) or heavy chain (HC). Where the cysteine may bond with a cysteine in the LC or HC, the underlined chain is the predicted predominant disulphide bond arrangement.

Figure 5 shows the sequences of the C_H1 and hinge region of IgG4 antibodies according to the present invention.

Figure 6 shows the sequences of the C_H1, hinge region, C_H2 and C_H3 of IgG4 antibodies according to the present invention.

Figure 7 shows the Western Blot analysis of antibodies according to the present invention with the top gel showing the results using an Anti-human Fc Antibody and the bottom gel showing the results using an Anti-Kappa Antibody.

Figure 8 shows the Western Blot analysis of antibodies according to the present invention with the top gel showing the results using an Anti-human Fc Antibody and the bottom gel showing the results using an Anti-human Kappa Antibody.

Figure 9 shows the Western Blot analysis of antibodies according to the present invention with the top gel showing the results using an Anti-human Fc Antibody and the bottom gel showing the results using an Anti-human Kappa Antibody.

Figure 10 shows the Western Blot analysis of an antibody according to the present invention with the top gel showing the results using an Anti-human Fc Antibody and the bottom gel showing the results using an Anti-human Kappa Antibody.

Figure 11 shows the results of a Thermofluor analysis of antibodies of the present invention which shows the Fab and C_H2 domain thermostabilties.

Figure 12 shows the results of a Thermofluor analysis of antibodies of the present invention which shows the Fab and C_H2 domain thermostabilties.

Figure 13 shows the results of a Thermofluor analysis of antibodies of the present invention which shows the Fab and C_H2 domain thermostabilties.

Figure 14 shows the results of a Thermofluor analysis of antibodies of the present invention which shows the Fab and C_H2 domain thermostabilties.

Figure 15 shows the ranking of the Thermostabilities of selected antibodies of the present invention.

Figure 16 shows heavy chain exchange for IgG1 wild-type, IgG4 wild-type and various mutants at two concentrations of GSH and at various timepoints.

Figure 17 shows heavy chain exchange for IgG4 wild-type and various mutants at two concentrations of GSH at various timepoints.

Figure 18 shows heavy chain exchange for IgG4 wild-type and various mutants at two concentrations of GSH at various timepoints.

Figure 19 shows percentage change of heavy chain exchange for various mutants in 0.5 mM GSH compared to wild-type IgG4

Figure 20 shows percentage change of heavy chain exchange for various mutants in 5 mM GSH compared to wild-type IgG4.

Figure 21 shows symmetrical arm exchange analysis of IgG4 mutants with alternative residues at position 241. IgG4 WT exchanged more than IgG4 P. Exchange activity of S241G and S241A were similar to each other and significantly less and approximately half of IgG4 WT. S241T exchanged at similar levels to IgG4 WT.

Brief Description of the Sequences

SEQ ID NOs: **1-223** shows various hinges.

SEQ ID NO: **224** shows a natural IgG1 hinge.

SEQ ID NO: **225** shows a natural IgG4 hinge.

SEQ ID NO: **226** shows the CH1 and hinge region sequence of an IgG1 wild-type antibody.

SEQ ID NO: **227** shows the CH1 and hinge region sequence of an IgG4 wild-type antibody.

SEQ ID NO: **228** shows a part of the constant region of a human wild-type kappa light chain.

SEQ ID NO: **229** shows an IgG4 lower hinge sequence (description page 22)

SEQ ID NO: **230** shows a part of the N-terminal sequence of the C_H1 domain of a human IgG1 antibody.

SEQ ID NO: **231** shows the hinge region of a human IgG1 antibody.

SEQ ID NO: **232** shows a part of the N-terminal sequence of the C_H1 domain of a human IgG2 antibody.

SEQ ID NO: **233** shows the hinge region of a human IgG2 antibody.

SEQ ID NO: **234** shows a part of the N-terminal sequence of the C_H1 domain of a human IgG3 antibody.

SEQ ID NO: **235** shows the hinge region of a human IgG3 antibody.

SEQ ID NO: **236** shows a part of the N-terminal sequence of the C_H1 domain of a human IgG4 antibody.

SEQ ID NO: **237** shows the hinge region of a human IgG4 antibody.

SEQ ID NO: **238** shows a part of the N-terminal sequence of the C_H1 domain of a human IgGD antibody.

SEQ ID NO: **239** shows a part of the hinge region of a human IgGD antibody.

SEQ ID NO: **240** shows a part of the N-terminal sequence of the C_H1 domain of a human IgGM antibody.

SEQ ID NO: **241** shows a part of the C-terminal sequence of the C_H1 domain of a human IgGM antibody.

SEQ ID NO: **242** shows a part of the C_H2 domain of a human IgGM antibody.

SEQ ID NOs: **243** to **278** show the C_H1 domain and hinge region sequences of antibodies 6, 7, 8, 15, 16, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 44, 45, 46, 47, 2, 3, 48, 28P, 44P, 1, 4 ,5 ,5P, 9, 10, 11, 12, 13 and 14 respectively.

SEQ ID NO: **279** show the wild type IgG4 C_H2 and C_H3 domain sequences.

SEQ ID NO: **280** shows the wild type IgG4 C_H2 and wild type IgG1 C_H3 domain sequences.

SEQ ID NOs: **281** to **306** show the C_H1 domain, hinge region, C_H2 domain and CH3 domain sequences of antibodies 6, 7, 8, 15, 16, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 44, 45, 46, 47, 2, 3, 48, 28P and 44P respectively.

SEQ ID NOs: 306 to **316** show the C_H1 domain, hinge region, C_H2 domain and C_H3 domain sequences of antibodies 1, 4, 5, 5P, 9, 10, 11, 12, 13 and 14 respectively.

SEQ ID NO: **317**, **318, 320** and **321** show various hinge sequences.

SEQ ID No: **319** is a location in the antibody sequence.

Detailed Description of the Preferred Embodiments of the Invention

The present invention will now be described in more detail.

A symmetric antibody as employed herein is antibody or antibody fragment wherein the heavy chains have a similar or identical sequence in the region outside the variable regions.

Similar as employed herein is wherein the amino acid sequence is 95% or greater identity over the whole sequence analyzed, for example 96, 97, 98 or 99% identity. The percentage identity can be assessed using software known to those skilled in the art.

Identical as employed herein refers to where there is a 100% sequence identity over the sequence analyzed, for example over the whole sequence.

In one embodiment the heavy chain sequences in the antibodies of the present disclosure are covalently linked, for example through an inter-chain disulfide bond, for example a bond that is present naturally in the corresponding wild-type fragment or a bond that has been genetically engineered to be present in the desired location in the chains.

In one aspect the antibodies of the present disclosure are characterized in that both of the heavy chain sequences or fragments have an IgG1 type hinge.

The wild-type IgG1 upper and core hinge has the sequence EPKSCDKTHTCPPCP (SEQ ID No: **224**).

The wild-type IgG4 upper and core hinge has the sequence EPKYGPPCPSCP (SEQ ID No: **225**).

IgG1 type hinge as employed herein is intended to refer to wherein one or more, for example 1 to 5, such as 1, 2 or 3 amino acids are inserted into the IgG4 hinge, in particular between EPKYGPP (SEQ ID No: **319**) and CPSC and/or one or more of the amino acids YGPP in the IgG4 hinge are replaced, for example to correspond to an amino acid in the IgG1 hinge,

in particular G (from YGPP in the IgG4 hinge) is replaced with C or where Y (from YGPP in the IgG4 hinge) is replaced with C or S.

Thus the present invention also provides a symmetric bispecific antibody comprising IgG4 heavy chains with an upper hinge, core and lower hinge, wherein said upper hinge and core in the heavy chain or each heavy chain therein has a length of 13 to 17, such as 15 amino acids.

In one embodiment the symmetric bispecific antibody with a first IgG4 heavy chain has an upper hinge and core of 15 amino acids in length.

In one embodiment the upper hinge and core of the heavy chains comprises the natural 12 amino acids found in an IgG4 hinge and a further three amino acids, for example 3 alanine residues, or 3 glycine residues or a combination thereof.

In one embodiment the hinge has the one of the following sequences:

ESKYGPPAAACPSCP	SEQ ID No: **1**;	ESKYGPPGGGCPSCP	SEQ ID No: **2**;
ESKYGPPTHTCPSCP	SEQ ID No: **3**;	ESKYGDKTHTCPSCP	SEQ ID No: **4**;
EPSKYGPPAAACPSCP	SEQ ID No: **5**;	EPSKYGPPGGGCPSCP	SEQ ID No: **6**;
EPSKYGPPTHTCPSCP	SEQ ID No: **7**;	EPSKYGDKTHTCPSCP	SEQ ID No: **8**;
ESKSYGPPAAACPSCP	SEQ ID No: **9**;	ESKSYGPPGGGCPSCP	SEQ ID No: **10**;
ESKSYGPPTHTCPSCP	SEQ ID No: **11**;	ESKSYGDKTHTCPSCP	SEQ ID No: **12**;
ESKYGPPAAACPPCP	SEQ ID No: **13**;	ESKYGPPGGGCPPCP	SEQ ID No: **14**;
ESKYGPPTHTCPPCP	SEQ ID No: **15**;	ESKYGDKTHTCPPCP	SEQ ID No: **16**;
EPSKYGPPAAACPPCP	SEQ ID No: **17**;	EPSKYGPPGGGCPPCP	SEQ ID No: **18**;
EPSKYGPPTHTCPPCP	SEQ ID No: **19**;	EPSKYGDKTHTCPPCP	SEQ ID No: **20**;
ESKSYGPPAAACPPCP	SEQ ID No: **21**;	ESKSYGPPGGGCPPCP	SEQ ID No: **22**;
ESKSYGPPTHTCPPCP	SEQ ID No: **23**;	ESKSYGDKTHTCPPCP	SEQ ID No: **24**

In one embodiment the upper hinge and core in an IgG4 heavy chain of the disclosure consists of an IgG1-type hinge i.e. EPKSCDKTHTCPPC SEQ ID No: **25** or a derivative thereof such as:

EPKSCDKAAACPPCP	SEQ ID No: **26**;	EPKSCDKGGGCPPCP	SEQ ID No: **27**;
EPKSCDKTHTSPPCP	SEQ ID No: **28**;	EPKSCDKTHTCPPSP	SEQ ID No: **29**;
EPKSCDKTHTSPPSP	SEQ ID No: **30**;	EPKSCDKAAASPPCP	SEQ ID No: **31**;
EPKSCDKAAACPPSP	SEQ ID No: **32**;	EPKSCDKAAASPPSP	SEQ ID No: **33**;
EPKSCDKGGGSPPCP	SEQ ID No: **34**;	EPKSCDKGGGCPPSP	SEQ ID No: **35**;
EPKSCDKGGGSPPSP	SEQ ID No: **36**		

In one embodiment the antibody according to the present disclosure comprises an upper hinge and core.

In one embodiment the upper hinge and core region is selected from one of the following sequences:

ESKYGPPCPSCP	SEQ ID No: **37**;	ESKYGDKCPSCP	SEQ ID No: **38**;
EPSKYGPPCPSCP	SEQ ID No: **39**;	EPSKYGDKCPSCP	SEQ ID No: **40**;
ESKSYGPPCPSCP	SEQ ID No: **41**;	ESKSYGDKCPSCP	SEQ ID No: **42**;
ESKYGPPAACPSCP	SEQ ID No: **43**;	ESKYGPPGGCPSCP	SEQ ID No: **44**;
ESKYGPPHTCPSCP	SEQ ID No: **45**;	ESKYGDKHTCPSCP	SEQ ID No: **46**;
EPSKYGPPAACPSCP	SEQ ID No: **47**;	EPSKYGPPGGCPSCP	SEQ ID No: **48**;
EPSKYGPPHTCPSCP	SEQ ID No: **49**;	EPSKYGDKHTCPSCP	SEQ ID No: **50**;
ESKSYGPPAACPSCP	SEQ ID No: **51**;	ESKSYGPPGGCPSCP	SEQ ID No: **52**;
ESKSYGPPHTCPSCP	SEQ ID No: **53**;	ESKSYGDKHTCPSCP	SEQ ID No: **54**;
ESKYGPPACPSCP	SEQ ID No: **55**;	ESKYGPPGCPSCP	SEQ ID No: **56**;
ESKYGPPTTCPSCP	SEQ ID No: **57**;	ESKYGDKTTCPSCP	SEQ ID No: **58**;
EPSKYGPPACPSCP	SEQ ID No: **59**;	EPSKYGPPGCPSCP	SEQ ID No: **60**;
EPSKYGPPTTCPSCP	SEQ ID No: **61**;	EPSKYGDKTTCPSCP	SEQ ID No: **62**;
ESKSYGPPACPSCP	SEQ ID No: **63**;	ESKSYGPPGCPSCP	SEQ ID No: **64**;
ESKSYGPPTTCPSCP	SEQ ID No: **65**;	ESKSYGDKTTCPSCP	SEQ ID No: **66**;
ESKYGPPTHCPSCP	SEQ ID No: **67**;	ESKYGDKTHCPSCP	SEQ ID No: **68**;
EPSKYGPPTHCPSCP	SEQ ID No: **69**;	EPSKYGDKTHCPSCP	SEQ ID No: **70**;
ESKSYGPPTHCPSCP	SEQ ID No: **71**;	ESKSYGDKTHCPSCP	SEQ ID No: **72**;
ESKYGPPHTCPSCP	SEQ ID No: **73**;	ESKYGDKHTCPSCP	SEQ ID No: **74**;
EPSKYGPPHTCPSCP	SEQ ID No: **75**;	EPSKYGDKHTCPSCP	SEQ ID No: **76**;
ESKSYGPPHTCPSCP	SEQ ID No: **77**;	ESKSYGDKHTCPSCP	SEQ ID No: **78**;
ESKYGPPTCPSCP	SEQ ID No: **79**;	ESKYGDKTCPSCP	SEQ ID No: **80**;
EPSKYGPPTCPSCP	SEQ ID No: **81**;	EPSKYGDKTCPSCP	SEQ ID No: **82**;
ESKSYGPPTCPSCP	SEQ ID No: **83**;	ESKSYGDKTCPSCP	SEQ ID No: **84**;
ESKYGPPHCPSCP	SEQ ID No: **85**;	ESKYGDKHCPSCP	SEQ ID No: **86**;
EPSKYGPPHCPSCP	SEQ ID No: **87**;	EPSKYGDKHCPSCP	SEQ ID No: **88**;
ESKSYGPPHCPSCP	SEQ ID No: **89**;	ESKSYGDKHCPSCP	SEQ ID No: **90**;
EPKSCDKAACPPCP	SEQ ID No: **91**;	EPKSCDKGGCPPCP	SEQ ID No: **92**;
EPKSCDKHTSPPCP	SEQ ID No: **93**;	EPKSCDKHTCPPSP	SEQ ID No: **94**;
EPKSCDKHTSPPSP	SEQ ID No: **95**;	EPKSCDKAASPPCP	SEQ ID No: **96**;

	EPKSCDKAACPPSP	SEQ ID No: **97**;	EPKSCDKAASPPSP	SEQ ID No: **98;**
	EPKSCDKGGSPPCP	SEQ ID No: **99**;	EPKSCDKGGCPPSP	SEQ ID No: **100**;
	EPKSCDKGGSPPSP	SEQ ID No: **101**;	EPKSCDKACPPCP	SEQ ID No: **102**;
	EPKSCDKGCPPCP	SEQ ID No: **103**;	EPKSCDKTSPPCP	SEQ ID No: 104;
5	EPKSCDKTCPPSP	SEQ ID No: **105**;	EPKSCDKTSPPSP	SEQ ID No: **106**;
	EPKSCDKASPPCP	SEQ ID No: **107**;	EPKSCDKACPPSP	SEQ ID No: **108**;
	EPKSCDKASPPSP	SEQ ID No: **109**;	EPKSCDKGSPPCP	SEQ ID No: **110**;
	EPKSCDKGCPPSP	SEQ ID No: **111**;	EPKSCDKGSPPSP	SEQ ID No: **112**;
	EPKSCDKCPPCP	SEQ ID No: **113**;	EPKSCDKCPPCP	SEQ ID No: **114**;
10	EPKSCDKSPPCP	SEQ ID No: **115**;	EPKSCDKSPPSP	SEQ ID No: **116**;
	EPKSCDKSPPCP	SEQ ID No: **117**;	EPKSCDKCPPSP	SEQ ID No: **118**;
	EPKSCDKSPPSP	SEQ ID No: **119**;	EPKSCDKSPPCP	SEQ ID No: **120**;
	EPKSCDKCPPSP	SEQ ID No: **121**;	EPKSCDKSPPSP	SEQ ID No: **122**;
	EPKSCDKTTSPPCP	SEQ ID No: **123**;	EPKSCDKTTCPPSP	SEQ ID No: **124**;
15	EPKSCDKTTSPPSP	SEQ ID No: **125**;	EPKSCDKTHSPPCP	SEQ ID No: **126**;
	EPKSCDKTHCPPSP	SEQ ID No: **127**;	EPKSCDKTHSPPSP	SEQ ID No: **128**;
	ESKYGPPCPPCP	SEQ ID No: **129**;	ESKYGPPCPPCP	SEQ ID No: **130**;
	ESKYGPPCPPCP	SEQ ID No: **131**;	ESKYGDKCPPCP	SEQ ID No: **132**;
	EPSKYGPPCPPCP	SEQ ID No: **133**;	EPSKYGPPCPPCP	SEQ ID No: **134**;
20	EPSKYGPPCPPCP	SEQ ID No: **135**;	EPSKYGDKCPPCP	SEQ ID No: **136**;
	ESKSYGPPCPPCP	SEQ ID No: **137**;	ESKSYGPPCPPCP	SEQ ID No: **138**;
	ESKSYGPPCPPCP	SEQ ID No: **139**;	ESKSYGDKCPPCP	SEQ ID No: **140**;
	ESKYGPPAACPPCP	SEQ ID No: **141**;	ESKYGPPGGCPPCP	SEQ ID No: **142**;
	ESKYGPPHTCPPCP	SEQ ID No: **143**;	ESKYGDKHTCPPCP	SEQ ID No: **144**;
25	EPSKYGPPAACPPCP	SEQ ID No: **145**;	EPSKYGPPGGCPPCP	SEQ ID No: 146
	EPSKYGPPHTCPPCP	SEQ ID No: **147**;	EPSKYGDKHTCPPCP	SEQ ID No: **148**;
	ESKSYGPPAACPPCP	SEQ ID No: **149**;	ESKSYGPPGGCPPCP	SEQ ID No: **150**;
	ESKSYGPPHTCPPCP	SEQ ID No: **151**;	ESKSYGDKHTCPPCP	SEQ ID No: **152**;
	ESKYGPPACPPCP	SEQ ID No: **153**;	ESKYGPPGCPPCP	SEQ ID No: **154**;
30	ESKYGPPTTCPPCP	SEQ ID No: **155**;	ESKYGDKTTCPPCP	SEQ ID No: **156**;
	EPSKYGPPACPPCP	SEQ ID No: **157**;	EPSKYGPPGCPPCP	SEQ ID No: **158**;
	EPSKYGPPTTCPPCP	SEQ ID No: **159**;	EPSKYGDKTTCPPCP	SEQ ID No: **160**;
	ESKSYGPPACPPCP	SEQ ID No: **161**;	ESKSYGPPGCPPCP	SEQ ID No: **162**;
	ESKSYGPPTTCPPCP	SEQ ID No: **163**;	ESKSYGDKTTCPPCP	SEQ ID No: **164**;

	ESKYGPPTHCPPCP	SEQ ID No: **165**;	ESKYGDKTHCPPCP	SEQ ID No: **166**;
	EPSKYGPPTHCPPCP	SEQ ID No: **167**;	EPSKYGDKTHCPPCP	SEQ ID No: **168**;
	ESKSYGPPTHCPPCP	SEQ ID No: **169**;	ESKSYGDKTHCPPCP	SEQ ID No: **170**;
	ESKYGPPHTCPPCP	SEQ ID No: **171**;	ESKYGDKHTCPPCP	SEQ ID No: **172**;
5	EPSKYGPPHTCPPCP	SEQ ID No: **173**;	EPSKYGDKHTCPPCP	SEQ ID No: **174**;
	ESKSYGPPHTCPPCP	SEQ ID No: **175**;	ESKSYGDKHTCPPCP	SEQ ID No: **176**;
	ESKYGPPTCPPCP	SEQ ID No: **177**;	ESKYGDKTCPPCP	SEQ ID No: **178**;
	EPSKYGPPTCPPCP	SEQ ID No: **179**;	EPSKYGDKTCPPCP	SEQ ID No: **180**;
	ESKSYGPPTCPPCP	SEQ ID No: **181**;	ESKSYGDKTCPPCP	SEQ ID No: **182**;
10	ESKYGPPHCPPCP	SEQ ID No: **183**;	ESKYGDKHCPPCP	SEQ ID No: **184**;
	EPSKYGPPHCPPCP	SEQ ID No: **185**;	EPSKYGDKHCPPCP	SEQ ID No: **186**;
	ESKSYGPPHCPPCP	SEQ ID No: **187**;	ESKSYGDKHCPPCP	SEQ ID No: **188**;
	EPKSCDKTHTCPPCP	SEQ ID No: **189**;	EPKSCDKTHTCPSCP	SEQ ID No: **190**;
	ESKYCPPACPSCP	SEQ ID No: **191**;	ESKYCPPAACPSCP	SEQ ID No: **192**;
15	ESKYCPPAAACPSCP	SEQ ID No: **193**;	ESKYCPPAAASPSCP	SEQ ID No: **194**;
	ESKYCPPAAACPSSP	SEQ ID No: **195**;	ESKCGPPAAACPSCP	SEQ ID No: **196**;
	ESKYCPPAAAACPSCP	SEQ ID No: **197**;	ESKYCPPAAAAACPSCP	SEQ ID No: **198**;
	ESKYCPPGGGCPSCP	SEQ ID No: **199**;	ESKYCPPSSSCPSCP	SEQ ID No: **200**;
	ESKYCPPTCPSCP	SEQ ID No: **201**;	ESKYCPPTHCPSCP	SEQ ID No: **202**;
20	ESKYCPPTHTCPSCP	SEQ ID No: **203**;	ESKYCPKTHTCPSCP	SEQ ID No: **204**;
	ESKYCDKTHTCPSCP	SEQ ID No: **205**;	ESKYCDKTHCPSCP	SEQ ID No: **206**;
	ESKYCDKTCPSCP	SEQ ID No: **207**;	ESKYCDKAAACPSCP	SEQ ID No: **208**;
	ESKYCDKCPSCP	SEQ ID No: **209**;	ESKSCDKTHTCPSCP	SEQ ID No: **210**;
	EPKYCDKTHTCPSCP	SEQ ID No: **211**;	EPKSCPPCPSCP	SEQ ID No: **212**;
25	ESKSCPPCPSCP	SEQ ID No: **213**;	EPKYCPPCPSCP	SEQ ID No: **214**;
	ECKYGPPCPSCP	SEQ ID No: **215**;	ECKYGPPSPSCP	SEQ ID No: 216;
	ECKYGPPCPSSP	SEQ ID No: **217**;	ESCYGPPCPSCP	SEQ ID No: **218**;
	ESCYGPPSPSCP	SEQ ID No: **219**;	ESCYGPPCPSSP	SEQ ID No: **220**;
	ESKCGPPCPSCP	SEQ ID No: **221**;	ESKCGPPSPSCP	SEQ ID No: **222**;
30	ESKCGPPCPSSP	SEQ ID No: **223**;	EPKSCDKCPPSP	SEQ ID No: **317**.

In one embodiment the core hinge region in one or both heavy chain sequences or fragments thereof has the sequence CPPCP SEQ ID No: **318**.

Whilst not wishing to be bound by theory it is thought that this sequence is likely to block dynamic exchange of the antibody arms at "*in vivo*" type concentrations for example

concentration of less than 0.5mM reductant, in particular concentrations of reductant in the order of 5uM are thought to be physiologically relevant (Zilmer et al., 2005 Drug Design Reviews vol. 2, no. 2, pp. 121–127, 2005).

In one embodiment of the present invention, each heavy chain of the bispecific antibody has identical upper and core hinge regions selected from the sequences above, and may also have an identical lower hinge region. In a further embodiment, each heavy chain of the bispecific antibody has identical C_H1 regions, and may also have identical C_H2 and C_H3 regions. Accordingly, each heavy chain may have identical heavy chain constant region sequences.

"Different variable regions" as employed herein is intended to refer to wherein the said variable regions have specificity for different antigens. That is to say that the antigen to which each variable region is specific is a different antigen or a different part of an antigen, eg a different epitope.

"Specific" as employed herein refers to the fact the binding domains recognized a target antigen with greater affinity and/avidity than other antigens to which it is not specific (for example 10, 20, 50, 10 or 1000 greater). It does not necessarily imply that the specific binding region does not bind any non-target antigens but rather the interaction with the target is such that it can be used to purify the target antigen (to which it is specific) from a complex mixture of antigens, including antigens in the same family of proteins.

In one embodiment the antibody according to the present disclosure is isolated.

Isolated as employed herein is intended to refer to an antibody that is isolated from the human body, for example: prepared by recombinant techniques, purified using a technique such as chromatography, and/or in a pharmaceutical formulation.

The present invention also provides an expression vector comprising a sequence which encodes the antibodies of the present invention and a host cell comprising the expression vector.

The present invention also provides an antibody as defined above for use in the treatment of a disease or disorder. Further provided is a method for the treatment of a disease or disorder comprising administering a therapeutically effective amount of an antibody as defined above.

In one embodiment the antibody according the present disclosure comprises one or two heavy chain sequences independently selected from a heavy chain sequence disclosed herein.
The terms "protein" and "polypeptide" are used interchangeably herein, unless the context indicates otherwise. "Peptide" is intended to refer to 10 or less amino acids.

The terms "polynucleotide" includes a gene, DNA, cDNA, RNA, mRNA etc unless the context indicates otherwise.

As used herein, the term "comprising" in context of the present specification should be interpreted as "including".

The term "wild-type" in the context of the present invention means an antibody as it may occur in nature or may be isolated from the environment, which does not comprise any genetically engineered mutations.

The designation for a substitution mutant herein consists of a letter followed by a number followed by a letter. The first letter designates the amino acid in the wild-type protein. The number refers to the amino acid position where the amino acid substitution is being made, and the second letter designates the amino acid that is used to replace the wild-type amino acid. The residues in antibody variable and constant domains are conventionally numbered according to a system devised by Kabat *et al.* This system is set forth in Kabat *et al.*, 1987, in Sequences of Proteins of Immunological Interest, US Department of Health and Human Services, NIH, USA (hereafter "Kabat *et al.* (*supra*)").

The Kabat residue designations do not always correspond directly with the linear numbering of the amino acid residues. The actual linear amino acid sequence may contain fewer or additional amino acids than in the strict Kabat numbering corresponding to a shortening of, or insertion into, a structural component, whether framework or complementarity determining region (CDR), of the basic variable domain structure. The correct Kabat numbering of residues may be determined for a given antibody by alignment of residues of homology in the sequence of the antibody with a "standard" Kabat numbered sequence. Alternatively, the numbering of amino acid residues may be performed by the EU-index or EU numbering system (also described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). A further numbering system of amino acid residues in antibodies is the IMGT numbering system (Lefranc, M.-P. et al., Dev. Comp. Immunol., 29, 185-203 (2005)).

The Kabat numbering system is used in the present specification except where otherwise indicated that the EU numbering system or IMGT numbering system is used.

Between the four IgG4 isotypes, the intrachain disulphide bonding arrangements in the heavy and light chain are similar whereas the interchain disulphide bonding arrangements are unique for each isotype [Reviewed by (Wypych,J., Li,M., Guo,A., Zhang,Z., Martinez,T., Allen,M.J., Fodor,S., Kelner,D.N., Flynn,G.C., Liu,Y.D., Bondarenko,P.V., Ricci,M.S.,

Dillon,T.M., Balland,A., 2008. Human IgG2 antibodies display disulphide-mediated structural isoforms. J Biol Chem. 283, 16194-16205)].

As shown in Figure 1b, the hinge region sequences of the four IgG4 isotypes differ. The complete or genetic hinge region typically consists of residues 226 to 251 (numbering based on Kabat numbering system). Figure 1b shows the upper, core and lower sections of the hinge regions of the four IgG4 isotypes. For the IgG1 isotype, the upper hinge region is residues 226 to 238, the core hinge region is residues 239 to 243 and the lower hinge region is residues 244 to 251. For the IgG4 isotype, the upper hinge region is residues 226 to 238, the core hinge region is residues 239 to 243 and the lower hinge region is residues 244 to 251. The new mutant IgG4 antibodies according to the present invention have been developed by modifying the interchain disulphide bond arrangements within IgG4, specifically the C_L-C_{H1} interchain disulphide bond arrangement between the light chain (LC) and heavy chain (HC) has been modified.

Figure 1b shows sections of the human IgG heavy and light chain sequences for the IgG 1-4 isotypes indicating the cysteine positions (underlined) that form the C_L-C_H1 interchain disulphide bonds. The inter C_L-C_H1 disulphide bond of IgG1 is formed between the LC C214 (Kabat numbering system) and C233 (Kabat numbering system) of the HC just before the hinge region. In contrast, the C_H1-C_L disulphide bond for IgG2, 3 and 4 is formed between the LC C214 and C127 N-terminal to the intrachain disulphide bond of the HC. The LC and HC sequences surrounding the cysteine residues involved in the C_L-C_H1 disulphide bond formation are shown and aligned in Figure 1b.

The present invention has investigated how the C_L-C_H1 disulphide bond affects the properties of an IgG4 antibody including the thermostability, structural stability and affinity of the antibody.

Mutants of IgG4 were generated by substitution of the cysteine residue in C_{H1} at position 127 with another amino acid as well as substituting one or more of the amino acids in the upper hinge region, preferably amino acids at positions selected from 227, 228, 229 and 230, numbered according to the Kabat numbering system, with cysteine. Positions 227, 228, 229 or 230 are at or near to the position that the IgG1 cysteine 233 is situated.

Each heavy chain may comprise further mutations including the substitution of one or both cysteine residues 239 and 242 in the IgG4 hinge region with another amino acid. A mutation to lengthen the IgG4 hinge region by three amino acids between positions 238 and 239 to be the same length as the IgG1 hinge was also included in some antibodies. The S241P mutation was also introduced in some antibodies.

The formation of half molecules of IgG4 can be reduced by introduction of a Ser to Pro mutation at position 241 (numbered according to the Kabat numbering system) in the hinge (Angal,S. et al., 1993. A single amino acid substitution abolishes the heterogeneity of chimeric mouse/human (IgG4) antibody. Mol Immunol 30, 105-108). In addition, this point mutation did not influence the compact structure of IgG4 thereby allowing IgG4 to retain its reduced ability to activate complement.

However, *in vitro* exchange of these mutated antibodies can be promoted by using high concentrations of antibodies, for example 1-10mM or more, such as 2, 3, 4, 5, 6, 7, 8, 9mM.It has been found that the mutant IgG4 antibodies according to the present invention show advantageous properties, for example improved stability.

In one embodiment, the mutant IgG4 antibodies according to the present invention show increased thermostability compared to a wild-type IgG4 antibody. It has been surprisingly found that the mutant IgG4 antibodies which have been mutated to replace the cysteine at position 127 in the C_H1 domain with another amino acid and in which a cysteine has been introduced in the heavy chain hinge region between positions 227 to 230 show improved thermostability compared to a wild type IgG4 antibody. The mutation to remove cysteine at position 127 alters the position at which the inter-chain disulphide bond forms between the heavy chain and the light chain (C_L-C_{H1}) and forces the light chain to form a disulphide bond with a cysteine which is introduced between positions 227 and 230 in the hinge region of the heavy chain. Hence in one embodiment, an IgG4 antibody is provided in which the cysteine 127 is substituted for another amino acid and the cysteine of the light chain is linked via a disulphide bond to an engineered cysteine at position 227, 228, 229 or 230.

A further improvement to thermostability was also surprisingly found by adding three amino acids to the IgG4 hinge region in order to lengthen the IgG4 hinge region.

It has also been surprisingly found that the mutant IgG4 antibodies which have been mutated to replace the cysteine at position 127 in the C_H1 domain with another amino acid and to replace the cysteine at position 239 or at position 242 in the heavy chain hinge region with another amino acid showed improved thermostability compared to a wild type IgG4 antibody.

In one embodiment the antibodies of the present invention show reduced formation of so-called half-molecules, which are formed of a single light chain and a single heavy chain (HL). Antibodies of the present invention which comprise a mutation at C239 but do not carry a mutation at C242 generally show reduced half-molecule formation. Without being bound by theory it is thought that this is due to removal of the Cysteine at position 239 reduces the formation of intra-chain disulphide bond in the heavy chain and therefore reduces the number

of half-molecules compared to antibodies which do not carry a mutation at C239 or the C242. Antibodies which carry a mutation at C242 but do not carry a mutation at C239 appear to form more half-molecule compared to antibodies which carry a mutation at C239 but do not carry a mutation at C242. Without being bound by theory, it is believed that the cysteine at position 239 is more reactive compared to the cysteine at position 242 and is capable of forming a disulphide bond with either a heavy chain hinge cysteine or the light chain cysteine.

Antibodies which carry mutation at both C239 and C242 form a high proportion of half-molecules due to no inter-chain disulphide bond formation between two heavy chains. However, antibodies comprising mutations at both C239 and C242 are still capable of forming whole antibody molecules due to the bonding of heavy chains via non-covalent bonds. Reduced half-molecule formation is also observed in antibodies carrying the S241P mutation.

Antibodies according the present invention also show comparable affinity towards the target antigen compared the wild-type IgG4 antibody.

Mutations to the heavy chain constant regions of the bispecific antibodies of the present invention are described in more detail below. The methods for replacing amino acids are well known in the art of molecular biology. Such methods include for example site directed mutagenesis using methods such as PCR to delete and/or substitute amino acids or *de novo* design of synthetic sequences.

Figure 2a shows the hinge residues of IgG1 wild type, IgG4 wild type and the positions where mutations have been introduced in the antibodies of the present invention. Numbering based on Kabat numbering system.

The antibodies according to the present invention comprise a mutation at position 127 (C127), wherein the cysteine residue is replaced by another amino acid, preferably an amino acid that does not contain a thiol group. By replace or substitute we mean that where the interchain cysteine 127 would normally be found in the antibody heavy chain another amino acid is in its place. The mutation at C127 may be any suitable mutation to one, two or three of the nucleotides encoding the amino acid at position 127 which changes the amino acid residue from cysteine to another suitable amino acid. Examples of suitable amino acids include serine, threonine, alanine, glycine or any polar amino acid. A particularly preferred amino acid is serine.

The substitution of the cysteine at position 127 with another amino acid removes the cysteine in the C_H1 domain which normally forms a disulphide bond with a cysteine in the light chain in the wild-type IgG4. Therefore, in order to form a light chain and heavy chain pairing

via an inter-chain disulphide bond the light chain must form a disulphide bond with a cysteine which is positioned in the hinge region of the heavy chain.

In a first aspect of the invention, antibodies according to the present invention comprise a heavy chain wherein one or more of the amino acids at positions selected from 227, 228, 229 and 230, numbered according to the Kabat numbering system, is substituted with cysteine. Accordingly, antibodies according to the present invention may carry one or more of the following mutations: S227C; K228C; Y229C; G230C

In one embodiment only one residue selected from 227, 228, 229 and 230 is substituted with a cysteine residue.

In one embodiment antibodies of the present invention carry the mutation Y229C or G230C.

The inclusion of a cysteine residue at a position selected from 227, 228, 229 and 230, in the hinge region of the heavy chain provides a new position for an inter-chain disulphide bond to form between the heavy chain and the light chain. It has been found by the present inventors that this new inter-chain disulphide bond arrangement provides IgG4 antibodies having improved thermostability compared to a wild-type IgG4 antibody.

Further mutations may be introduced to the antibodies of this aspect of the present invention. In one embodiment the cysteine at position 239 (C239) and/or the cysteine at position 242 (C242), numbered according to the Kabat numbering system, in the heavy chain are substituted with another amino acid, preferably an amino acid that does not contain a thiol group. By replace or substitute we mean that where the cysteine 239 and/or the cysteine 242 would normally be found in the antibody heavy chain another amino acid is in its place. The mutation at C239 and/or C242 may be any suitable mutation to one, two or three of the nucleotides encoding the amino acid which changes the amino acid residue from cysteine to another suitable amino acid. Examples of suitable amino acids include serine, threonine, alanine, glycine or any polar amino acid. A particularly preferred amino acid is serine.

In one embodiment the cysteine at position 239 in the heavy chain is substituted with another amino acid and the cysteine at position 242 in the heavy chain is substituted with another amino acid. In this embodiment, the substitution of both C239 and C242 removes both cysteine residues in the hinge region of the heavy chain which normally form inter-heavy chain disulphide bonds with the corresponding cysteines in another heavy chain. The resulting half-molecules may form whole antibody molecules through non-covalent bonding between two heavy chains.

In an alternative embodiment the cysteine at position 239 in the heavy chain is substituted with another amino acid. In this embodiment the cysteine at position 242 is not substituted with another amino acid.

In a further alternative embodiment the cysteine at position 242 in the heavy chain is substituted with another amino acid. In this embodiment the cysteine at position 239 is not substituted with another amino acid.

The substitution of either C239 or C242, leaves one cysteine in the heavy chain which is capable of forming an inter-heavy chain disulphide bond with a cysteine in another heavy chain. Without being bound by theory it is thought that the substitution of one cysteine in the hinge region, particularly substitution of C239, reduces the formation of an intra-chain disulphide bond in the hinge region and therefore may reduce the formation of half antibody molecules.

In one embodiment of the present invention, wherein the serine at position 227 is substituted with a cysteine, the antibody preferably does not comprise mutations at positions C239 and C242. In another embodiment, wherein the serine at position 227 is substituted with a cysteine, the cysteine at position 239 in the heavy chain is preferably substituted with another amino acid but the cysteine at position 242 is not substituted with another amino acid.

In one embodiment the antibodies of the present invention comprise an IgG4 heavy chain which is mutated to insert one or more amino acids between amino acids 226-243. The number of amino acids inserted may be 1 to 10, 1 to 5, 1 to 3, preferably 1, 2, 3 or 4 amino acids are inserted. The amino acids are preferably inserted between amino acids 238 and 239. Any suitable amino acids may be inserted in the hinge region, such as alanines, glycines, serines or threonines and combinations thereof. Preferably three alanines (AAA), three glycines (GGG), three serines (SSS) or three threonines (TTT) are inserted or a threonine, histidine and another threonine (THT). It has been found that antibodies of the present invention comprising an IgG4 heavy chain which has been mutated to insert three amino acids in the hinge region show improved thermostability.

A further mutation which may be introduced in the antibodies according to the present invention is the mutation S241P. This mutation has been previously shown to reduce the formation of half molecules (Angal,S. et al., 1993. A single amino acid substitution abolishes the heterogeneity of chimeric mouse/human (IgG4) antibody. Mol Immunol 30, 105-108). It has been surprisingly found that mutant antibodies of the present invention which comprise the S241P mutation demonstrate some heavy chain exchange *in vitro* under strong reducing conditions compared to IgG4 P (IgG4 with S241P). This allows the creation of bispecific

antibodies *in vitro* from mutant IgG4 antibodies of the present invention. The antibodies according to the present invention may comprise one or more further mutations in the hinge region. For example the antibodies may further comprise one or more of the following mutations S227P, Y229S, P237D and P238K.

In one embodiment the antibody according to the present invention effectively comprises an IgG1 hinge region from residue 226 to 243 (upper hinge and core hinge). Accordingly, the antibody of the present invention comprises a hinge region wherein the glycine at position 230 is substituted with cysteine, the serine at position 227 is substituted with proline, the tyrosine at position 229 is substituted with serine, the proline at position 237 is substituted with aspartic acid, the proline at position 238 is substituted with lysine, the amino acid sequence threonine-histidine-threonine is inserted between positions 238 and 239 and the serine at position 241 is substituted with proline. These mutations may also be written as S227P, Y229S, G230C, P237D, P238KTHT and S241P, as shown in Figure 2a. It has been found that the introduction of these further mutations to the IgG4 hinge region provides an antibody having improved thermostability.

The antibody according to the present invention preferably has an IgG4 lower hinge from residue 244 to 251 (APEFLGGP SEQ ID No: **229**). Without being bound by theory it is believed that the IgG4 lower hinge region contributes to the lack of effector function of an IgG4 antibody.

In a second aspect of the present invention, symmetric bispecific antibody is provided wherein in one or both heavy chains the inter-chain cysteine at position 127 is substituted with another amino acid, as described above, and the cysteine at position 239 or the cysteine at position 242, numbered according to the Kabat numbering system, in the heavy chain is substituted with another amino acid. In this second aspect, none of the residues at positions 227, 228, 229 and 230 are substituted with a cysteine residue.

A symmetric bispecific antibody of the class IgG4 comprising two heavy chains which each comprise a variable domain, C_H1 domain and hinge region, , wherein in each heavy chain the inter-chain cysteine at position 127, numbered according to the Kabat numbering system, is substituted with another amino acid; and the cysteine at position 239 and/or the cysteine at position 242, numbered according to the Kabat numbering system, is substituted with another amino acid, wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

Antibodies according to the second aspect of the present invention have surprisingly been found to have improved thermostability compared to a wild-type IgG4 antibody.

In the second aspect of the present invention, the antibody may comprise one or more further mutations. In one embodiment the antibody comprises an IgG4 heavy chain which is mutated to insert three amino acids between amino acids 226-243, preferably between amino acids 238 and 239, as described above. In a further embodiment the antibody comprises the mutation S241P. In a further embodiment, the antibody may further comprise one or more of the following mutations S227P, Y229S, P237D and P238K.

Figures 3a and 4a also show the mutations introduced in IgG4 antibodies according to the present invention. Figures 3b and 4b show the positions of the cysteine residues in the IgG4 antibodies of the present invention and also show the predicted bonding of the cysteine to a cysteine in the light chain (LC) or another heavy chain (HC). For cysteine residues which show (LC or HC), it is possible that the cysteine is binding to a cysteine in the light chain or the heavy chain but where either the LC or HC is underlined this is the disulphide bond which is believed to predominantly occur.

In one embodiment, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region and each heavy chain comprises the mutations of an antibody selected from 2, 3, 6, 7, 8, 15, 16, 28, 28P, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 44, 44P, 45, 46, 47 and 48, as shown in Table 1. Accordingly, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region and each heavy chain comprises one of the following sequences: SEQ ID NO: **243**, SEQ ID NO: **244**, SEQ ID NO: **245** , SEQ ID NO: **246**, SEQ ID NO: **247** , SEQ ID NO: **248**, SEQ ID NO: **249**, SEQ ID NO: **250**, SEQ ID NO: **251**, SEQ ID NO: **252**, SEQ ID NO: **253**, SEQ ID NO: **254**, SEQ ID NO: **255**, SEQ ID NO: **256**, SEQ ID NO: **257**, SEQ ID NO:**258**, SEQ ID NO:**259**, SEQ ID NO:**260**, SEQ ID NO: **261**, SEQ ID NO: **262**, SEQ ID NO:**263**, SEQ ID NO:**264**, SEQ ID NO: **265**, SEQ ID NO:**266**, SEQ ID NO: **267** and SEQ ID NO: **268**.

In a preferred embodiment the antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, and comprises one of the following sequences: SEQ ID NO: **243**, SEQ ID NO:**244**, SEQ ID NO:**245**, SEQ ID NO: **246**, SEQ ID NO: **247**, SEQ ID NO: **248**, SEQ ID NO: **249**, SEQ ID NO: **250**, SEQ ID NO: **251**, SEQ ID NO: **252**, SEQ ID NO: **253**, SEQ ID NO: **254**, SEQ ID NO: **255**, SEQ ID NO: **256**, SEQ ID NO:**257**, SEQ ID NO: **258**, SEQ ID NO: 259, SEQ ID NO: **260**, SEQ ID NO: **261**, SEQ ID NO: **262**, SEQ ID NO: **263**, SEQ ID NO: **264**, SEQ ID NO: **265**, SEQ ID NO: **266**, SEQ ID NO: **267** and SEQ ID NO: **268**. More preferably, the antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain

and a hinge region and each heavy chain comprises one of the following sequences: SEQ ID NO: **243**, SEQ ID NO: **244**, SEQ ID NO: **245** , SEQ ID NO: **246** , SEQ ID NO: **247**, SEQ ID NO: **248**, SEQ ID NO: **249**, SEQ ID NO: **250**, SEQ ID NO: **251**, SEQ ID NO: **252**, SEQ ID NO: **253**, SEQ ID NO: **254**, SEQ ID NO: **255**, SEQ ID NO: **256**, SEQ ID NO: **257**, SEQ ID NO: **258**, SEQ ID NO: **259**, SEQ ID NO: **260**, SEQ ID NO: **261**, SEQ ID NO: **262**, SEQ ID NO: **263**, SEQ ID NO: **264**, SEQ ID NO: **265**, SEQ ID NO: **266**, SEQ ID NO: **267** and SEQ ID NO: **268**.

In a further preferred embodiment, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain and each heavy chain comprises the mutations of an antibody selected from 2, 3, 6, 7, 8, 15, 16, 28, 28P, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 44, 44P, 45, 46, 47 and 48, as shown in Table 1. Accordingly, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain and each heavy chain comprises one of the following sequences: SEQ ID NO: **281**, SEQ ID NO: **282**, SEQ ID NO: **283** , SEQ ID NO: **284**, SEQ ID NO: **285**, SEQ ID NO: **286**, SEQ ID NO: **287**, SEQ ID NO: **288**, SEQ ID NO: **289**, SEQ ID NO: **290**, SEQ ID NO: **291**, SEQ ID NO: **292**, SEQ ID NO: **293**, SEQ ID NO: **294**, SEQ ID NO: **295**, SEQ ID NO: **296**, SEQ ID NO: **297**, SEQ ID NO: **298**, SEQ ID NO: **299**, SEQ ID NO: **300**, SEQ ID NO: **301**, SEQ ID NO: **302**, SEQ ID NO: **303**, SEQ ID NO: **304**, SEQ ID NO: **305** and SEQ ID NO: **306**.

A particularly preferred antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, wherein the heavy chain comprises SEQ ID NO: **36** (antibody 28P), SEQ ID NO: **37** (antibody 44P) or SEQ ID NO: **35** (antibody 48). A further particularly preferred antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain wherein the heavy chain comprises SEQ ID NO:**62** (antibody 28P), SEQ ID NO: **63** (antibody 44P) or SEQ ID NO:**61** (antibody 48). Antibodies 28P, 44P and 48 are particularly preferred because they exhibit significantly improved thermostability and further exhibit reduced half-molecule formation.

Table 1 below lists example antibodies with mutations which have been introduced compared to the IgG4 wild-type sequence. Table 1 also includes wild-type IgG1 and IgG4 antibodies and control antibodies. **Table 1:**

Antibody Number	**Heavy Chain Mutations (Kabat Numbering)**	**C_H1 domain & hinge SEQ ID NO:**	**C_H1,Hinge, C_H2 & C_H3 SEQ ID NO:**

1	C127S	269	307
2	C127S, C239S	264	302
3	C127S, C242S	265	303
4	C127S, C242S, C239S	270	308
5	G230C	271	309
5P	G230C, S241P	272	310
6	C127S, G230C, C239S	243	281
7	C127S, G230C, C242S	244	282
8	C127S, G230C, C239S, C242S	245	283
9	G230C, C239S	273	311
10	G230C, C242S	274	312
11	G230C, C239S, C242S	275	313
12	C239S	276	314
13	C242S	277	315
14	C239S, C242S	278	316
15	C127S, G230C	246	284
16	C127S, G230C, S241P	247	285
17	Human IgG4 wild type	227	-
18	S241P	-	-
19	Human IgG1 wild type	226	-
28	C127S Y229C	248	286
28P	C127S Y229C, S241P	267	305
29	C127S Y229C C239S	249	287
30	C127S Y229C C242S	250	288
31	C127S Y229C C239S C242S	251	289
32	C127S K228C	252	290
33	C127S K228C C239S	253	291
34	C127S K228C C242S	254	292
35	C127S K228C C239S C242S	255	293
36	C127S S227C	256	294
37	C127S S227C C239S	257	295
38	C127S S227C C242S	258	296
39	C127S S227C C239S C242S	259	297
44	C127S G230C P238PAAA	260	298
44P	C127S G230C P238PAAA, S241P	268	306
45	C127S G230C P238PAAA C239S	261	299
46	C127S G230C P238PAAA C242S	262	300
47	C127S G230C P238PAAA C239S C242S	263	301
48	C127S, S227P, Y229S, G230C, P237D, P238KTHT, S241P	266	304
49	C127S G230C P238PA		
50	C127S G230C P238PAA S241P		
51	C127S, G230C, P238PAAAA		
52	C127S, G230C, P238PAAAAA		
55	C127S, G230C, P238PTHT		
56	C127S, G230C, P237D, P238KTHT		
57	C127S, G230C, P238PGGG		
60	C127S, S227P, G230C		
62	C127S, Y229S, G230C		

64	C127S, S227P, Y229S, G230C		
65	C127S, S227P, Y229S, G230C, P237D, P238KTHT		
66	C127S, G230C, P237D, P238KTH		
67	C127S, G230C, P237D, P238KT		
68	C127S, G230C, P237D, P238K		
69	C127S, G230C P237D, P238KAAA		
71	C127S, S227P, G230C, P237D, P238KTHT		
73	C127S, Y229S, G230C, P237D, P238KTHT		
74	C127S Y229C core hinge SPPCP		
75	C127S G230C core hinge CPPSP		
76	C127S Y229C core hinge CPPSP		
77	C127S G230C core hinge SPPCP		

Figures 3a and 4a also show the mutations introduced in IgG4 antibodies according to the present invention. Figures 3b and 4b show the positions of the cysteine residues in the IgG4 antibodies of the present invention and also show the predicted bonding of the cysteine to a cysteine in the light chain (LC) or another heavy chain (HC). For cysteine residues which show (LC or HC), it is possible that the cysteine is binding to a cysteine in the light chain or the heavy chain but where either the LC or HC is underlined this is the disulphide bond which is believed to predominantly occur.

In a preferred embodiment, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region and each heavy chain comprises the mutations of an antibody selected from 2, 3, 6, 7, 8, 15, 16, 28, 28P, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 44, 44P, 45, 46, 47 and 48, as shown in Table 1. Accordingly, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region and each heavy chain comprises one of the following sequences: SEQ ID NO: **243**, SEQ ID NO: **244**, SEQ ID NO: **245**, SEQ ID NO: **246**, SEQ ID NO: **247**, SEQ ID NO: **248**, SEQ ID NO: **249**, SEQ ID NO: **250**, SEQ ID NO: **251**, SEQ ID NO: **252**, SEQ ID NO: **253**, SEQ ID NO: **254**, SEQ ID NO: **255**, SEQ ID NO: **256**, SEQ ID NO: **257**, SEQ ID NO: **258**, SEQ ID NO: **259**, SEQ ID NO: **260**, SEQ ID NO: **261**, SEQ ID NO: **262**, SEQ ID NO: **263**, SEQ ID NO: **264**, SEQ ID NO: **265**, SEQ ID NO: **266**, SEQ ID NO: **267** and SEQ ID NO: 268.

In a preferred embodiment the antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, and comprises one of the following sequences: SEQ ID NO: **243**, SEQ ID NO: **244**, SEQ ID NO: **245**, SEQ ID NO: **246**, SEQ ID NO: **247**, SEQ ID NO: **248**, SEQ ID NO: **249**, SEQ ID NO:

250, SEQ ID NO: **251**, SEQ ID NO: **252**, SEQ ID NO: **253**, SEQ ID NO: **254**, SEQ ID NO: **255**, SEQ ID NO: **256**, SEQ ID NO: **257**, SEQ ID NO: **258**, SEQ ID NO: **259**, SEQ ID NO: **260**, SEQ ID NO: **261**, SEQ ID NO: **262**, SEQ ID NO: **263**, SEQ ID NO: **264**, SEQ ID NO: **265**, SEQ ID NO: **266**, SEQ ID NO: **267** and SEQ ID NO: **268**. More preferably, the antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region and each heavy chain comprises one of the following sequences: SEQ ID NO: **243**, SEQ ID NO: **244**, SEQ ID NO: **245**, SEQ ID NO: **246**, SEQ ID NO: **247** , SEQ ID NO: **248**, SEQ ID NO: **249**, SEQ ID NO: **250**, SEQ ID NO: **251**, SEQ ID NO: **252**, SEQ ID NO: **253**, SEQ ID NO: **254**, SEQ ID NO: **255**, SEQ ID NO: **256**, SEQ ID NO: **257**, SEQ ID NO: **258**, SEQ ID NO: **259**, SEQ ID NO: **260**, SEQ ID NO: **261**, SEQ ID NO: **262**, SEQ ID NO: **263**, SEQ ID NO: **264**, SEQ ID NO: **265**, SEQ ID NO: **266**, SEQ ID NO: **267** and SEQ ID NO: **268**.

In a further preferred embodiment, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain and each heavy chain comprises the mutations of an antibody selected from 2, 3, 6, 7, 8, 15, 16, 28, 28P, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 44, 44P, 45, 46, 47 and 48, as shown in Table 1. Accordingly, the present invention provides an antibody comprising two heavy chains which each comprise a variable region, a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain and each heavy chain comprises one of the following sequences: SEQ ID NO: **281**, SEQ ID NO: **282**, SEQ ID NO: **283** , SEQ ID NO: **284**, SEQ ID NO: **285**, SEQ ID NO: **286**, SEQ ID NO: **287**, SEQ ID NO: **288**, SEQ ID NO: **289**, SEQ ID NO: **290**, SEQ ID NO: **291**, SEQ ID NO: **292**, SEQ ID NO: **293**, SEQ ID NO: **294**, SEQ ID NO: **295**, SEQ ID NO: **296**, SEQ ID NO: **297**, SEQ ID NO: **298**, SEQ ID NO: **299**, SEQ ID NO: **300**, SEQ ID NO: **301**, SEQ ID NO: **302**, SEQ ID NO: **303**, SEQ ID NO: **304**, SEQ ID NO: **305** and SEQ ID NO: **306**.

A particularly preferred antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, wherein the heavy chain comprises SEQ ID NO: **267** (antibody 28P), SEQ ID NO: **268** (antibody 44P) or SEQ ID NO: **266** (antibody 48). A further particularly preferred antibody of the present invention comprises two heavy chains which each comprise a variable region, a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain wherein the heavy chain comprises SEQ ID NO: **305** (antibody 28P), SEQ ID NO: **306** (antibody 44P) or SEQ ID NO: **304** (antibody 48). Antibodies 28P, 44P and 48 are particularly preferred because they exhibit significantly improved thermostability and further exhibit reduced half-molecule formation.

Antibodies 2, 3 and 8 have been shown to form significant quantity of so-called half-molecules (HL). These mutants may form whole antibody molecules (H2L2) *in vitro* under non-denaturing conditions but any non-covalent associations between the heavy chains and/or between heavy and light chains is removed under non-reducing SDS-PAGE conditions. Whilst it often taught to be desirable to reduce the formation of half-molecules, antibodies which have an increased tendency to form half-molecules may be advantageous for certain uses. Antibodies which form stable half-molecules (HL) and little or no whole antibody (H2L2) due to the antibody heavy chain being incapable to form a covalent or non-covalent association with another heavy chain are of particular interest. Antibodies which form stable half-molecules may be advantageous for the production of monovalent antibodies. Antibodies which form half-molecules may also provide a useful way to produce a bispecific antibody due to the formation of whole antibodies from half-molecules having different specificities, wherein the whole antibody is bispecific and monovalent for each antigen. The heavy chains of such a bispecific antibody would be associated non-covalently.

Antibody 3 retains C239 in the hinge region but appears unable to form interhinge heavy chain disulphide bonds, presumably due to efficient formation of a disulphide between the C-terminal light chain cysteine and the hinge C239. A comparison of antibodies 2 and 3 shows the extent of the 'reach' of the C-terminal cysteine of the light chain, in that the light chain disulphide bonds more efficiently to C239 than to C242 in the hinge region. Furthermore antibody 3 shows increased stability compared to antibody 2.

Whilst the mutated antibodies according to the present invention are described above with respect to the IgG4 isotype, the skilled person will appreciate that the mutations made to the IgG4 antibody may also be applied to other antibody isotypes or classes which have the same disulphide bond arrangement as an IgG4 antibody in order to provide an improved antibody. Specific examples of antibodies which have the same disulphide bond arrangement as an IgG4 antibody are IgG3 antibodies, IgM antibodies and IgD antibodies. As shown in Figure 1b, IgG3 and IgM have a cysteine at position 127 in the C_H1 domain and IgD has a cysteine at position 128 in the C_H1 domain which is equivalent to the C127 in the C_H1 domain of IgG4 which forms an inter-chain disulphide bond with a cysteine in the light chain. Further, it can also be seen from Figure 1b that upper hinge regions of IgG3 and IgD and the C-terminal region of the C_H1 domain and the N-terminal region of the C_H2 domain in IgM do not contain a cysteine residue which is equivalent to the residues of the upper hinge region of IgG1. Accordingly, the present invention further provides an IgG3 antibody, an IgD antibody and an IgM antibody wherein the cysteine in the C_H1 domain which forms an inter-chain disulphide

bond with a cysteine in a light chain is substituted with another amino acid and wherein one or more amino acids which are in a structurally analogous position to the upper hinge region of IgG1 or IgG4 are substituted with cysteine.

Accordingly, the present invention also provides a symmetric bispecific antibody of the class IgG3 comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, wherein in each heavy chain:

a. the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is substituted with another amino acid; and
b. one or more of the amino acids positioned in the upper hinge region is substituted with cysteine

wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different..

In a preferred embodiment of the IgG3 antibody aspect of the present invention, the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is the cysteine at position 127, numbered according to the Kabat numbering system, as shown in Figure 1b and 2b.

In a preferred embodiment of the IgG3 antibody aspect of the present invention, the one or more amino acids positioned in the upper hinge region which may be substituted with cysteine are one or more of the amino acids at positions selected from 226, 227, 228 229, 230, 232 and 233, numbered according to the Kabat numbering system, as shown in Figures 1b and 2b.

The present invention further provides a symmetric bispecific antibody of the class IgM comprising two heavy chains which each comprise a variable region, a C_H1 domain and a C_H2 domain, wherein in each heavy chain:

a. the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is substituted with another amino acid; and
b. one or more of the amino acids positioned in the C_H1 domain or C_H2 domain is substituted with cysteine

wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

In a preferred embodiment of the IgM antibody aspect of the present invention, the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is the cysteine at position 127, numbered according to the Kabat numbering system, as shown in Figures 1b and 2c.

In a preferred embodiment of the IgM antibody aspect of the present invention, one or more amino acids positioned in the C-terminal end of the C_H1 domain or the N-terminal end of the C_H2 domain are substituted with cysteine. Preferred amino acids position in the C-terminal end of the C_H1 domain which may be substituted with cysteine are one or more of the amino acids at positions selected from 223, 223A, 223B and 223C, numbered according to the Kabat numbering system, as shown in Figures 1b and 2c. Preferred amino acids position in the N-terminal end of the C_H2 domain which may be substituted with cysteine are one or more of the amino acids at positions selected from 243G, 243H and 243I, numbered according to the Kabat numbering system, as shown in Figures 1b and 2c. Accordingly any one or more of amino acids 223 to 243 may be substituted with cysteine.

The present invention further provides a symmetric bispecific antibody of the class IgD comprising two heavy chains which each comprise a variable region, a C_H1 domain and a hinge region, wherein in each heavy chain:

a. the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is substituted with another amino acid; and
b. one or more of the amino acids positioned in the hinge region is substituted with cysteine

wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

In a preferred embodiment of the IgD antibody aspect of the present invention, the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is the cysteine at position 128 numbered according to the Kabat numbering system, as shown in Figures 1b and 2d.

The hinge region of an IgD antibody may be defined as R224-P243, according to the Kabat numbering system.

In a preferred embodiment of the IgD antibody aspect of the present invention, the one or more amino acids positioned in the hinge region which are substituted with cysteine are one or more of the amino acids at positions selected from 227, 228, 229, 230, 231, 232 and 233, numbered according to the Kabat numbering system, as shown in Figures 1b and 2d.

The IgG3, IgD or IgM antibodies provided by the present invention may comprise one or more further mutations to the hinge region as discussed above with respect to the IgG4 antibody.

In this aspect of the present invention, the antibody is preferably of the class IgG4.

The term 'antibody' as used herein includes intact (whole) antibodies and functionally active fragments which comprise two heavy chains which each comprise a V_H domain, a C_H1 domain and a hinge region. The antibody according to the present invention preferably comprises at least one light chain. Accordingly, the term "antibody" in the present invention covers bi, tri or tetra-valent antibodies, a dimer of Fab' and $F(ab')_2$ fragmentsand whole antibody molecules comprising two light chain and heavy chain pairings.

As is well known in the art, a typical Fab' molecule comprises a heavy and a light chain pair in which the heavy chain comprises a variable region V_H, a constant domain C_H1 and a hinge region and the light chain comprises a variable region V_L and a constant domain C_L.

In one embodiment there is provided a dimer of Fab' according to the present disclosure for example dimerisation may be through the hinge.

In one embodiment the heavy chain comprises a C_H2 domain and a C_H3 domain and optionally a C_H4 domain. In one embodiment the antibody comprises two heavy chains each of which is as defined above in the first or second aspect of the present invention. The antibodies according to the present invention also preferably comprise two light chains, wherein the constant regions of the light chains are preferably identical. In this embodiment wherein the antibody comprises two heavy chains and two light chains, preferably both heavy chain constant region sequences are identical as defined above by the first or second aspect of the present invention, and both light chain constant region sequences are identical.

In a preferred embodiment the antibody of the present invention is a whole antibody comprising two light chains and two heavy chains, wherein each heavy chain comprises an IgG4 C_H1 wherein the cysteine at position 127, numbered according to the Kabat numbering system is substituted with another amino acid, an IgG1 upper and middle hinge region, an IgG4 lower hinge region, a C_H2 domain and a C_H3 domain.

The complete hinge region of an IgG4 antibody typically consists of residues 226 to 251 (numbering based on Kabat numbering system. However the hinge region may be shortened or lengthened as required. For example, antibodies according to the first aspect of the present invention, the wild type amino acid is substituted with a cysteine residue at position 227, 228, 229 or 230, the hinge region may end after the new cysteine residue at position 227, 228, 229 or 230. Antibodies according to the present invention may also comprise one or more further amino acids positioned N-terminal and/or C-terminal of the hinge region. In addition other characteristics of the hinge can be controlled, such as the distance of the hinge cysteine(s) from the light chain interchain cysteine, the distance between the cysteines of the hinge and the composition of other amino acids in the hinge that may affect properties of the hinge such as

flexibility e.g. glycines may be incorporated into the hinge to increase rotational flexibility or prolines may be incorporated to reduce flexibility. Alternatively combinations of charged or hydrophobic residues may be incorporated into the hinge to confer multimerisation or purification properties. Other modified hinge regions may be entirely synthetic and may be designed to possess desired properties such as length, composition and flexibility.

The constant region domains, in particular in the Fc domain, where present, employed in the present invention, are preferably of IgG4 isotype where antibody effector functions are not required. According each heavy chain preferably comprises an IgG4 C_H2 domain and a C_H3 domain, as shown in SEQ ID NO: **64**.

It will be appreciated that sequence variants of the Fc constant region domains may also be used.

In one embodiment each heavy chain comprises IgG4 C_H2 and C_H3 domains wherein the arginine at position 409 (EU numbering) is substituted with lysine, threonine, methionine or leucine in order to inhibit aggregate formation at low pH (US 2008/0063635 Takahashi et al.) Mutations at L235, D265, D270, K322, P331 and P329 (numbered according to EU numbering system) are also taught in order to attenuate CDC activity (US 2008/0063635 Takahashi et al.).

Each heavy chain may comprise the mutations as taught in WO2008/145142 Van de Winkel et al. which discloses stable IgG4 antibodies that have a reduced ability to undergo Fab-arm exchange by substitution of the arginine residue at position 409, the Phe residue at position 405 or the Lys at position 370 (numbered according to EU numbering system).

In one embodiment each heavy chain comprises an IgG4 C_H2 domain and an IgG1 C_H3 domain, as shown in SEQ ID NO: 280.

In the embodiment of the present invention wherein the antibody is a mutated IgG3, IgD or IgM antibody, each heavy chain preferably comprises a C_H2 domain and a C_H3 domain, and optionally a C_H4 domain. In the IgG3 antibody each heavy chain preferably comprises IgG3 C_H2 domain and a IgG3 C_H3 domain. In the IgD antibody each heavy chain preferably comprises IgD C_H2 domain and a IgD C_H3 domain. In the IgM antibody each heavy chain preferably comprises IgM C_H2 domain, a IgM C_H3 domain and a IgM C_H4 domain.

In one embodiment mutations at C127 in the C_H1 domain may be made at equivalent positions in other IgG isotopes (1, 2, 3) or in other antibody classes. These mutant antibodies may comprise one or more further mutations, for example in the hinge region and/or C_H2 domain and/or C_H3 domain. Examples of specific mutations in the hinge region and C_H2 and C_H3 domains are described previously with respect to the other aspects of the present invention.

Specific examples of the above mutant antibodies are the mutant IgG4 antibodies 4, 5, 5P, 9, 10, 11 and 14 listed in Table 1.

Accordingly the present invention provides an antibody comprising two heavy chains, wherein each heavy chain comprises a C_H1 domain and a hinge region and each heavy chain comprises the mutations of an antibody selected from 4, 5, 5P, 9, 10, 11 and 14, as shown in Table 1. Accordingly, the present invention provides an antibody comprising two heavy chains, wherein each heavy chain comprises a C_H1 domain and a hinge region and each heavy chain comprises one of the following sequences: SEQ ID NO: **270**, SEQ ID NO: **271**, SEQ ID NO: **272**, SEQ ID NO: **273**, SEQ ID NO: **274**, SEQ ID NO: **275** and SEQ ID NO: **276**.

In a further embodiment, the present invention provides an antibody comprising two heavy chains, wherein each heavy chain comprises a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain and each heavy chain comprises the mutations of an antibody selected from 4, 5, 5P, 9, 10, 11 and 14, as shown in Table 1. Accordingly, the present invention provides an antibody comprising two heavy chains, wherein each heavy chain comprises a C_H1 domain, a hinge region, a C_H2 domain and a C_H3 domain and each heavy chain comprises one of the following sequences: SEQ ID NO: **308**, SEQ ID NO: **309**, SEQ ID NO: **310**, SEQ ID NO: **311**, SEQ ID NO: **312**, SEQ ID NO: **313** and SEQ ID NO: **316**.

Antibodies 4 (C127S, C239S and C242S) and 14 (C239S and C242S) have been shown to form significant quantity of so-called half-molecules (HL). These mutants may form whole antibody molecules (H2L2) *in vitro* under non-denaturing conditions but any non-covalent associations between the heavy chains and/or between heavy and light chains is removed under non-reducing SDS-PAGE conditions. Whilst it often taught to be desirable to reduce the formation of half-molecules, antibodies which have an increased tendency to form half-molecules may be advantageous for certain uses, for example in vitro formation of half molecules may facilitate heavy chain exchange and facilitate the preparation of bispecific IgG4 antibodies according to the present disclosure.

Antibodies 2, 3 and 8, as described above, have also been shown to form significant quantities of half-molecules and, therefore, may also be used in situations where half-molecule formation is desirable.

Antibody 3 retains C239 in the hinge region but appears unable to form interhinge heavy chain dulphide bonds, presumably due to efficient formation of a disulphide between the C-terminal light chain cysteine and the hinge C239. A comparison of antibodies 2 and 3 shows the extent of the 'reach' of the C-terminal cysteine of the light chain, in that the light chain

disulphide bonds more efficiently to C239 than to C242 in the hinge region. Furthermore antibody 3 shows increased stability compared to antibody 2.

Antibodies 5 (G230C), 5P (G230C and S241P), 9 (G230C and C239S), 10 (G230C and C242S) and 11 (G230C, C239S and C242S) comprises two cysteines (a cysteine at position 127 in CH1 and at 230 in the upper hinge) with which the cysteine in the light chain may form a disulphide bond. Accordingly, these antibodies may comprise a non-disulphide bonded cysteine in the heavy chain C_H1 or hinge region which can advantageously be used for attachment of an effector molecule at the non-.disulphide bonded cysteine. Further antibody 5 comprises two hinge cysteines at C239 and C242 and, therefore, will be resistant to a mild reduction step required to activate the free thiol of the non-disulphide bonded cysteine to insert an effector molecule. Further antibody 11, comprises no hinge cysteines at 239 and 242, and therefore this reduces the chance of any effector molecules being attached to these positions in the hinge.

The term 'antibody' as used herein includes intact (whole) antibodies and functionally active fragments which comprise two heavy chains which each comprise a V_H domain, a C_H1 domain and a hinge region. The antibody according to the present invention preferably comprises at least one light chain. Accordingly, the term "antibody" in the present invention covers bi, tri or tetra-valent antibodies, Fab' and $F(ab')_2$ fragments, half-antibody molecules or half-molecules comprising a single light chain and heavy chain pairing and whole antibody molecules comprising two light chain and heavy chain pairings.

As is well known in the art, a typical Fab' molecule comprises a heavy and a light chain pair in which the heavy chain comprises a variable region $V_{H,}$ a constant domain C_H1 and a hinge region and the light chain comprises a variable region V_L and a constant domain C_L.
In one embodiment there is provided a dimer of Fab' according to the present disclosure for example dimerisation may be through the hinge.

In one embodiment the heavy chain comprises a C_H2 domain and a C_H3 domain and optionally a C_H4 domain. In one embodiment the antibody comprises two heavy chains each of which is as defined above in the first or second aspect of the present invention. The antibodies according to the present invention also preferably comprise two light chains. In this embodiment wherein the antibody comprises two heavy chains, preferably both heavy chain sequences are identical as defined above by the first or second aspect of the present invention.
In a preferred embodiment the antibody of the present invention is a whole antibody comprising two light chains and two heavy chains, wherein each heavy chain comprises an IgG4 C_H1 wherein the cysteine at position 127, numbered according to the Kabat numbering system is

substituted with another amino acid, an IgG1 upper and middle hinge region, an IgG4 lower hinge region, a C_H2 domain and a C_H3 domain.

The complete hinge region of an IgG4 antibody typically consists of residues 226 to 251 (numbering based on Kabat numbering system. However the hinge region may be shortened or lengthened as required. For example, antibodies according to the first aspect of the present invention, the wild type amino acid is substituted with a cysteine residue at position 227, 228, 229 or 230, the hinge region may end after the new cysteine residue at position 227, 228, 229 or 230. Antibodies according to the present invention may also comprise one or more further amino acids positioned N-terminal and/or C-terminal of the hinge region. In addition other characteristics of the hinge can be controlled, such as the distance of the hinge cysteine(s) from the light chain interchain cysteine, the distance between the cysteines of the hinge and the composition of other amino acids in the hinge that may affect properties of the hinge such as flexibility e.g. glycines may be incorporated into the hinge to increase rotational flexibility or prolines may be incorporated to reduce flexibility. Alternatively combinations of charged or hydrophobic residues may be incorporated into the hinge to confer multimerisation or purification properties. Other modified hinge regions may be entirely synthetic and may be designed to possess desired properties such as length, composition and flexibility.

The constant region domains, in particular in the Fc domain, where present, employed in the present invention, are preferably of IgG4 isotype where antibody effector functions are not required. According each heavy chain preferably comprises an IgG4 C_H2 domain and a C_H3 domain, as shown in SEQ ID NO: **279**.

In one embodiment, the antibody is a monoclonal, fully human, humanized or chimeric antibody fragment. In one embodiment the antibody is fully human or humanised.

Monoclonal antibodies may be prepared by any method known in the art such as the hybridoma technique (Kohler & Milstein, *Nature*, 1975, 256, 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al., Immunology Today*, 1983, 4, 72) and the EBV-hybridoma technique (Cole *et al.,* "Monoclonal Antibodies and Cancer Therapy", pp. 77-96, Alan R. Liss, Inc., 1985).

Antibodies for use in the invention may also be generated using single lymphocyte antibody methods by cloning and expressing immunoglobulin variable region cDNAs generated from single lymphocytes selected for the production of specific antibodies by, for example, the methods described by Babcook, J. *et al.*, *Proc. Natl. Acad. Sci. USA*, 1996, 93(15), 7843-7848, WO 92/02551, WO2004/051268 and WO2004/106377.

Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule which optionally comprise one or more donor residues from the non-human species (see, for example, US 5,585,089).

The antibodies for use in the present invention can also be generated using various phage display methods known in the art and include those disclosed by Brinkman *et al.*, *J. Immunol. Methods*, 1995, 182, 41-50; Ames *et al.*, *J. Immunol. Methods*, 1995, 184, 177-186; Kettleborough *et al. Eur. J. Immunol.*, 1994, 24, 952-958; Persic *et al.*, *Gene*, 1997 187, 9-18; and Burton *et al.*, *Advances in Immunology*, 1994, 57, 191-280; WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; and WO 95/20401; and US 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743; and 5,969,108. Also, transgenic mice, or other organisms, including other mammals, may be used to generate humanized antibodies.

Fully human antibodies are those antibodies in which the variable regions and the constant regions (where present) of both the heavy and the light chains are all of human origin, or substantially identical to sequences of human origin, not necessarily from the same antibody. Examples of fully human antibodies may include antibodies produced for example by the phage display methods described above and antibodies produced by mice in which the murine immunoglobulin variable and/or constant region genes have been replaced by their human counterparts eg. as described in general terms in EP0546073 B1, US 5,545,806, US 5,569,825, US 5,625,126, US 5,633,425, US 5,661,016, US5,770,429, EP 0438474 B1 and EP0463151 B1. The antibody starting material for use in the present invention may be prepared by the use of recombinant DNA techniques involving the manipulation and re-expression of DNA encoding the antibody variable and constant region(s). Standard molecular biology techniques may be used to modify, add or delete amino acids or domains as desired. Any alterations to the variable or constant regions are still encompassed by the terms 'variable' and 'constant' regions as used herein.

The antibody starting material may be obtained from any species including for example mouse, rat, rabbit, hamster, camel, llama, goat or human. Parts of the antibody may be obtained from more than one species, for example the antibody may be chimeric. In one example, the constant regions are from one species and the variable regions from another. The antibody starting material may also be modified. In another example, the variable region of the antibody has been created using recombinant DNA engineering techniques. Such engineered versions include those created for example from natural antibody variable regions by insertions,

deletions or changes in or to the amino acid sequences of the natural antibodies. Particular examples of this type include those engineered variable region domains containing at least one CDR and, optionally, one or more framework amino acids from one antibody and the remainder of the variable region domain from a second antibody. The methods for creating and manufacturing these antibodies are well known in the art (see for example, Boss et al., US 4,816,397; Cabilly et al., US 6,331,415; Shrader et al., WO 92/02551; Ward et al., 1989, Nature, 341, 544; Orlandi et al., 1989, Proc.Natl.Acad.Sci. USA, 86, 3833; Riechmann et al., 1988, Nature, 322, 323; Bird et al, 1988, Science, 242, 423; Queen et al., US 5,585,089; Adair, WO91/09967; Mountain and Adair, 1992, Biotechnol. Genet. Eng. Rev, 10, 1-142; Verma et al., 1998, Journal of Immunological Methods, 216, 165-181).

In one embodiment the antibody comprises a variable domain pair forming a binding domain is a cognate pair. Cognate pair as employed herein is intended to refer to a natural pair of variable domains, that is to say isolated from a single antibody or antibody expressing cell.

Variable domains may have been optimized and/or humanized.

Optimised/humanized variable domains derived from a cognate pair will still be considered a cognate pair after optimization/humanization.

Thus the invention extends to human, humanized or chimeric molecules.

In one embodiment the molecule specifically binds a target antigen. Specifically binds as employed herein is intended to refer to molecules having high affinity for a target antigen (to which it is specific) and which binds antigens to which it is not specific with a low or much lower affinity (or not at all). Methods of measuring affinity are known to those skilled in the art and include such assays as BIAcore™.

The antibody molecules of the present invention suitably have a high binding affinity, in particular, nanomolar or picomolar. Affinity may be measured using any suitable method known in the art, including BIAcore™. In one embodiment the molecule of the present invention has a binding affinity of about 100 pM or better. In one embodiment the molecule of the present invention has a binding affinity of about 50pM or better. In one embodiment the molecule of the present invention has a binding affinity of about 40pM or better. In one embodiment the molecule of the present invention has a binding affinity of about 30pM or better. In one embodiment the molecule of the present invention is fully human or humanised and has a binding affinity of about 100pM or better.

A derivative of a naturally occurring domain as employed herein is intended to refer to where one, two, three, four or five amino acids in a naturally occurring sequence have been

replaced or deleted, for example to optimize the properties of the domain such as by eliminating undesirable properties but wherein the characterizing feature(s) of the domain is/are retained.

In one embodiment the antibody molecules of the present invention comprise one or more albumin binding peptides. *In vivo* the peptide binds albumin, which increases the half-life of the molecule.

The albumin binding peptide may be appended from one or more variable regions, a hinge or C-terminal of the molecule or any location that does not interfere with the molecules antigen binding properties.

Examples of albumin binding peptides are provided in WO 2007/106120.

It will also be understood by one skilled in the art that the antibody may undergo a variety of posttranslational modifications. The type and extent of these modifications often depends on the host cell line used to express the molecule as well as the culture conditions. Such modifications may include variations in glycosylation, methionine oxidation, diketopiperazine formation, aspartate isomerization and asparagine deamidation. A frequent modification is the loss of a carboxy-terminal basic residue (such as lysine or arginine) due to the action of carboxypeptidases (as described in Harris, RJ. *Journal of Chromatography* 705:129-134, 1995).

If desired a molecule for use in the present invention may be conjugated to one or more effector molecule(s). It will be appreciated that the effector molecule may comprise a single effector molecule or two or more such molecules so linked as to form a single moiety that can be attached to the antibody molecule of the present invention. Where it is desired to obtain an antibody according to the invention linked to an effector molecule, this may be prepared by standard chemical or recombinant DNA procedures in which the antibody is linked either directly or via a coupling agent to the effector molecule. Techniques for conjugating such effector molecules to an antibody are well known in the art (see, Hellstrom *et al.*, Controlled Drug Delivery, 2nd Ed., Robinson *et al.*, eds., 1987, pp. 623-53; Thorpe *et al.*, 1982 , Immunol. Rev., 62:119-58 and Dubowchik *et al.*, 1999, Pharmacology and Therapeutics, 83, 67-123). Particular chemical procedures include, for example, those described in WO 93/06231, WO 92/22583, WO 89/00195, WO 89/01476 and WO03031581. Alternatively, where the effector molecule is a protein or polypeptide the linkage may be achieved using recombinant DNA procedures, for example as described in WO 86/01533 and EP0392745.

The term effector molecule as used herein includes, for example, antineoplastic agents, drugs, toxins, biologically active proteins, for example enzymes, other antibody or antibody fragments, synthetic or naturally occurring polymers, nucleic acids and fragments thereof e.g.

DNA, RNA and fragments thereof, radionuclides, particularly radioiodide, radioisotopes, chelated metals, nanoparticles and reporter groups such as fluorescent compounds or compounds which may be detected by NMR or ESR spectroscopy.

Examples of effector molecules may include cytotoxins or cytotoxic agents including any agent that is detrimental to (*e.g.* kills) cells. Examples include combrestatins, dolastatins, epothilones, staurosporin, maytansinoids, spongistatins, rhizoxin, halichondrins, roridins, hemiasterlins, taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof.

Effector molecules also include, but are not limited to, antimetabolites (*e.g.* methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.* mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.* daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.* dactinomycin (formerly actinomycin), bleomycin, mithramycin, anthramycin (AMC), calicheamicins or duocarmycins), and anti-mitotic agents (*e.g.* vincristine and vinblastine).

Other effector molecules may include chelated radionuclides such as ^{111}In and ^{90}Y, Lu^{177}, Bismuth^{213}, Californium^{252}, Iridium^{192} and Tungsten^{188}/Rhenium^{188}; or drugs such as but not limited to, alkylphosphocholines, topoisomerase I inhibitors, taxoids and suramin.

Other effector molecules include proteins, peptides and enzymes. Enzymes of interest include, but are not limited to, proteolytic enzymes, hydrolases, lyases, isomerases, transferases. Proteins, polypeptides and peptides of interest include, but are not limited to, immunoglobulins, toxins such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin, a protein such as insulin, tumour necrosis factor, α-interferon, β-interferon, nerve growth factor, platelet derived growth factor or tissue plasminogen activator, a thrombotic agent or an anti-angiogenic agent, *e.g.* angiostatin or endostatin, or, a biological response modifier such as a lymphokine, interleukin-1 (IL-1), interleukin-2 (IL-2), granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), nerve growth factor (NGF) or other growth factor and immunoglobulins.

Other effector molecules may include detectable substances useful for example in diagnosis. Examples of detectable substances include various enzymes, prosthetic groups,

fluorescent materials, luminescent materials, bioluminescent materials, radioactive nuclides, positron emitting metals (for use in positron emission tomography), and nonradioactive paramagnetic metal ions. See generally U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics. Suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; suitable prosthetic groups include streptavidin, avidin and biotin; suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride and phycoerythrin; suitable luminescent materials include luminol; suitable bioluminescent materials include luciferase, luciferin, and aequorin; and suitable radioactive nuclides include ^{125}I, ^{131}I, ^{111}In and ^{99}Tc.

In another example the effector molecule may increase the half-life of the antibody *in vivo*, and/or reduce immunogenicity of the antibody and/or enhance the delivery of an antibody across an epithelial barrier to the immune system. Examples of suitable effector molecules of this type include polymers, albumin, albumin binding proteins or albumin binding compounds such as those described in WO 05/117984.

Where the effector molecule is a polymer it may, in general, be a synthetic or a naturally occurring polymer, for example an optionally substituted straight or branched chain polyalkylene, polyalkenylene or polyoxyalkylene polymer or a branched or unbranched polysaccharide, e.g. a homo- or hetero- polysaccharide.

Specific optional substituents which may be present on the above-mentioned synthetic polymers include one or more hydroxy, methyl or methoxy groups.

Specific examples of synthetic polymers include optionally substituted straight or branched chain poly(ethyleneglycol), poly(propyleneglycol) poly(vinylalcohol) or derivatives thereof, especially optionally substituted poly(ethyleneglycol) such as methoxypoly(ethyleneglycol) or derivatives thereof.

Specific naturally occurring polymers include lactose, amylose, dextran, glycogen or derivatives thereof.

"Derivatives" as used herein is intended to include reactive derivatives, for example thiol-selective reactive groups such as maleimides and the like. The reactive group may be linked directly or through a linker segment to the polymer. It will be appreciated that the residue of such a group will in some instances form part of the product as the linking group between the antibody of the disclosure and the polymer.

The size of the polymer may be varied as desired, but will generally be in an average molecular weight range from 500Da to 50000Da, for example from 5000 to 40000Da such as

from 20000 to 40000Da. The polymer size may in particular be selected on the basis of the intended use of the product for example ability to localize to certain tissues such as tumors or extend circulating half-life (for review see Chapman, 2002, Advanced Drug Delivery Reviews, 54, 531-545). Thus, for example, where the product is intended to leave the circulation and penetrate tissue, for example for use in the treatment of a tumour, it may be advantageous to use a small molecular weight polymer, for example with a molecular weight of around 5000Da. For applications where the product remains in the circulation, it may be advantageous to use a higher molecular weight polymer, for example having a molecular weight in the range from 20000Da to 40000Da.

Suitable polymers include a polyalkylene polymer, such as a poly(ethyleneglycol) or, especially, a methoxypoly(ethyleneglycol) or a derivative thereof, and especially with a molecular weight in the range from about 15000Da to about 40000Da.

In one example an antibody for use in the present invention is attached to poly(ethyleneglycol) (PEG) moieties. In one particular example the PEG molecules may be attached through any available amino acid side-chain or terminal amino acid functional group located in the antibody, for example any free amino, imino, thiol, hydroxyl or carboxyl group. Such amino acids may occur naturally in the antibody or may be engineered into the antibody using recombinant DNA methods (see for example US 5,219,996; US 5,667,425; WO 98/25971). In one example the molecule of the present invention is a modified antibody wherein the modification is the addition to the C-terminal end of its heavy chain one or more amino acids to allow the attachment of an effector molecule. Multiple sites can be used to attach two or more PEG molecules.

In one embodiment a PEG molecule is linked to a cysteine 171 in the light chain, for example see WO2008/038024 incorporated herein by reference.

Suitably PEG molecules are covalently linked through a thiol group of at least one cysteine residue located in the antibody. Each polymer molecule attached to the modified antibody may be covalently linked to the sulphur atom of a cysteine residue located in the antibody. The covalent linkage will generally be a disulphide bond or, in particular, a sulphur-carbon bond. Where a thiol group is used as the point of attachment appropriately activated effector molecules, for example thiol selective derivatives such as maleimides and cysteine derivatives may be used. An activated polymer may be used as the starting material in the preparation of polymer-modified antibody as described above. The activated polymer may be any polymer containing a thiol reactive group such as an α-halocarboxylic acid or ester, e.g. iodoacetamide, an imide, e.g. maleimide, a vinyl sulphone or a disulphide. Such starting

materials may be obtained commercially (for example from Nektar, formerly Shearwater Polymers Inc., Huntsville, AL, USA) or may be prepared from commercially available starting materials using conventional chemical procedures. Particular PEG molecules include 20K methoxy-PEG-amine (obtainable from Nektar, formerly Shearwater; Rapp Polymere; and SunBio) and M-PEG-SPA (obtainable from Nektar, formerly Shearwater).

The present invention also provides isolated DNA encoding an antibody molecule described herein.

In a further aspect there is provided a vector comprising said DNA.

General methods by which the vectors may be constructed, transfection methods and culture methods are well known to those skilled in the art. In this respect, reference is made to "Current Protocols in Molecular Biology", 1999, F. M. Ausubel (ed), Wiley Interscience, New York and the Maniatis Manual produced by Cold Spring Harbor Publishing.

In a further aspect there is provided a host cell comprising said vector and/or DNA.

Any suitable host cell/vector system may be used for expression of the DNA sequences encoding the molecule of the present invention. Bacterial, for example *E. coli*, and other microbial systems may be used or eukaryotic, for example mammalian, host cell expression systems may also be used. Suitable mammalian host cells include CHO, myeloma or hybridoma cells.

The present invention also provides a process for the production of an antibody molecule as described herein comprising culturing a host cell containing a vector (and/or DNA) of the present invention under conditions suitable for leading to expression of protein from DNA encoding an antibody molecule of the present invention, and isolating an antibody molecule.

For production of products comprising both heavy and light chains, the cell line may be transfected with two vectors, a first vector encoding a light chain polypeptide and a second vector encoding a heavy chain polypeptide. Alternatively, a single vector may be used, the vector including sequences encoding light chain and heavy chain polypeptides.

The antibody molecules according to the present disclosure are expressed at suitable levels from host cells making them conducive to commercial processing.

The antibody may be specific for any target antigen. The antigen may be a cell-associated protein, for example a cell surface protein on cells such as bacterial cells, yeast cells, T-cells, endothelial cells or tumour cells, or it may be a soluble protein. Antigens of interest may also be any medically relevant protein such as those proteins upregulated during disease or infection, for example receptors and/or their corresponding ligands. Particular examples of cell

surface proteins include adhesion molecules, for example integrins such as β1 integrins e.g. VLA-4, E-selectin, P selectin or L-selectin, CD2, CD3, CD4, CD5, CD7, CD8, CD11a, CD11b, CD18, CD19, CD20, CD23, CD25, CD33, CD38, CD40, CD40L, CD45, CDW52, CD69, CD134 (OX40), ICOS, BCMP7, CD137, CD27L, CDCP1, CSF1 or CSF1-Receptor, DPCR1, DPCR1, dudulin2, FLJ20584, FLJ40787, HEK2, KIAA0634, KIAA0659, KIAA1246, KIAA1455, LTBP2, LTK, MAL2, MRP2, nectin-like2, NKCC1, PTK7, RAIG1, TCAM1, SC6, BCMP101, BCMP84, BCMP11, DTD, carcinoembryonic antigen (CEA), human milk fat globulin (HMFG1 and 2), MHC Class I and MHC Class II antigens, KDR and VEGF, PD-1, DC-SIGN, TL1A, DR3, IL-7 receptor A and where appropriate, receptors thereof.

Soluble antigens include interleukins such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-12, IL-13, IL-14, IL-16 or IL-17, such as IL17A and/or IL17F, viral antigens for example respiratory syncytial virus or cytomegalovirus antigens, immunoglobulins, such as IgE, interferons such as interferon α, interferon β or interferon γ, tumour necrosis factor TNF (formerly known as tumour necrosis factor-α and referred to herein as TNF or TNFα), tumor necrosis factor-β, colony stimulating factors such as G-CSF or GM-CSF, and platelet derived growth factors such as PDGF-α, and PDGF-β, WISP-1 and where appropriate receptors thereof. Other antigens include bacterial cell surface antigens, bacterial toxins, viruses such as influenza, EBV, HepA, B and C, bioterrorism agents, radionuclides and heavy metals, and snake and spider venoms and toxins.

In one embodiment there is provided a method of generating a symmetric bispecific antibody comprising the step of mixing a first IgG4 antibody with a second IgG4 antibody *ex vivo*, under conditions conducive to heavy chain exchange, wherein the antigen specificity of variable regions in the first the antibody are different to antigen specificity of the variable regions in the second antibody.

In vitro conditions conducive to heavy chain exchange include reducing conditions. Suitable reducing agents include GSH, 2-mercaptoethanol, 2-mercaptoethylamine, TBP, TCEP, cysteine-HCl and DTT.

Suitable concentrations of the reducing agents are in the range 0.01 to 10mM such as 0.5 to 5mM. In addition, reduction may be achieved using redox buffers, that is to say different relative ratios of oxidised and reduced variants of reagents such as for example: GSH :GSSG and Cys:diCys

Suitable conditions include ratios of antibodies are in the 0.5:5 to 5:05, such as 1:1 or 1:2.

Suitable temperature include 15 to 40°C, such as 37°C.

The reducing conditions may be selected to be between the reductive stabilities of the homodimers and the heterodimers.

In an alternative embodiment the antibodies if the disclosure are prepared employing a mixed cell culture, for example~50% exchange occurs. This may yield in the region of 1-2g/l of the desired bispecific.

In one embodiment there is provided an antibody or fragment obtained or obtainable from a process or method described herein.

In one embodiment, the antibody may be used to functionally alter the activity of the antigen of interest. For example, the antibody may neutralize, antagonize or agonise the activity of said antigen, directly or indirectly.

The antibody molecules of the present invention are useful in the treatment and/or prophylaxis of a pathological condition.

Thus there is provided an antibody according to the present invention for use in treatment, by administering a therapeutically effective amount thereof, for example in a pharmaceutical formulation. In one embodiment the antibody according to the invention is administered topically to the lungs, for example by inhalation.

The antibodies provided by the present invention are useful in the treatment of diseases or disorders including inflammatory diseases and disorders, immune disease and disorders, fibrotic disorders and cancers.

The term “inflammatory disease” or “disorder” and “immune disease or disorder” includes rheumatoid arthritis, psoriatic arthritis, still's disease, Muckle Wells disease, psoriasis, Crohn's disease, ulcerative colitis, SLE (Systemic Lupus Erythematosus), asthma, allergic rhinitis, atopic dermatitis, multiple sclerosis, vasculitis, Type I diabetes mellitus, transplantation and graft-versus-host disease.

The term “fibrotic disorder” includes idiopathic pulmonary fibrosis (IPF), systemic sclerosis (or scleroderma), kidney fibrosis, diabetic nephropathy, IgA nephropathy, hypertension, end-stage renal disease, peritoneal fibrosis (continuous ambulatory peritoneal dialysis), liver cirrhosis, age-related macular degeneration (ARMD), retinopathy, cardiac reactive fibrosis, scarring, keloids, burns, skin ulcers, angioplasty, coronary bypass surgery, arthroplasty and cataract surgery.

The term “cancer” includes a malignant new growth that arises from epithelium, found in skin or, more commonly, the lining of body organs, for example: breast, ovary, prostate, lung, kidney, pancreas, stomach, bladder or bowel. Cancers tend to infiltrate into adjacent tissue and spread (metastasise) to distant organs, for example: to bone, liver, lung or the brain.

The present invention also provides a pharmaceutical or diagnostic composition comprising an antibody of the present invention in combination with one or more of a pharmaceutically acceptable excipient, diluent or carrier. Accordingly, provided is the use of an antibody of the invention for the manufacture of a medicament. The composition will usually be supplied as part of a sterile, pharmaceutical composition that will normally include a pharmaceutically acceptable carrier. A pharmaceutical composition of the present invention may additionally comprise a pharmaceutically-acceptable adjuvant.

The present invention also provides a process for preparation of a pharmaceutical or diagnostic composition comprising adding and mixing the antibody of the present invention together with one or more of a pharmaceutically acceptable excipient, diluent or carrier.

The antibody of the disclosure may be the sole active ingredient in the pharmaceutical or diagnostic composition or may be accompanied by other active ingredients including other antibody ingredients, for example anti-TNF, anti- IL-1β, anti-T cell, anti-IFNγ or anti-LPS antibodies, or non-antibody ingredients such as xanthines. Other suitable active ingredients include antibodies capable of inducing tolerance, for example, anti-CD3 or anti-CD4 antibodies.

In a further embodiment the antibody or composition according to the disclosure is employed in combination with a further pharmaceutically active agent, for example a corticosteroid (such as fluticasonoe propionate) and/or a beta-2-agonist (such as salbutamol, salmeterol or formoterol) or inhibitors of cell growth and proliferation (such as rapamycin, cyclophosphmide, methotrexate) or alternative a CD28 and /or CD40 inhibitor. In one embodiment the inhibitor is a small molecule. In another embodiment the inhibitor is an antibody specific to the target.

The pharmaceutical compositions suitably comprise a therapeutically effective amount of the antibody of the invention. The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent needed to treat, ameliorate or prevent a targeted disease or condition, or to exhibit a detectable therapeutic or preventative effect. The therapeutically effective amount can be estimated initially either in cell culture assays or in animal models, usually in rodents, rabbits, dogs, pigs or primates. The animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

The precise therapeutically effective amount for a human subject will depend upon the severity of the disease state, the general health of the subject, the age, weight and gender of the

subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities and tolerance/response to therapy. This amount can be determined by routine experimentation and is within the judgment of the clinician. Generally, a therapeutically effective amount will be from 0.01 mg/kg to 50 mg/kg, for example 0.1 mg/kg to 20 mg/kg. Pharmaceutical compositions may be conveniently presented in unit dose forms containing a predetermined amount of an active agent of the invention per dose.

Compositions may be administered individually to a patient or may be administered in combination (*e.g.* simultaneously, sequentially or separately) with other agents, drugs or hormones.

The dose at which an antibody of the present invention is administered depends on the nature of the condition to be treated, for example the extent of the disease/inflammation present and on whether the molecule is being used prophylactically or to treat an existing condition.

The frequency of dose will depend on the half-life of the antibody and the duration of its effect. If the antibody has a short half-life (e.g. 2 to 10 hours) it may be necessary to give one or more doses per day. Alternatively, if the antibody has a long half-life (e.g. 2 to 15 days) it may only be necessary to give a dosage once per day, once per week or even once every 1 or 2 months.

The pharmaceutically acceptable carrier should not itself induce the production of antibodies harmful to the individual receiving the composition and should not be toxic. Suitable carriers may be large, slowly metabolised macromolecules such as proteins, polypeptides, liposomes, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers and inactive virus particles.

Pharmaceutically acceptable salts can be used, for example mineral acid salts, such as hydrochlorides, hydrobromides, phosphates and sulphates, or salts of organic acids, such as acetates, propionates, malonates and benzoates.

Pharmaceutically acceptable carriers in therapeutic compositions may additionally contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents or pH buffering substances, may be present in such compositions. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries and suspensions, for ingestion by the patient.

Suitable forms for administration include forms suitable for parenteral administration, e.g. by injection or infusion, for example by bolus injection or continuous infusion. Where the product is for injection or infusion, it may take the form of a suspension, solution or emulsion in an oily or aqueous vehicle and it may contain formulatory agents, such as suspending,

preservative, stabilising and/or dispersing agents. Alternatively, the molecule of the disclosure may be in dry form, for reconstitution before use with an appropriate sterile liquid.

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals. However, in one or more embodiments the compositions are adapted for administration to human subjects.

Suitably in formulations according to the present disclosure, the pH of the final formulation is not similar to the value of the isoelectric point of the antibody, for example if the pH of the formulation is 7 then a pI of from 8-9 or above may be appropriate. Whilst not wishing to be bound by theory it is thought that this may ultimately provide a final formulation with improved stability, for example the antibody remains in solution.

The pharmaceutical compositions of this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, transcutaneous (for example, see WO98/20734), subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, intravaginal or rectal routes. Hyposprays may also be used to administer the pharmaceutical compositions of the invention. Typically, the therapeutic compositions may be prepared as injectables, either as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared.

Direct delivery of the compositions will generally be accomplished by injection, subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Dosage treatment may be a single dose schedule or a multiple dose schedule.

It will be appreciated that the active ingredient in the composition will be an antibody. As such, it will be susceptible to degradation in the gastrointestinal tract. Thus, if the composition is to be administered by a route using the gastrointestinal tract, the composition will need to contain agents which protect the antibody from degradation but which release the antibody once it has been absorbed from the gastrointestinal tract.

A thorough discussion of pharmaceutically acceptable carriers is available in Remington's Pharmaceutical Sciences (Mack Publishing Company, N.J. 1991).

In one embodiment the formulation is provided as a formulation for topical administrations including inhalation.

Suitable inhalable preparations include inhalable powders, metering aerosols containing propellant gases or inhalable solutions free from propellant gases. Inhalable powders according to the disclosure containing the active substance may consist solely of the abovementioned

active substances or of a mixture of the abovementioned active substances with physiologically acceptable excipient.

These inhalable powders may include monosaccharides (e.g. glucose or arabinose), disaccharides (e.g. lactose, saccharose, maltose), oligo- and polysaccharides (e.g. dextranes), polyalcohols (e.g. sorbitol, mannitol, xylitol), salts (e.g. sodium chloride, calcium carbonate) or mixtures of these with one another. Mono- or disaccharides are suitably used, the use of lactose or glucose, particularly but not exclusively in the form of their hydrates.

Particles for deposition in the lung require a particle size less than 10 microns, such as 1-9 microns for example from 0.1 to 5 μm, in particular from 1 to 5 μm. The particle size of the active ingredient (such as the antibody) is of primary importance.

The propellent gases which can be used to prepare the inhalable aerosols are known in the art. Suitable propellent gases are selected from among hydrocarbons such as n-propane, n-butane or isobutane and halohydrocarbons such as chlorinated and/or fluorinated derivatives of methane, ethane, propane, butane, cyclopropane or cyclobutane. The abovementioned propellent gases may be used on their own or in mixtures thereof.

Particularly suitable propellent gases are halogenated alkane derivatives selected from among TG 11, TG 12, TG 134a and TG227. Of the abovementioned halogenated hydrocarbons, TG134a (1,1,1,2-tetrafluoroethane) and TG227 (1,1,1,2,3,3,3-heptafluoropropane) and mixtures thereof are particularly suitable.

The propellent-gas-containing inhalable aerosols may also contain other ingredients such as cosolvents, stabilisers, surface-active agents (surfactants), antioxidants, lubricants and means for adjusting the pH. All these ingredients are known in the art.

The propellant-gas-containing inhalable aerosols according to the invention may contain up to 5 % by weight of active substance. Aerosols according to the invention contain, for example, 0.002 to 5 % by weight, 0.01 to 3 % by weight, 0.015 to 2 % by weight, 0.1 to 2 % by weight, 0.5 to 2 % by weight or 0.5 to 1 % by weight of active ingredient.

Alternatively topical administrations to the lung may also be by administration of a liquid solution or suspension formulation, for example employing a device such as a nebulizer, for example, a nebulizer connected to a compressor (e.g., the Pari LC-Jet Plus(R) nebulizer connected to a Pari Master(R) compressor manufactured by Pari Respiratory Equipment, Inc., Richmond, Va.).

The antibody of the invention can be delivered dispersed in a solvent, e.g., in the form of a solution or a suspension. It can be suspended in an appropriate physiological solution, e.g., saline or other pharmacologically acceptable solvent or a buffered solution. Buffered solutions

known in the art may contain 0.05 mg to 0.15 mg disodium edetate, 8.0 mg to 9.0 mg NaCl, 0.15 mg to 0.25 mg polysorbate, 0.25 mg to 0.30 mg anhydrous citric acid, and 0.45 mg to 0.55 mg sodium citrate per 1 mL of water so as to achieve a pH of about 4.0 to 5.0. A suspension can employ, for example, lyophilised molecule.

The therapeutic suspensions or solution formulations can also contain one or more excipients. Excipients are well known in the art and include buffers (e.g., citrate buffer, phosphate buffer, acetate buffer and bicarbonate buffer), amino acids, urea, alcohols, ascorbic acid, phospholipids, proteins (e.g., serum albumin), EDTA, sodium chloride, liposomes, mannitol, sorbitol, and glycerol. Solutions or suspensions can be encapsulated in liposomes or biodegradable microspheres. The formulation will generally be provided in a substantially sterile form employing sterile manufacture processes.

This may include production and sterilization by filtration of the buffered solvent/solution used for the for the formulation, aseptic suspension of the molecule in the sterile buffered solvent solution, and dispensing of the formulation into sterile receptacles by methods familiar to those of ordinary skill in the art.

Nebulizable formulation according to the present disclosure may be provided, for example, as single dose units (e.g., sealed plastic containers or vials) packed in foil envelopes. Each vial contains a unit dose in a volume, e.g., 2 mL, of solvent/solution buffer.

The antibody of the present disclosure are thought to be particularly suitable for delivery via nebulisation.

Comprising in the context of the present specification is intended to meaning including. Where technically appropriate embodiments of the invention may be combined.

The invention will now be described with reference to the following examples, which are merely illustrative and should not in any way be construed as limiting the scope of the present invention.

Examples

1 Mutagenesis of IgG4 heavy chain and generating mutated IgG4 heavy chain single gene vectors.

Amino acid mutations were performed using the Quickchange® Lightening Multi Site Directed Mutagenesis (SDM) kit or the Quickchange® II DSM kit (obtained from Stratagene®) (catalogue numbers 210516 and 200521 respectively) and performed according to manufacturer's instructions.

Mutations were verified by DNA sequencing. The IgG4 heavy chains of antibodies 1 to 47 in the following table were produced:

Antibody Number	Heavy Chain Mutations (Kabat Numbering)	C_H1 domain & Hinge SEQ ID NO:	C_H1,Hinge, C_H2 & C_H3 SEQ ID NO:
1	C127S	269	307
2	C127S, C239S	264	302
3	C127S, C242S	265	303
4	C127S, C242S, C239S	270	308
5	G230C	271	309
5P	G230C, S241P	272	310
6	C127S, G230C, C239S	243	281
7	C127S, G230C, C242S	244	282
8	C127S, G230C, C239S, C242S	245	283
9	G230C, C239S	273	311
10	G230C, C242S	274	312
11	G230C, C239S, C242S	275	313
12	C239S	276	314
13	C242S	277	315
14	C239S, C242S	278	316
15	C127S, G230C	246	284
16	C127S, G230C, S241P	247	285
17	Human IgG4 wild type	227	-
18	S241P	-	-
19	Human IgG1 wild type	226	-
28	C127S Y229C	248	286
28P	C127S Y229C, S241P	267	305
29	C127S Y229C C239S	249	287
30	C127S Y229C C242S	250	288
31	C127S Y229C C239S C242S	251	289
32	C127S K228C	252	290
33	C127S K228C C239S	253	291
34	C127S K228C C242S	254	292
35	C127S K228C C239S C242S	255	293
36	C127S S227C	256	294
37	C127S S227C C239S	257	295
38	C127S S227C C242S	258	296
39	C127S S227C C239S C242S	259	297
44	C127S G230C P238PAAA	260	298
44P	C127S G230C P238PAAA, S241P	268	306
45	C127S G230C P238PAAA C239S	261	299
46	C127S G230C P238PAAA C242S	262	300
47	C127S G230C P238PAAA C239S C242S	263	301
48	C127S, S227P, Y229S, G230C, P237D, P238KTHT, S241P	266	304

The heavy chain of antibody 48 (Sequence ID NO: **266**) was generated by PCR and restriction enzyme cloning. The PCR product was generated by a forward oligo encoding the IgG1 upper and core hinge region sequence and a restriction site BglII and a reverse oligo encoding the restriction enzyme DraIII. The PCR fragment was then digested with above mentioned enzymes and ligated into the hG4 single gene vector containing the appropriate variable region.

2. Expression of the mutated IgG4 antibodies

All mutant DNA was transfected into CHOK1 cells. Cells ($2x10^8$ cells/ml) were resuspended in 1 ml Earles Balance Salt Solution (Sigma) and mixed with 400 μg of DNA (200 μg heavy chain DNA and 200 μg kappa light chain DNA). 800μl aliquots were transferred to 0.4 cm cuvettes (Biorad). For a 500 ml culture, six cuvettes were electroporated under the following parameters: 1 ms, 9.6 Amps; 10 ms, 0 Amps; 40 ms, 3.2 Amps. The transfected cells were incubated for 24 hrs, shaking at 140 rpm in a 5% CO_2 humidified environment at 37°C and continued from day 2 post transfection at 32°C for 10-13 days. On day 4 post transfection 1.6 mls 1 M sodium butyrate was added to the culture. Once the cells reached 40% viability or up to day 13, the supernatant was harvested. Cultures were centrifuged for 45 minutes at 4000 rpm. The supernatant was put through a 0.22 μM Stericup filter (Millipore) to be purified.

3. Purification of mutated IgG4 antibodies

Supernatants (200-500 ml) were purified using a Protein A 5 ml HiTrap MabSelect SuRe column (GE Healthcare, Amersham UK). Samples were prepared by adding $1/50^{th}$ of the supernatant volume of 2 M Tris-HCl pH 8.5. Samples were loaded onto the column at 1 ml/min. The column was washed with PBS pH 7.4. To elute the samples, 0.1 M sodium citrate, pH 3.4 was run through the column at 1 ml/min and 0.5 ml fractions were collected. Peak fractions were neutralised by adding 0.125 ml of 2 M Tris-HCl pH8.5 to each. UV detection was set at 280 nm.

4. Characterization of purified mutated IgG4 antibodies

SDS PAGE analysis:

Crude supernatant was centrifuged at 1200 rpm for 5 mins and quantified on the OCTET. Antibody samples (25-30ng) were prepared by adding the appropriate amounts of antibody, 4x Loading Buffer (Invitrogen) and 2 μl 100mM NEM. A total volume of 20 μl was made up using dH_2O. The samples were then boiled for 3 mins at 100°C and loaded onto a 15 well 1.5 mm 4-20% Tris-Glycine gel. Gels were run at 150 V for 1.5 hrs in 1x Tank buffer. Antibodies were transferred to a nitrocellulose membrane using the iBlot dry transfer system set to transfer for 8 mins. The membrane was incubated for 1 hr at room temperature (RT) in PBS-TM on a shaking platform, followed by incubation with a rabbit anti-human IgG Fc HRP conjugated

antibody (Jackson Immunoresearch) or goat anti-human Kappa light chain HRP conjugated antibody (Bethyl) for 1 hr, shaking at RT. This was followed by 3 washes of 5 mins each with PBS-T. The blots were revealed using a metal enhanced DAB substrate kit according to the manufacturer's instructions (Pierce).

The results of the Western blot analysis is shown in Figures 7, 8, 9 and 10. In Figure 7-10, H stands for heavy chain and L for light chain, H2L2 is a whole antibody molecule comprising two heavy chains and two light chains and HL is a half molecule comprising one heavy chain and one light chain.

Figure 7 shows the Western blot analysis for antibodies 15, 16, 6, 7, 8, 17, 18, 19, 5, 5P, 9, 10, 11, 1, 2, 3, 4, 12, 13 and 14. It can be seen from Figure 7 that the antibodies show a good level of H2L2 except for antibodies 4, 8 and 14 which show no or very little H2L2 due to the presence of both hinge mutations C239S and C242S. However, antibodies 4, 8 and 14 can form H2L2 by non-covalent bonding between the heavy chains. Mutant 3 also shows little H2L2, this mutant retains C239 but is unable to form inter heavy chain disulphides in the hinge, presumably due to efficient formation of a disulphide between the C-terminal light chain (LC) cysteine and the hinge C239. It can also be seen that antibodies which comprise the mutation C239S but not C242S (antibodies 2, 6, 9 and 12) show reduced formation of HL compared to antibodies which comprise neither C239S nor C242S or antibodies which comprise C242S but not C239S. Antibodies 5P and 16 which comprise the S241P mutation also show reduced formation of HL. A comparison of mutants 2 and 3 shows the extent of the 'reach' of the C-terminal cysteine of light chain to form a disulphide bond with the heavy chain, it appears that the light chain cysteine bonds more efficiently to C239 than to C242 in the heavy chain.

Figure 8 shows the Western blot analysis for antibodies 15, 6, 7, 8, 28, 29, 30, 31, 17, 19, 32, 33, 33, 34, 35, 36, 37, 38 and 39. It can be seen from Figure 8 that the antibodies show a good level of H2L2 except for antibodies 8, 31, 35 and 39 which show no or very little H2L2 due to the presence of mutations C239S and C242S in the hinge region and therefore no disulphide bonds form between two heavy chains. However, antibodies 8, 31, 35 and 39 can form H2L2 by non-covalent bonding between the heavy chains. It can also be seen that antibodies which comprise the mutation C239S but not C242S (antibodies 6, 29, 33 and 37) show reduced formation of HL compared to antibodies which comprise neither C239S nor C242S or antibodies which comprise C242S but not C239S. Mutant 15 is able to form a disulphide bond between the light chain and G230C in the CH1 and inter heavy chain disulphides hence resulting in a fully assembled and disulphide bonded protein. Furthermore, a comparison of mutants 15(C127S G230C), 28(C127S Y229C), 32(C127S K228C) and 36(C127S S227C)

shows that the position of the introduced cysteine in the upper hinge improves inter LC-HC disulphide bond formation. G230 and Y229 are particularly preferred positions to introduce a cysteine. Mutant 28 (C127S Y229C) shows a low level of HL and H2 and therefore has low disulphide bond heterogeneity.

Figure 9 shows the Western blot analysis for antibodies 15, 6, 7, 8, 44, 45, 46, 47, 17 and 19. It can be seen from Figure 9 that the antibodies show a good level of H2L2 except for antibodies 8 and 47 which show no or very little H2L2 due to the presence of mutations C239S and C242S in the hinge region and therefore no disulphide bonds form between two heavy chains. However, antibodies 8 and 47 can form H2L2 by non-covalent bonding between the heavy chains. It can also be seen that antibodies which comprise the mutation C239S but not C242S (antibodies 6 and 45) show reduced formation of HL compared to antibodies which comprise neither C239S nor C242S or antibodies which comprise C242S but not C239S. In particular, mutant 44 shows that insertion of three amino acids in the upper hinge can also reduce the formation of HL and H2 and hence has lower levels of disulphide heterogeneity than the comparable mutant 15.

Figure 10, shows the Western blot analysis for antibodies 48, 17, 18 and 19. It can be seen from Figure 10, that antibody 48 shows a good level of H2L2 and very little HL. Mutant 48 contains the IgG1 upper hinge sequence EPKSCDKTHT SEQ ID NO: **320** in place of the IgG4 upper hinge sequence along with a core hinge S241P mutation. Hence mutant 48 has the upper and core hinge sequence EPKSCDKTHTCPPCP SEQ ID NO: 321. Mutant 48 shows lower levels of disulphide bond heterogeneity compared to the wild type IgG4 antibody 17 and approximately equivalent low levels of disulphide bond heterogeneity compared to the IgG4 S241P mutant 18 and wild type IgG1 antibody 19.

Thermofluor assay:

Thermostabilities of purified mAbs were analyzed in a thermofluor assay using SYPRO® Orange to monitor the thermal unfolding process of proteins. 5 µl of mAb at 1 mg/ml, 5 µl of 30xdye, and 40 µl of PBS were added together. Ten µl of the mix was dispensed in quadruplicate to a 384 PCR optical well plate and was run on the 7900HT Fast Real-Time PCR System (Agilent Technologies UK Ltd, Wokingham UK). This PCR System contains a heating device for accurate temperature control set at 20°C to 99°C; a charged coupled device simultaneously monitors the fluorescence changes in the wells.

Figures 11, 12, 13, 14 and 15 show the results of the thermostability analysis of the IgG4 Antibody mutants compared to wild-type IgG1 and IgG4 antibodies.

A comparison of mutant 15 with wild type IgG4 (mutant 17) shows and increase in the Fab Tm due to the altered disulphide arrangement. A comparison of mutant 15 and 28 shows further improvement in Fab Tm for mutant 28 comprising Y229C mutation compared to mutant 15 comprising G230C mutation. A comparison of mutant 15 and 44 shows that the Fab Tm of a G230C mutant can be further increased further by insertion of three amino acids in the upper hinge. Comparison of mutants 17 and 18 show that the S241P middle hinge mutation does not increase Fab Tm even though it significantly reduces HL formation. Mutant 48 also shows significantly improved Fab Tm when compared to both wild type IgG4 (mutant 17) and mutant 15.

Figure 15 shows the overall ranking of the thermostabilites of selected IgG4 mutants according to the present invention. Mutants 48, 44, 44P, 46, 45, 6, 29, 30, 28, 28P, 31, 8, 47 and 15 all show significantly higher Fab Tm values compared to the wild type IgG4 (mutant 17) and wild type IgG4 S241P (mutant 18).

5. Fab arm exchange

a) In vitro heavy chain exchange

A first IgG4 antibody and its potential exchange partner were mixed in a 1:1 molar ratio at a total concentration of 100 ug/ml in phosphate buffered saline (PBS) (in mM: 150 NaCl, 10 NaH_2PO_4; pH 7.4). To allow disulphide bond reduction, samples were supplemented with reduced Glutathione (GSH; Sigma) to a final concentration of 0, 0.5 or 5 mM. At the start of the experiment (t = 0 hours) an aliquot of the mixture was taken, quenched with N-ethylmaleimide (NEM; Sigma) to a final concentration of 10 mM (to inactivate potentially reactive thiol groups) and incubated alongside the rest of the mixture for 16 hours at 37oC (t = 16 hours). After incubation, the t = 16 hours sample was quenched as above.

b)Detection and quantification of heavy chain exchange in vitro

The presence of functionally active bispecific antibodies was determined using a sandwich MSD assay in which quenched reaction samples provided in Example 5 a), serially diluted in 1 % BSA in PBS (PB), were pre-incubated with 1 ug/ml biotinylated-antigen 1 (antigen of first antibody) in PB for 1 h at RT with agitation (200 r.p.m) before being transferred to PB pre-blocked streptavidin coated MSD plates (Meso Scale Diagnostics). After 1 h incubation at RT with agitation, wells were washed three times with PBS/0.1 % Tween-20 before being incubated with 1 ug/ml of sulfo-tagged antigen 2 (antigen of second antibody in PB. After incubation, plates were washed as above and signals revealed and measured using the manufactures *read* buffer and Image Sector 6000 instrument, respectively. Background values obtained from control parallel reactions in which biotinylated-antigen was substituted for a non-

biotinylated alternative, were subtracted from all signals. Duplicate values from at least 3 independent experiments were used in all calculations.

The higher the MSD signal the larger the amount of heavy chain exchange that has occurred.

The following antibodies were analysed:

Antibody	Mutations compared to wild type IgG4
IgG1 wt (wild type)	-
IgG4 wt (wild type)	-
IgG4 P	S241P
IgG4 mutant 28	C127S Y229C
IgG4 mutant 28 P	C127S Y229C S241P
IgG4 mutant 15	C127S G230C
IgG4 mutant 44	C127S G230C P238PAAA
IgG4 mutant 44P	C127S G230C P238PAAA, S241P
IgG4 mutant 48	C127S, S227P, Y229S, G230C, P237D, P238KTHT, S241P

Figures 16 to 20 show the results of the quantification Fab arm exchange *in vitro*, where the y-axis show the MSD signal, wherein the higher the level of the bar the higher the quantity of Fab arm exchange.

Figure 16 shows heavy chain exchange for IgG1 wild-type, IgG4 wild-type and mutants IgG4P, 28, 28P, 15, 44, 44P and 48 at two concentrations of GSH and at various timepoints.

Figure 17 shows heavy chain exchange for IgG4 wild-type and mutants 15, 44 and 48 at two concentrations of GSH at various timepoints. It can be seen that the more the IgG4 hinge is mutated to be of the IgG1 type the more exchange is reduced, as shown by mutant 48 having the lease exchange.

Figure 18 shows heavy chain exchange for IgG4 wild-type and mutants 15 and 28 at two concentrations of GSH at various timepoints. It can be seen that the mutation at position 229 (mutant 28) reduces exchange over 4 to 16 hours at both concentrations of reducing agent to a greater extent compared to the mutation at position 230 (mutant 15).

Figure 19 shows percentage change for mutants IgG4P, 15, 28, 44 and 48 in 0.5 mM GSH compared to wild-type IgG4. The exchange can be ranked as follows: IgG4 wt > 15 = 44 > 48 > 28.

Figure 20 shows percentage change for various mutants in 5 mM GSH compared to wild-type IgG4. The exchange can be ranked IgG4 wt > 15 = 44 > 48 > 28.

In good agreement with the literature (Labrijn 2011, Lewis 2009, Stubenrauch 2010, Labrijn 2009) we show that the S241P mutation in the IgG4 core-hinge represents a tool for preventing Fab-arm exchange. It can also be seen that mutant bispecific antibodies of the present invention would demonstrate less Fab arm exchange than has been shown at 0.5 mM GSH, which is 100 times higher than the 4-6 uM physiological GSH concentration of plasma (Zilmer. et al, 2005. Drug Design Reviews). Accordingly, bispecific antibodies may be created *in vitro* by Fab arm exchange under reducing conditions, which would then have significantly reduced Fab arm exchange *in vivo* compared to IgG4 wt.

Antibody Affinity:

The affinity of selected mutant IgG4 antibodies of the present invention to the target soluble cytokine may be measured by Biacore™. The assay format is capture of the IgG's on an anti-Fc surface followed by titration of soluble cytokine.

The term "k_d" (s^{-1}), refers to the dissociation rate constant of the antibody-antigen interaction. Said value is also referred to as the k_{off} value.

The term "k_a" (M^{-1} s^{-1}), as used herein, refers to the association rate constant of the antibody-antigen interaction.

The term "K_D" (M) or "K_D" (pM), as used herein, refers to the dissociation equilibrium constant of the antibody-antigen interaction.

Size exclusion (SEC) HPLC Analysis:

Approximately 50ug purified antibody was run on the HPLC using a S200 column. Abs 1 to 19 were used for the analysis. This result shows that non-covalently associated H2L2 is formed despite alterations to the DSB arrangements of a human IgG4 molecule.

Claims

1. A symmetric bispecific antibody of the class IgG4 comprising two heavy chains which each comprise a variable domain, C_H1 domain and a hinge region, wherein in each heavy chain: the cysteine in the C_H1 domain which forms an inter-chain disulphide bond with a cysteine in a light chain is substituted with another amino acid; and
optionally one or more of the amino acids positioned in the upper hinge region is substituted with cysteine, wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

2. A symmetric bispecific antibody according to claim 1, wherein the hinge region is an IgG1 type hinge.

3. A symmetric bispecific antibody according to claim 1 or 2 wherein the antibody is isolated.

4. A symmetric bispecific antibody according to any one of claims 1 to 3 where an inter-chain cysteine at position 127, numbered according to the Kabat numbering system, in the C_H1 domain in one or both heavy chains is substituted with another amino acid.

5. A symmetric bispecific antibody according to any one of claims 1 to 4, wherein the one or more amino acids positioned in the upper hinge region of the first heavy chain is substituted with cysteine is selected from 227, 228, 229 and 230, numbered according to the Kabat numbering system.

6. A symmetric bispecific antibody according to claim 5, wherein the glycine at position 230, numbered according to the Kabat numbering system, is substituted with cysteine.

7. A symmetric bispecific antibody according to claim 5, wherein the tyrosine at position 229, numbered according to the Kabat numbering system, is substituted with cysteine.

8. A symmetric bispecific antibody according to claim 5, wherein the lysine at position 228, numbered according to the Kabat numbering system, is substituted with cysteine.

9. A symmetric antibody according to claim 5, wherein the serine at position 227, numbered according to the Kabat numbering system, is substituted with cysteine.

10. A symmetric bispecific antibody according to any of claims 1 to 9, wherein the cysteine at position 239 and the cysteine at position 242, numbered according to the Kabat numbering system, in one or both heavy chains is/are substituted with another amino acid.

11. A symmetric bispecific antibody according to any of claim 1 to 10, wherein the cysteine at position 239, numbered according to the Kabat numbering system, in the first heavy chain is substituted with another amino acid.

12. A symmetric bispecific antibody according to any of claims 1 to 11, wherein the cysteine at position 242, numbered according to the Kabat numbering system, in the first heavy chain is substituted with another amino acid.

13. A symmetric bispecific antibody of the class IgG4 comprising two heavy chains which each comprise a variable domain, C_H1 domain and hinge region, wherein in each heavy chain the inter-chain cysteine at position 127, numbered according to the Kabat numbering system, is substituted with another amino acid; and the cysteine at position 239 and/or the cysteine at position 242, numbered according to the Kabat numbering system, is substituted with another amino acid, wherein the constant region sequence of each heavy chain is similar or identical and the variable region in each heavy chain is different.

14. A symmetric bispecific antibody according to any of claims 10 to 13, wherein the cysteine at position 239 and/or the cysteine at position 242 of a first heavy chain is substituted by a non-thiol containing amino acid.

15. A symmetric bispecific antibody according to claim 14, wherein the non-thiol containing amino acid is serine.

16. A symmetric bispecific antibody according to any preceding claim, wherein the cysteine at position 127 is substituted by a non-thiol containing amino acid.

17. A symmetric bispecific antibody according to claim 16, wherein the non-thiol containing amino acid is serine.

18. A symmetric bispecific antibody according to any preceding claim, wherein one or both heavy chains is/are mutated to insert three amino acids between amino acids 226-243, numbered according to the Kabat numbering system.

19. A symmetric bispecific antibody according to claim 18, wherein one or both heavy chains is/are mutated to insert three amino acids between positions 238 and 239, numbered according to the Kabat numbering system.

20. A symmetric bispecific antibody according to claim 19, wherein three alanines are inserted between positions 238 and 239, of the first heavy chain numbered according to the Kabat numbering system.

21. A symmetric bispecific antibody according to claim 19, wherein a threonine, a histidine and a further theronine are inserted between positions 238 and 239, of one or both of the heavy chains numbered according to the Kabat numbering system.

22. A symmetric bispecific antibody according to any preceding claim, wherein the serine at position 241, of one or both of the heavy chains numbered according to the Kabat numbering system, is/are substituted with proline.

23. A symmetric bispecific antibody according to any preceding claim, wherein in one or both of the heavy chains the glycine at position 230 is substituted with cysteine, the serine at position 227 is/are substituted with proline, the tyrosine at position 229 is substituted with serine, the proline at position 237 is substituted with aspartic acid, the proline at position 238 is substituted with lysine, the amino acid sequence threonine-histidine-threonine is inserted between positions 238 and 239 and the serine at position 241 is substituted with proline.

24. A symmetric bispecific antibody according to any preceding claim, wherein both the heavy chains comprises a C_H2 domain and/or a C_H3 domain.

25. A symmetric bispecific antibody according to any preceding claim, wherein hinge region in each heavy chain is identical.

26. A symmetric bispecific antibody according to any one of claims 1 to 25, wherein each heavy chain comprises an upper hinge region and core region of 12 to 17 amino acids in length, for example 15 amino acids in length.

27. A symmetric bispecific antibody according to any preceding claim, which further comprises one or two light chains.

28. An expression vector comprising a sequence which encodes an antibody as defined in any one of claims 1 to 27.

29. A host cell comprising a vector as defined in claim 28.

30. An antibody as defined in any one of claims 1 to 27 for use in the treatment of a disease or disorder.

31. A method of generating a symmetric bispecific antibody comprising the step of mixing a first IgG4 antibody with a second IgG4 antibody *ex vivo*, under conditions conducive to heavy chain exchange, wherein the antigen specificity of variable regions in the first the antibody are different to antigen specificity of the variable regions in the second antibody.

32. A method according to claim 31, wherein the conditions conducive to heavy chain exchange are reducing conditions, for example in the presence of a suitable buffer.

33. A method according to claim 31 or claim 32, wherein the first IgG4 antibody and the second IgG4 antibody each comprise a C_H1 domain and a hinge region as defined in any of claims 1 to 26.