Bispecific, tetravalent antigen binding proteins

The present invention relates to bispecific, tetravalent antigen binding proteins, methods for their production, pharmaceutical compositions containing said antibodies, and uses thereof.

Background of the Invention

Engineered proteins, such as bi- or multispecific antibodies capable of binding two or more antigens are known in the art. Such multispecific binding proteins can be generated using cell fusion, chemical conjugation, or recombinant DNA techniques.

A wide variety of recombinant multispecific antibody formats have been developed in the recent past, e.g. tetravalent bispecific antibodies by fusion of, e.g. an IgG antibody format and single chain domains (see e.g. Coloma, M.J., et. al., Nature Biotech. 15 (1997) 159-163; WO 2001/077342; and Morrison, S.L., Nature Biotech. 25 (2007) 1233-1234.

Also several other new formats wherein the antibody core structure (IgA, IgD, IgE, IgG or IgM) is no longer retained such as dia-, tria- or tetrabodies, minibodies, several single chain formats (scFv, Bis-scFv), which are capable of binding two or more antigens, have been developed (Holliger, P., et. al, Nature Biotech 23 (2005) 1126-1136; Fischer, N., and Léger, O., Pathobiology 74 (2007) 3-14; Shen, J., et. al., J. Immunol. Methods 318 (2007) 65-74; Wu, C., et al., Nature Biotech. 25 (2007) 1290-1297).

All such formats use linkers either to fuse the antibody core (IgA, IgD, IgE, IgG or IgM) to a further binding protein (e.g. scFv) or to fuse e.g. two Fab fragments or scFv (Fischer, N., and Léger, O., Pathobiology 74 (2007) 3-14). While it is obvious that linkers have advantages for the engineering of bispecific antibodies, they may also cause problems in therapeutic settings. Indeed, these foreign peptides might elicit an immune response against the linker itself or the junction between the protein and the linker. Further more, the flexible nature of these peptides makes them more prone to proteolytic cleavage, potentially leading to poor antibody stability, aggregation and increased immunogenicity. In addition one may want to retain effector functions, such as e.g. complement-dependent cytotoxicity (CDC) or

antibody dependent cellular cytotoxicity (ADCC), which are mediated through the Fc part by maintaining a high degree of similarity to naturally occurring antibodies.

Thus ideally, one should aim at developing bispecific antibodies that are very similar in general structure to naturally occurring antibodies (like IgA, IgD, IgE, IgG or IgM) with minimal deviation from human sequences.

In one approach bispecific antibodies that are very similar to natural antibodies have been produced using the quadroma technology (see Milstein, C., and Cuello, A.C., Nature 305 (1983) 537-540) based on the somatic fusion of two different hybridoma cell lines expressing murine monoclonal antibodies with the desired specificities of the bispecific antibody. Because of the random pairing of two different antibody heavy and light chains within the resulting hybrid-hybridoma (or quadroma) cell line, up to ten different antibody species are generated of which only one is the desired, functional bispecific antibody. Due to the presence of mispaired byproducts, and significantly reduced production yields, means sophisticated purification procedures are required (see e.g. Morrison, S.L., Nature Biotech. 25 (2007) 1233-1234). In general the same problem of mispaired byproducts remains if recombinant expression techniques are used.

An approach to circumvent the problem of mispaired byproducts, which is known as 'knobs-into-holes', aims at forcing the pairing of two different antibody heavy chains by introducing mutations into the CH3 domains to modify the contact interface. On one chain bulky amino acids were replaced by amino acids with short side chains to create a 'hole'. Conversely, amino acids with large side chains were introduced into the other CH3 domain, to create a 'knob'. By coexpressing these two heavy chains (and two identical light chains, which have to be appropriate for both heavy chains), high yields of heterodimer formation ('knob-hole') versus homodimer formation ('hole-hole' or 'knob-knob') was observed (Ridgway, J.B., et al., Protein Eng. 9 (1996) 617-621; and WO 96/027011). The percentage of heterodimer could be further increased by remodeling the interaction surfaces of the two CH3 domains using a phage display approach and the introduction of a disulfide bridge to stabilize the heterodimers (Merchant, A.M, et al., Nature Biotech 16 (1998) 677-681; Atwell, S., et al., J. Mol. Biol. 270 (1997) 26–35). New approaches for the knobs-into-holes technology are described in e.g. in EP 1 870 459 A1. Although this format appears very attractive, no data describing progression towards the clinic are currently available. One important constraint of this strategy is that the light chains of the two parent antibodies have to be identical

to prevent mispairing and formation of inactive molecules. Thus this technique is not appropriate for easily developing recombinant, bispecific antibodies against two antigens starting from two antibodies against the first and the second antigen, as either the heavy chains of these antibodies an/or the identical light chains have to be optimized. The same problem of mispairing remains when instead of bivalent, bispecific antibodies, tetravalent bispecific antibodies are expressed e.g. by fusion of additional Fab fragments (each identical to the Fab fragment of the respective antibody binding to first or second antigen) to each heavy chain C-terminus of the heterodimer. (see Fig 2)

WO 2006/093794 relates to heterodimeric protein binding compositions. WO 99/37791 describes multipurpose antibody derivatives. Morrison, S.L., et al the J. Immunolog, 160 (1998) 2802-2808 refers to the influence of variable region domain exchange on the functional properties of IgG.

Summary of the Invention

The invention comprises a bispecific, tetravalent antigen binding protein, comprising:

a) a modified heavy chain of a first antibody,
which specifically binds to a first antigen,
and to which C-terminus of said heavy chain additionally the VH-CH1 domains of said first antibody are fused via their N-terminus;
b) two light chains of said first antibody of a);
c) a modified heavy chain of a second antibody,
which specifically binds to a second antigen,
wherein the CH1 domain is replaced by the CL domain of said second antibody and to which C-terminus of said heavy chain additionally the VH-CL domains of said second antibody are fused via their N-terminus; and
d) two modified light chains of said second antibody of c),
wherein the CL domain is replaced by the CH1 domain of said second antibody.

A further embodiment of the invention is a method for the preparation of an antigen binding protein according to the invention

comprising the steps of
a) transforming a host cell with

- vectors comprising nucleic acid molecules encoding a bispecific antigen binding protein according to the invention

b) culturing the host cell under conditions that allow synthesis of said antibody molecule; and

c) recovering said antibody molecule from said culture.

A further embodiment of the invention is a host cell comprising

- vectors comprising nucleic acid molecules encoding an antigen binding protein according to the invention

A further embodiment of the invention is a pharmaceutical composition comprising an antigen binding protein according to the invention and at least one pharmaceutically acceptable excipient.

A further embodiment of the invention is a method for the treatment of a patient in need of therapy, characterized by administering to the patient a therapeutically effective amount of an antigen binding protein according to the invention.

According to the invention, the ratio of a desired bispecific, tetravalent antigen binding protein compared to undesired side products can be improved by the replacement of the CH1 with CL domain in the modified heavy chain under c) and the corresponding two modified light chains under d). In this way the undesired mispairing of the light chains of the antibody which specifically binds two a first antigen (of b) with the wrong VH-CH1 domains of the modified antibody heavy chains (of c) of the antibody which specifically binds two a second antigen can be reduced. And analogously the mispairing of the modified light chains of d) with the heavy chains of a). (see Fig 2 without these modifications and mispairing and Fig 3 with these CH1 – CL replacements (or exchanges) and no mispairing).

Detailed Description of the Invention

The invention comprises a bispecific, tetravalent antigen binding protein, comprising:

a) a modified heavy chain of a first antibody,
which specifically binds to a first antigen,
and to which C-terminus of said heavy chain additionally the VH-CH1 domains of said first antibody are fused via a peptide connector to their N-terminus;

b) two light chains of said first antibody of a);

c) a modified heavy chain of a second antibody,
which specifically binds to a second antigen,
wherein the CH1 domain is replaced by the CL domain of said second antibody and to which C-terminus of said heavy chain additionally the VH-CL domains of said second antibody are fused via a peptide connector to their N-terminus; and

d) two modified light chains of said second antibody of c),
wherein the CL domain is replaced by the CH1 domain of said second antibody.

According to the invention, the ratio of a desired bispecific, tetravalent antigen binding protein compared to undesired side products (due to mispairing of the light chains of the antibody with the wrong antibody heavy chains) can be improved by the replacement of the CH1 with CL domain in the modified heavy chain under c) and the corresponding two modified light chains under d). Mispairing in this connection means the association of i) the light chains of an antibody which specifically binds to a first antigen b) with modified heavy chain of an antibody which specifically binds to a second antigen); or ii) the light chains of an antibody which specifically binds to a second antigen b) with modified heavy chain of an antibody which specifically binds to a first antigen (see Fig 2) which leads to undesired inactive or not fully functional byproducts.

In an additional aspect of the invention such improved ratio of a desired bispecific, tetravalent antibody compared to undesired side products can be further improved by modifications of the CH3 domains of said antibodies which specifically bind to a first and second antigen.

Thus in one preferred embodiment of the invention the CH3 domains of said bispecific, tetravalent antigen binding protein (in the modified heavy chains of a and c)) according to the invention can be altered by the "knob-into-holes" technology which is described in detail with several examples in e.g. WO 96/027011, Ridgway, J.B., et al., Protein Eng 9 (1996) 617-621; and Merchant, A.M., et al., Nat Biotechnol 16 (1998) 677-681. In this method the interaction surfaces of the two CH3 domains are altered to increase the heterodimerisation of both heavy chains containing these two CH3 domains. Each of the two CH3 domains (of the two heavy chains) can be the "knob", while the other is the "hole". The introduction of a disulfide bridge further stabilizes the heterodimers (Merchant, A.M., et al., Nature Biotech 16 (1998) 677-681; Atwell, S., et al. J. Mol. Biol. 270 (1997) 26-35) and increases the yield.

Thus in one aspect of the invention said bispecific, tetravalent antigen binding protein is further characterized in that

the CH3 domain of the modified heavy chain of the antibody of a) and the CH3 domain of the modified heavy chain of the antibody of b) each meet at an interface which comprises an original interface between the antibody CH3 domains;

- wherein said interface is altered to promote the formation of the bispecific, tetravalent antigen binding protein, wherein the alteration is characterized in that:
  i) the CH3 domain of one heavy chain is altered,

so that within the original interface the CH3 domain of one heavy chain that meets the original interface of the CH3 domain of the other heavy chain within the bispecific, tetravalent antigen binding protein,

an amino acid residue is replaced with an amino acid residue having a larger side chain volume, thereby generating a protuberance within the interface of the CH3 domain of one heavy chain which is positionable in a cavity within the interface of the CH3 domain of the other heavy chain

and

ii) the CH3 domain of the other heavy chain is altered,
so that within the original interface of the second CH3 domain that meets the original interface of the first CH3 domain within the bispecific, tetravalent antigen binding protein

an amino acid residue is replaced with an amino acid residue having a smaller side chain volume, thereby generating a cavity within the interface of the second CH3 domain within which a protuberance within the interface of the first CH3 domain is positionable.

Preferably said amino acid residue having a larger side chain volume is selected from the group consisting of arginine (R), phenylalanine (F), tyrosine (Y), tryptophan (W).

Preferably said amino acid residue having a smaller side chain volume is selected from the group consisting of alanine (A), serine (S), threonine (T), valine (V).

In one aspect of the invention both CH3 domains are further altered by the introduction of cysteine (C) as amino acid in the corresponding positions of each

CH3 domain such that a disulfide bridge between both CH3 domains can be formed.

In one preferred embodiment, said bispecific, tetravalent antigen binding protein comprises a T366W mutation in the CH3 domain of the "knobs chain" and T366S, L368A, Y407V mutations in the CH3 domain of the "hole chain". An additional interchain disulfide bridge between the CH3 domains can also be used (Merchant, A.M., et al., Nature Biotech. 16 (1998) 677-681) e.g. by introducing a Y349C mutation into the CH3 domain of the "knobs" or "hole" chain and a E356C mutation or a S354C mutation into the CH3 domain of the other chain. Thus in a another preferred embodiment, said bispecific, tetravalent antigen binding protein comprises S354C, T366W mutations in one of the two CH3 domains and Y349C, T366S, L368A, Y407V mutations in the other of the two CH3 domains or said bispecific, tetravalent antigen binding protein comprises E356C, T366W mutations in one of the two CH3 domains and Y349C, T366S, L368A, Y407V mutations in the other of the two CH3 domains or said bispecific, tetravalent antigen binding protein comprises Y349C, T366W mutations in one of the two CH3 domains and E356C, T366S, L368A, Y407V mutations in the other of the two CH3 domains or said bispecific, tetravalent antigen binding protein comprises Y349C, T366W mutations in one of the two CH3 domains and S354C, T366S, L368A, Y407V mutations in the other of the two CH3 domains; (the additional Y349C mutation in one CH3 domain and the additional E356C or S354C mutation in the other CH3 domain forming a interchain disulfide bridge) (numbering always according to EU index of Kabat). But also other knobs-in-holes technologies as described by EP 1 870 459 A1, can be used alternatively or additionally. A preferred example for said trispecific or tetraspecific antibody are R409D; K370E mutations in the CH3 domain of the "knobs chain" and D399K; E357K mutations in the CH3 domain of the "hole chain" (numbering always according to EU index of Kabat).

In another preferred embodiment said trispecific or tetraspecific antibody comprises a T366W mutation in the CH3 domain of the "knobs chain" and T366S, L368A, Y407V mutations in the CH3 domain of the "hole chain" and additionally R409D; K370E mutations in the CH3 domain of the "knobs chain" and D399K; E357K mutations in the CH3 domain of the "hole chain."

In another preferred embodiment said trispecific or tetraspecific antibody comprises Y349C, T366W mutations in one of the two CH3 domains and S354C,

T366S, L368A, Y407V mutations in the other of the two CH3 domains or said trispecific or tetraspecific antibody comprises Y349C, T366W mutations in one of the two CH3 domains and S354C, T366S, L368A, Y407V mutations in the other of the two CH3 domains and additionally R409D; K370E mutations in the CH3 domain of the "knobs chain" and D399K; E357K mutations in the CH3 domain of the "hole chain".

The term "antibody" as used herein denotes a full length antibody consisting of two antibody heavy chains and two antibody light chains (see Fig. 1). A heavy chain of full length antibody is a polypeptide consisting in N-terminal to C-terminal direction of an antibody heavy chain variable domain (VH), an antibody constant heavy chain domain 1 (CH1), an antibody hinge region (HR), an antibody heavy chain constant domain 2 (CH2), and an antibody heavy chain constant domain 3 (CH3), abbreviated as VH-CH1-HR-CH2-CH3; and optionally an antibody heavy chain constant domain 4 (CH4) in case of an antibody of the subclass IgE. Preferably the heavy chain of full length antibody is a polypeptide consisting in N-terminal to C-terminal direction of VH, CH1, HR, CH2 and CH3. The light chain of full length antibody is a polypeptide consisting in N-terminal to C-terminal direction of an antibody light chain variable domain (VL), and an antibody light chain constant domain (CL), abbreviated as VL-CL. The antibody light chain constant domain (CL) can be κ (kappa) or λ (lambda). The antibody chains are linked together via inter-polypeptide disulfide bonds between the CL domain and the CH1 domain (i.e. between the light and heavy chain) and between the hinge regions of the full length antibody heavy chains. Examples of typical full length antibodies are natural antibodies like IgG (e.g. IgG 1 and IgG2), IgM, IgA, IgD, and IgE.) The antibodies according to the invention can be from a single species e.g. human, or they can be chimerized or humanized antibodies. The full length antibodies according to the invention comprise two antigen binding sites each formed by a pair of VH and VL, which both specifically bind to the same (first) antigen. The C-terminus of the heavy or light chain of said full length antibody denotes the last amino acid at the C-terminus of said heavy or light chain. Said antibody comprises two identical Fab fragments consisting of the VH and CH1 domain of the heavy chain and the VL and CL domain of the light chain. (see Fig. 1).

In an antigen binding protein according to the invention, the CH1 and the CL domains of the second antibody which specifically binds to a second antigen are

replaced by each other leading to the modified light chains under d) and the modified antibody heavy chain under c) to which C-terminus of said heavy chain additionally the VH-CL domains of said antibody (which specifically binds to a second antigen) are fused via a peptide connector to their N-terminus.

The“ VH-CH1 domains” of said antibody (which specifically binds to a first antigen) refers to the VH and CH1 domain of said antibody in N- to C-terminal direction. And the“ VH-CCL domains” of said antibody (which specifically binds to a second antigen) refers to the VH and CH1 domain of said antibody in N- to C-terminal direction.

The term “peptide connector” as used within the invention denotes a peptide with amino acid sequences, which is preferably of synthetic origin. These peptide connectors according to invention are used to fuse the antigen binding peptides to the C-or N-terminus of the full length and/or modified full length antibody chains to form a bispecific antigen binding protein according to the invention. Preferably said peptide connectors under c) are peptides with an amino acid sequence with a length of at least 5 amino acids, preferably with a length of 5 to 100, more preferably of 10 to 50 amino acids. In one embodiment said peptide connector is (GxS)n or (GxS)nGm with G = glycine, S = serine, and (x = 3, n= 3, 4, 5 or 6, and m= 0, 1, 2 or 3) or (x = 4,n= 2, 3, 4 or 5 and m= 0, 1, 2 or 3), preferably x = 4 and n= 2 or 3, more preferably with x = 4, n= 2. In one embodiment said peptide connector is $(G_4S)_2$.

The terms “binding site” or “antigen-binding site” as used herein denotes the region(s) of an antigen binding protein according to the invention to which a ligand (e.g. the antigen or antigen fragment of it) actually binds and which is derived from an antibody molecule or a fragment thereof (e.g. a Fab fragment). The antigen-binding site according to the invention comprises an antibody heavy chain variable domain (VH) and an antibody light chain variable domain (VL) of an antibody or antibody fragment which specifically binds to the desired antigen.

The antigen-binding sites (i.e. the pairs of VH/VL) that specifically bind to the desired antigen can be derived a) from known antibodies to the antigen or b) from new antibodies or antibody fragments obtained by de novo immunization methods using inter alia either the antigen protein or nucleic acid or fragments thereof or by phage display.

An antigen-binding site of an antigen binding protein of the invention contains six complementarity determining regions (CDRs) which contribute in varying degrees to the affinity of the binding site for antigen. There are three heavy chain variable domain CDRs (CDRH1, CDRH2 and CDRH3) and three light chain variable domain CDRs (CDRL1, CDRL2 and CDRL3). The extent of CDR and framework regions (FRs) is determined by comparison to a compiled database of amino acid sequences in which those regions have been defined according to variability among the sequences.

Antibody specificity refers to selective recognition of the antibody or antigen binding protein for a particular epitope of an antigen. Natural antibodies, for example, are monospecific. Bispecific antibodies are antibodies which have two different antigen-binding specificities. Where an antibody has more than one specificity, the recognized epitopes may be associated with a single antigen or with more than one antigen.

The term "monospecific" antibody or antigen binding protein as used herein denotes an antibody or antigen binding protein that has one or more binding sites each of which bind to the same epitope of the same antigen.

The term "valent" as used within the current application denotes the presence of a specified number of binding sites in an antibody molecule. A natural antibody for example or a full length antibody according to the invention has two binding sites and is bivalent. The term "tetravalent", denotes the presence of four binding sites in an antigen binding protein. The term "bispecific, tetravalent," as used herein denotes antigen binding protein according to the invention that has four antigen-binding sites of which two bind to a first antigen and two a second antigen (or another epitope of the antigen). Antigen binding proteins of the present invention have four binding sites and are tetravalent.

The full length antibodies of the invention comprise immunoglobulin constant regions of one or more immunoglobulin classes. Immunoglobulin classes include IgG, IgM, IgA, IgD, and IgE isotypes and, in the case of IgG and IgA, their subtypes. In a preferred embodiment, an full length antibody of the invention has a constant domain structure of an IgG type antibody.

The terms "monoclonal antibody" or "monoclonal antibody composition" as used herein refer to a preparation of antibody or antibody or antigen binding protein molecules of a single amino acid composition.

The term "chimeric antibody" refers to an antibody comprising a variable region, i.e., binding region, from one source or species and at least a portion of a constant region derived from a different source or species, usually prepared by recombinant DNA techniques. Chimeric antibodies comprising a murine variable region and a human constant region are preferred. Other preferred forms of "chimeric antibodies" encompassed by the present invention are those in which the constant region has been modified or changed from that of the original antibody to generate the properties according to the invention, especially in regard to C1q binding and/or Fc receptor (FcR) binding. Such chimeric antibodies are also referred to as "class-switched antibodies.". Chimeric antibodies are the product of expressed immunoglobulin genes comprising DNA segments encoding immunoglobulin variable regions and DNA segments encoding immunoglobulin constant regions. Methods for producing chimeric antibodies involve conventional recombinant DNA and gene transfection techniques are well known in the art. See, e.g., Morrison, S.L., et al., Proc. Natl. Acad. Sci. USA 81 (1984) 6851-6855; US 5,202,238 and US 5,204,244.

The term "humanized antibody" refers to antibodies in which the framework or "complementarity determining regions" (CDR) have been modified to comprise the CDR of an immunoglobulin of different specificity as compared to that of the parent immunoglobulin. In a preferred embodiment, a murine CDR is grafted into the framework region of a human antibody to prepare the "humanized antibody." See, e.g., Riechmann, L., et al., Nature 332 (1988) 323-327; and Neuberger, M.S., et al., Nature 314 (1985) 268-270. Particularly preferred CDRs correspond to those representing sequences recognizing the antigens noted above for chimeric antibodies. Other forms of "humanized antibodies" encompassed by the present invention are those in which the constant region has been additionally modified or changed from that of the original antibody to generate the properties according to the invention, especially in regard to C1q binding and/or Fc receptor (FcR) binding.

The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germ line immunoglobulin sequences. Human antibodies are well-known in the state of the

art (van Dijk, M.A., and van de Winkel, J.G., Curr. Opin. Chem. Biol. 5 (2001) 368-374). Human antibodies can also be produced in transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire or a selection of human antibodies in the absence of endogenous immunoglobulin production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge (see, e.g., Jakobovits, A., et al., Proc. Natl. Acad. Sci. USA 90 (1993) 2551-2555; Jakobovits, A., et al., Nature 362 (1993) 255-258; Brueggemann, M., et al., Year Immunol. 7 (1993) 33-40). Human antibodies can also be produced in phage display libraries (Hoogenboom, H.R., and Winter, G.J., Mol. Biol. 227 (1992) 381-388; Marks, J.D., et al., J. Mol. Biol. 222 (1991) 581-597). The techniques of Cole, S.P.C., et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole, S.P.C., et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985); and Boerner, P., et al., J. Immunol. 147 (1991) 86-95). As already mentioned for chimeric and humanized antibodies according to the invention the term "human antibody" as used herein also comprises such antibodies which are modified in the constant region to generate the properties according to the invention, especially in regard to C1q binding and/or FcR binding, e.g. by "class switching" i.e. change or mutation of Fc parts (e.g. from IgG1 to IgG4 and/or IgG1/IgG4 mutation.)

The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies isolated from a host cell such as a NS0 or CHO cell or from an animal (e.g. a mouse) that is transgenic for human immunoglobulin genes or antibodies expressed using a recombinant expression vector transfected into a host cell. Such recombinant human antibodies have variable and constant regions in a rearranged form. The recombinant human antibodies according to the invention have been subjected to in vivo somatic hypermutation. Thus, the amino acid sequences of the VH and VL regions of the recombinant antibodies are sequences that, while derived from and related to human germ line VH and VL sequences, may not naturally exist within the human antibody germ line repertoire in vivo.

The "variable domain" (variable domain of a light chain (VL), variable region of a heavy chain (VH) as used herein denotes each of the pair of light and heavy chains which is involved directly in binding the antibody to the antigen. The domains of variable human light and heavy chains have the same general structure and each

domain comprises four framework (FR) regions whose sequences are widely conserved, connected by three "hypervariable regions" (or complementarity determining regions, CDRs). The framework regions adopt a β-sheet conformation and the CDRs may form loops connecting the β-sheet structure. The CDRs in each chain are held in their three-dimensional structure by the framework regions and form together with the CDRs from the other chain the antigen binding site. The antibody heavy and light chain CDR3 regions play a particularly important role in the binding specificity/affinity of the antibodies according to the invention and therefore provide a further object of the invention.

The terms "hypervariable region" or "antigen-binding portion of an antibody" when used herein refer to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region comprises amino acid residues from the "complementarity determining regions" or "CDRs". "Framework" or "FR" regions are those variable domain regions other than the hypervariable region residues as herein defined. Therefore, the light and heavy chains of an antibody comprise from N- to C-terminus the domains FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. CDRs on each chain are separated by such framework amino acids. Especially, CDR3 of the heavy chain is the region which contributes most to antigen binding. CDR and FR regions are determined according to the standard definition of Kabat, et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991).

As used herein, the terms “binding”, “specifically binding”, or “ which specifically binds to” refers to the binding of the antibody/antigen binding protein to an epitope of the antigen in an in vitro assay, preferably in an plasmon resonance assay (BIAcore, GE-Healthcare Uppsala, Sweden) with purified wild-type antigen. The affinity of the binding is defined by the terms ka (rate constant for the association of the antibody (or antibody or antigen binding protein) from the antibody/antigen complex), k_D (dissociation constant), and K_D (k_D/ka). Binding or specifically binding means a binding affinity (K_D) of 10^{-8} mol/l or less, preferably 10^{-9} M to 10^{-13} mol/l. Thus, a bispecific, tetravalent antigen binding protein according to the invention is specifically binding to each antigen for which it is specific with a binding affinity (K_D) of 10^{-8} mol/l or less, preferably 10^{-9} M to 10^{-13} mol/l.

Binding of the antibody to the FcγRIII can be investigated by a BIAcore assay (GE-Healthcare Uppsala, Sweden). The affinity of the binding is defined by the

terms ka (rate constant for the association of the antibody from the antibody/antigen complex), k_D (dissociation constant), and K_D (k_D/ka).

The term "epitope" includes any polypeptide determinant capable of specific binding to an antibody. In certain embodiments, epitope determinant include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl, or sulfonyl, and, in certain embodiments, may have specific three dimensional structural characteristics, and or specific charge characteristics. An epitope is a region of an antigen that is bound by an antibody.

In certain embodiments, an antibody is said to specifically bind an antigen when it preferentially recognizes its target antigen in a complex mixture of proteins and/or macromolecules.

In a further embodiment the bispecific antigen binding protein according to the invention is characterized in that said full length antibody is of human IgG1 subclass, or of human IgG1 subclass with the mutations L234A and L235A.

In a further embodiment the bispecific antigen binding protein according to the invention is characterized in that said full length antibody is of human IgG2 subclass.

In a further embodiment the bispecific antigen binding protein according to the invention is characterized in that said full length antibody is of human IgG3 subclass.

In a further embodiment the bispecific antigen binding protein according to the invention is characterized in that said full length antibody is of human IgG4 subclass or, of human IgG4 subclass with the additional mutation S228P.

Preferably the bispecific antigen binding protein according to the invention is characterized in that said full length antibody is of human IgG1 subclass, of human IgG4 subclass with the additional mutation S228P.

It has now been found that the bispecific antigen binding proteins according to the invention have improved characteristics such as biological or pharmacological activity, pharmacokinetic properties or toxicity. They can be used e.g. for the treatment of diseases such as cancer.

The term "constant region" as used within the current applications denotes the sum of the domains of an antibody other than the variable region. The constant region is not involved directly in binding of an antigen, but exhibits various effector functions. Depending on the amino acid sequence of the constant region of their heavy chains, antibodies are divided in the classes: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses, such as IgG1, IgG2, IgG3, and IgG4, IgA1 and IgA2. The heavy chain constant regions that correspond to the different classes of antibodies are called α, δ, ε, γ, and μ, respectively. The light chain constant regions (CL) which can be found in all five antibody classes are called κ (kappa) and λ (lambda).

The term "constant region derived from human origin" as used in the current application denotes a constant heavy chain region of a human antibody of the subclass IgG1, IgG2, IgG3, or IgG4 and/or a constant light chain kappa or lambda region. Such constant regions are well known in the state of the art and e.g. described by Kabat, E.A., (see e.g. Johnson, G. and Wu, T.T., Nucleic Acids Res. 28 (2000) 214-218; Kabat, E.A., et al., Proc. Natl. Acad. Sci. USA 72 (1975) 2785-2788).

While antibodies of the IgG4 subclass show reduced Fc receptor (FcγRIIIa) binding, antibodies of other IgG subclasses show strong binding. However Pro238, Asp265, Asp270, Asn297 (loss of Fc carbohydrate), Pro329, Leu234, Leu235, Gly236, Gly237, Ile253, Ser254, Lys288, Thr307, Gln311, Asn434, and His435 are residues which, if altered, provide also reduced Fc receptor binding (Shields, R.L., et al., J. Biol. Chem. 276 (2001) 6591-6604; Lund, J., et al., FASEB J. 9 (1995) 115-119; Morgan, A., et al., Immunology 86 (1995) 319-324; EP 0 307 434).

In one embodiment an antigen binding protein according to the invention has a reduced FcR binding compared to an IgG1 antibody and the full length parent antibody is in regard to FcR binding of IgG4 subclass or of IgG1 or IgG2 subclass with a mutation in S228, L234, L235 and/or D265, and/ or contains the PVA236 mutation. In one embodiment the mutations in the full length parent antibody are S228P, L234A, L235A, L235E and/or PVA236. In another embodiment the mutations in the full length parent antibody are in IgG4 S228P and in IgG1 L234A and L235A.

The constant region of an antibody is directly involved in ADCC (antibody-dependent cell-mediated cytotoxicity) and CDC (complement-dependent

cytotoxicity). Complement activation (CDC) is initiated by binding of complement factor C1q to the constant region of most IgG antibody subclasses. Binding of C1q to an antibody is caused by defined protein-protein interactions at the so called binding site. Such constant region binding sites are known in the state of the art and described e.g. by Lukas, T.J., et al., J. Immunol. 127 (1981) 2555-2560; Brunhouse, R. and Cebra, J.J., Mol. Immunol. 16 (1979) 907-917; Burton, D.R., et al., Nature 288 (1980) 338-344; Thomason, J.E., et al., Mol. Immunol. 37 (2000) 995-1004; Idusogie, E.E., et al., J. Immunol. 164 (2000) 4178-4184; Hezareh, M., et al., J. Virol. 75 (2001) 12161-12168; Morgan, A., et al., Immunology 86 (1995) 319-324; and EP 0 307 434. Such constant region binding sites are, e.g., characterized by the amino acids L234, L235, D270, N297, E318, K320, K322, P331, and P329 (numbering according to EU index of Kabat).

The term "antibody-dependent cellular cytotoxicity (ADCC)" refers to lysis of human target cells by an antigen binding protein according to the invention in the presence of effector cells. ADCC is measured preferably by the treatment of a preparation of antigen expressing cells with an antigen binding protein according to the invention in the presence of effector cells such as freshly isolated PBMC or purified effector cells from buffy coats, like monocytes or natural killer (NK) cells or a permanently growing NK cell line.

The term "complement-dependent cytotoxicity (CDC)" denotes a process initiated by binding of complement factor C1q to the Fc part of most IgG antibody subclasses. Binding of C1q to an antibody is caused by defined protein-protein interactions at the so called binding site. Such Fc part binding sites are known in the state of the art (see above). Such Fc part binding sites are, e.g., characterized by the amino acids L234, L235, D270, N297, E318, K320, K322, P331, and P329 (numbering according to EU index of Kabat). Antibodies of subclass IgG1, IgG2, and IgG3 usually show complement activation including C1q and C3 binding, whereas IgG4 does not activate the complement system and does not bind C1q and/or C3.

Cell-mediated effector functions of monoclonal antibodies can be enhanced by engineering their oligosaccharide component as described in Umana, P., et al., Nature Biotechnol. 17 (1999) 176-180, and US 6,602,684. IgG1 type antibodies, the most commonly used therapeutic antibodies, are glycoproteins that have a conserved N-linked glycosylation site at Asn297 in each CH2 domain. The two complex biantennary oligosaccharides attached to Asn297 are buried between the

CH2 domains, forming extensive contacts with the polypeptide backbone, and their presence is essential for the antibody to mediate effector functions such as antibody dependent cellular cytotoxicity (ADCC) (Lifely, M., R., et al., Glycobiology 5 (1995) 813-822; Jefferis, R., et al., Immunol. Rev. 163 (1998) 59-76; Wright, A., and Morrison, S., L., Trends Biotechnol. 15 (1997) 26-32). Umana, P., et al. Nature Biotechnol. 17 (1999) 176-180 and WO 99/54342 showed that overexpression in Chinese hamster ovary (CHO) cells of ß(1,4)-N-acetylglucosaminyltransferase III ("GnTIII"), a glycosyltransferase catalyzing the formation of bisected oligosaccharides, significantly increases the in vitro ADCC activity of antibodies. Alterations in the composition of the Asn297 carbohydrate or its elimination affect also binding to FcγR and C1q (Umana, P., et al., Nature Biotechnol. 17 (1999) 176-180; Davies, J., et al., Biotechnol. Bioeng. 74 (2001) 288-294; Mimura, Y., et al., J. Biol. Chem. 276 (2001) 45539-45547; Radaev, S., et al., J. Biol. Chem. 276 (2001) 16478-16483; Shields, R., L., et al., J. Biol. Chem. 276 (2001) 6591-6604; Shields, R., L., et al., J. Biol. Chem. 277 (2002) 26733-26740; Simmons, L., C., et al., J. Immunol. Methods 263 (2002) 133-147).

Methods to enhance cell-mediated effector functions of monoclonal antibodies are reported e.g. in WO 2005/018572, WO 2006/116260, WO 2006/114700, WO 2004/065540, WO 2005/011735, WO 2005/027966, WO 1997/028267, US 2006/0134709, US 2005/0054048, US 2005/0152894, WO 2003/035835, WO 2000/061739.

In one preferred embodiment of the invention, the bispecific antigen binding protein is glycosylated (if it comprises an Fc part of IgG1, IgG2, IgG3 or IgG4 subclass, preferably of IgG1 or IgG3 subclass) with a sugar chain at Asn297 whereby the amount of fucose within said sugar chain is 65% or lower (Numbering according to Kabat). In another embodiment is the amount of fucose within said sugar chain is between 5% and 65%, preferably between 20% and 40%. "Asn297" according to the invention means amino acid asparagine located at about position 297 in the Fc region. Based on minor sequence variations of antibodies, Asn297 can also be located some amino acids (usually not more than $\pm$3 amino acids) upstream or downstream of position 297, i.e. between position 294 and 300. In one embodiment the glycosylated antigen binding protein according to the invention the IgG subclass is of human IgG1 subclass, of human IgG1 subclass with the mutations L234A and L235A or of IgG3 subclass. In a further embodiment the amount of N-glycolylneuraminic acid (NGNA) is 1% or less and/or the amount of

N-terminal alpha-1,3-galactose is 1% or less within said sugar chain. The sugar chain show preferably the characteristics of N-linked glycans attached to Asn297 of an antibody recombinantly expressed in a CHO cell.

The term "the sugar chains show characteristics of N-linked glycans attached to Asn297 of an antibody recombinantly expressed in a CHO cell" denotes that the sugar chain at Asn297 of the full length parent antibody according to the invention has the same structure and sugar residue sequence except for the fucose residue as those of the same antibody expressed in unmodified CHO cells, e.g. as those reported in WO 2006/103100.

The term "NGNA" as used within this application denotes the sugar residue N-glycolylneuraminic acid.

Glycosylation of human IgG1 or IgG3 occurs at Asn297 as core fucosylated biantennary complex oligosaccharide glycosylation terminated with up to two Gal residues. Human constant heavy chain regions of the IgG1 or IgG3 subclass are reported in detail by Kabat, E., A., et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991), and by Brüggemann, M., et al., J. Exp. Med. 166 (1987) 1351-1361; Love, T.W., et al., Methods Enzymol. 178 (1989) 515-527. These structures are designated as G0, G1 (α-1,6- or α-1,3-), or G2 glycan residues, depending from the amount of terminal Gal residues (Raju, T.S., Bioprocess Int. 1 (2003) 44-53). CHO type glycosylation of antibody Fc parts is e.g. described by Routier, F.H., Glycoconjugate J. 14 (1997) 201-207. Antibodies which are recombinantly expressed in non-glycomodified CHO host cells usually are fucosylated at Asn297 in an amount of at least 85%. The modified oligosaccharides of the full length parent antibody may be hybrid or complex. Preferably the bisected, reduced/not-fucosylated oligosaccharides are hybrid. In another embodiment, the bisected, reduced/not-fucosylated oligosaccharides are complex.

According to the invention "amount of fucose" means the amount of said sugar within the sugar chain at Asn297, related to the sum of all glycostructures attached to Asn297 (e.g. complex, hybrid and high mannose structures) measured by MALDI-TOF mass spectrometry and calculated as average value. The relative amount of fucose is the percentage of fucose-containing structures related to all glycostructures identified in an N-Glycosidase F treated sample (e.g. complex, hybrid and oligo- and high-mannose structures, resp.) by MALDI-TOF.

The antigen binding protein according to the invention is produced by recombinant means. Thus, one aspect of the current invention is a nucleic acid encoding the antigen binding protein according to the invention and a further aspect is a cell comprising said nucleic acid encoding an antigen binding protein according to the invention. Methods for recombinant production are widely known in the state of the art and comprise protein expression in prokaryotic and eukaryotic cells with subsequent isolation of the antigen binding protein and usually purification to a pharmaceutically acceptable purity. For the expression of the antibodies as aforementioned in a host cell, nucleic acids encoding the respective modified light and heavy chains are inserted into expression vectors by standard methods. Expression is performed in appropriate prokaryotic or eukaryotic host cells like CHO cells, NS0 cells, SP2/0 cells, HEK293 cells, COS cells, PER.C6 cells, yeast, or E.coli cells, and the antigen binding protein is recovered from the cells (supernatant or cells after lysis). General methods for recombinant production of antibodies are well-known in the state of the art and described, for example, in the review articles of Makrides, S.C., Protein Expr. Purif. 17 (1999) 183-202; Geisse, S., et al., Protein Expr. Purif. 8 (1996) 271-282; Kaufman, R.J., Mol. Biotechnol. 16 (2000) 151-161; Werner, R.G., Drug Res. 48 (1998) 870-880.

The bispecific antigen binding proteins according to the invention are suitably separated from the culture medium by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography. DNA or RNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures. The hybridoma cells can serve as a source of such DNA and RNA. Once isolated, the DNA may be inserted into expression vectors, which are then transfected into host cells such as HEK 293 cells, CHO cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of recombinant monoclonal antibodies in the host cells.

Amino acid sequence variants (or mutants) of the bispecific antigen binding protein are prepared by introducing appropriate nucleotide changes into the antigen binding protein DNA, or by nucleotide synthesis. Such modifications can be performed, however, only in a very limited range, e.g. as described above. For example, the modifications do not alter the above mentioned antibody characteristics such as the IgG isotype and antigen binding, but may improve the yield of the recombinant production, protein stability or facilitate the purification.

The term "host cell" as used in the current application denotes any kind of cellular system which can be engineered to generate the antibodies according to the current invention. In one embodiment HEK293 cells and CHO cells are used as host cells. As used herein, the expressions "cell," "cell line," and "cell culture" are used interchangeably and all such designations include progeny. Thus, the words "transformants" and "transformed cells" include the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Variant progeny that have the same function or biological activity as screened for in the originally transformed cell are included.

Expression in NS0 cells is described by, e.g., Barnes, L.M., et al., Cytotechnology 32 (2000) 109-123; Barnes, L.M., et al., Biotech. Bioeng. 73 (2001) 261-270. Transient expression is described by, e.g., Durocher, Y., et al., Nucl. Acids. Res. 30 (2002) E9. Cloning of variable domains is described by Orlandi, R., et al., Proc. Natl. Acad. Sci. USA 86 (1989) 3833-3837; Carter, P., et al., Proc. Natl. Acad. Sci. USA 89 (1992) 4285-4289; and Norderhaug, L., et al., J. Immunol. Methods 204 (1997) 77-87. A preferred transient expression system (HEK 293) is described by Schlaeger, E.-J., and Christensen, K., in Cytotechnology 30 (1999) 71-83 and by Schlaeger, E.-J., in J. Immunol. Methods 194 (1996) 191-199.

The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, enhancers and polyadenylation signals.

A nucleic acid is "operably linked" when it is placed in a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading frame. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

Purification of antibodies is performed in order to eliminate cellular components or other contaminants, e.g. other cellular nucleic acids or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, agarose gel electrophoresis, and others well known in the art. See Ausubel, F., et al., ed. Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York (1987). Different methods are well established and widespread used for protein purification, such as affinity chromatography with microbial proteins (e.g. protein A or protein G affinity chromatography), ion exchange chromatography (e.g. cation exchange (carboxymethyl resins), anion exchange (amino ethyl resins) and mixed-mode exchange), thiophilic adsorption (e.g. with beta-mercaptoethanol and other SH ligands), hydrophobic interaction or aromatic adsorption chromatography (e.g. with phenyl-sepharose, aza-arenophilic resins, or m-aminophenylboronic acid), metal chelate affinity chromatography (e.g. with Ni(II)- and Cu(II)-affinity material), size exclusion chromatography, and electrophoretical methods (such as gel electrophoresis, capillary electrophoresis) (Vijayalakshmi, M.A., Appl. Biochem. Biotech. 75 (1998) 93-102).

One aspect of the invention is a pharmaceutical composition comprising an antigen binding protein according to the invention. Another aspect of the invention is the use of an antigen binding protein according to the invention for the manufacture of a pharmaceutical composition. A further aspect of the invention is a method for the manufacture of a pharmaceutical composition comprising an antigen binding protein according to the invention. In another aspect, the present invention provides a composition, e.g. a pharmaceutical composition, containing an antigen binding protein according to the present invention, formulated together with a pharmaceutical carrier.

Another aspect of the invention is said pharmaceutical composition for the treatment of cancer.

Another aspect of the invention is the bispecific antigen binding protein according to the invention for the treatment of cancer.

Another aspect of the invention is the use of an antigen binding protein according to the invention for the manufacture of a medicament for the treatment of cancer.

Another aspect of the invention is a method of treatment of a patient suffering from cancer by administering an antigen binding protein according to the invention to said patient in the need of such treatment.

As used herein, "pharmaceutical carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (e.g. by injection or infusion).

A composition of the present invention can be administered by a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. To administer a compound of the invention by certain routes of administration, it may be necessary to coat the compound with, or co-administer the compound with, a material to prevent its inactivation. For example, the compound may be administered to a subject in an appropriate carrier, for example, liposomes, or a diluent. Pharmaceutically acceptable diluents include saline and aqueous buffer solutions. Pharmaceutical carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art.

The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intra-arterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intra-articular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion.

The term cancer as used herein refers to proliferative diseases, such as lymphomas, lymphocytic leukemias, lung cancer, non small cell lung (NSCL) cancer, bronchioloalviolar cell lung cancer, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, gastric cancer, colon cancer, breast cancer, uterine cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the

vagina, carcinoma of the vulva, Hodgkin's Disease, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, prostate cancer, cancer of the bladder, cancer of the kidney or ureter, renal cell carcinoma, carcinoma of the renal pelvis, mesothelioma, hepatocellular cancer, biliary cancer, neoplasms of the central nervous system (CNS), spinal axis tumors, brain stem glioma, glioblastoma multiforme, astrocytomas, schwanomas, ependymonas, medulloblastomas, meningiomas, squamous cell carcinomas, pituitary adenoma and Ewings sarcoma, including refractory versions of any of the above cancers, or a combination of one or more of the above cancers.

These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms may be ensured both by sterilization procedures, supra, and by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol, sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

Regardless of the route of administration selected, the compounds of the present invention, which may be used in a suitable hydrated form, and/or the pharmaceutical compositions of the present invention, are formulated into pharmaceutically acceptable dosage forms by conventional methods known to those of skill in the art.

Actual dosage levels of the active ingredients in the pharmaceutical compositions of the present invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present invention employed, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general

health and prior medical history of the patient being treated, and like factors well known in the medical arts.

The composition must be sterile and fluid to the extent that the composition is deliverable by syringe. In addition to water, the carrier preferably is an isotonic buffered saline solution.

Proper fluidity can be maintained, for example, by use of coating such as lecithin, by maintenance of required particle size in the case of dispersion and by use of surfactants. In many cases, it is preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol or sorbitol, and sodium chloride in the composition.

As used herein, the expressions "cell," "cell line," and "cell culture" are used interchangeably and all such designations include progeny. Thus, the words "transformants" and "transformed cells" include the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Variant progeny that have the same function or biological activity as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

The term “transformation” as used herein refers to process of transfer of a vectors/nucleic acid into a host cell. If cells without formidable cell wall barriers are used as host cells, transfection is carried out e.g. by the calcium phosphate precipitation method as described by Graham and Van der Eh, Virology 52 (1978) 546ff. However, other methods for introducing DNA into cells such as by nuclear injection or by protoplast fusion may also be used. If prokaryotic cells or cells which contain substantial cell wall constructions are used, e.g. one method of transfection is calcium treatment using calcium chloride as described by Cohen, S.N, et al., PNAS 69 (1972) 2110-2114.

As used herein, "expression" refers to the process by which a nucleic acid is transcribed into mRNA and/or to the process by which the transcribed mRNA (also referred to as transcript) is subsequently being translated into peptides, polypeptides, or proteins. The transcripts and the encoded polypeptides are collectively referred to as gene product. If the polynucleotide is derived from genomic DNA, expression in a eukaryotic cell may include splicing of the mRNA.

A "vector" is a nucleic acid molecule, in particular self-replicating, which transfers an inserted nucleic acid molecule into and/or between host cells. The term includes vectors that function primarily for insertion of DNA or RNA into a cell (e.g., chromosomal integration), replication of vectors that function primarily for the replication of DNA or RNA, and expression vectors that function for transcription and/or translation of the DNA or RNA. Also included are vectors that provide more than one of the functions as described.

An "expression vector" is a polynucleotide which, when introduced into an appropriate host cell, can be transcribed and translated into a polypeptide. An "expression system" usually refers to a suitable host cell comprised of an expression vector that can function to yield a desired expression product.

The following examples, sequence listing and figures are provided to aid the understanding of the present invention, the true scope of which is set forth in the appended claims. It is understood that modifications can be made in the procedures set forth without departing from the spirit of the invention.

Description of the Sequence Listing

SEQ ID NO:1 modified heavy chain of <Ang-2> antibody with C-terminal fused <Ang-2> antibody VH-CH1 domains

SEQ ID NO:2 unmodified light chain <Ang-2> antibody

SEQ ID NO:3 modified heavy chain of <VEGF> antibody with CH1-CL exchange and with C-terminal fused <VEGF> antibody VH-CL domains

SEQ ID NO:4 modified light chain of <VEGF> antibody with CH1-CL exchange (<VEGF> antibody VL-CH1 domains)

Description of the Figures

Figure 1 Schematic structure of a full length antibody without CH4 domain specifically binding to a first antigen 1 with two pairs of heavy and light chain which comprise variable and constant domains in a typical order.

Figure 2 Schematic structure of two mispairing possibilities (out of four) leading to an exemplary undesired byproduct reducing the yield of a bispecific, tetravalent antibody,

which binds to a first antigen 1 and a second antigen 2 and in which no domains are exchanged.

Figure 3 Schematic structure of a bispecific, tetravalent antigen binding protein according to the invention - the mispairing is impaired by the replacement of CH1 and CL domain in the heavy and light chains of the antibody which specifically binds to the second antigen.

Figure 4 Schematic structure of an exemplary bispecific, tetravalent antigen binding protein according to the invention with knobs and hole.

Examples

Materials & general methods

General information regarding the nucleotide sequences of human immunoglobulins light and heavy chains is given in: Kabat, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991). Amino acids of antibody chains are numbered and referred to according to EU numbering (Edelman, G.M., et al., Proc. Natl. Acad. Sci. USA 63 (1969) 78-85; Kabat, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD, (1991)).

Recombinant DNA techniques

Standard methods are used to manipulate DNA as described in Sambrook, J. et al., Molecular cloning: A laboratory manual; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989. The molecular biological reagents are used according to the manufacturer's instructions.

Gene synthesis

Desired gene segments are prepared from oligonucleotides made by chemical synthesis. The gene segments, which are flanked by singular restriction endonuclease cleavage sites, are assembled by annealing and ligation of oligonucleotides including PCR amplification and subsequently cloned via the indicated restriction sites e.g. KpnI/ SacI or AscI/PacI into a pPCRScript (Stratagene) based pGA4 cloning vector. The DNA sequences of the subcloned gene fragments are confirmed by DNA sequencing. Gene synthesis fragments are ordered according to given specifications at Geneart (Regensburg, Germany).

DNA sequence determination

DNA sequences are determined by double strand sequencing performed at MediGenomix GmbH (Martinsried, Germany) or Sequiserve GmbH (Vaterstetten, Germany).

DNA and protein sequence analysis and sequence data management

The GCG's (Genetics Computer Group, Madison, Wisconsin) software package version 10.2 and Infomax's Vector NT1 Advance suite version 8.0 is used for sequence creation, mapping, analysis, annotation and illustration.

Expression vectors

For the expression of the described bispecific tetravalent antibodies variants of expression plasmids for transient expression (e.g. in HEK293 EBNA or HEK293-F) cells based either on a cDNA organization with or without a CMV-Intron A promoter or on a genomic organization with a CMV promoter are applied.

Beside the antibody expression cassette the vectors contained:

- an origin of replication which allows replication of this plasmid in E. coli, and
- a ß-lactamase gene which confers ampicillin resistance in E. coli.

The transcription unit of the antibody gene is composed of the following elements:

- unique restriction site(s) at the 5' end
- the immediate early enhancer and promoter from the human cytomegalovirus,
- followed by the Intron A sequence in the case of the cDNA organization,
- a 5'-untranslated region of a human antibody gene,
- a immunoglobulin heavy chain signal sequence,
- the human bispecific tetravalent antibody chain (wildtype or with domain exchange) either as cDNA or as genomic organization with an the immunoglobulin exon-intron organization
- a 3' untranslated region with a polyadenylation signal sequence, and
- unique restriction site(s) at the 3' end.

The fusion genes comprising the described antibody chains as described below are generated by PCR and/or gene synthesis and assembled with known recombinant methods and techniques by connection of the according nucleic acid segments e.g. using unique restriction sites in the respective vectors. The subcloned nucleic acid

sequences are verified by DNA sequencing. For transient transfections larger quantities of the plasmids are prepared by plasmid preparation from transformed E. coli cultures (Nucleobond AX, Macherey-Nagel).

Cell culture techniques

Standard cell culture techniques are used as described in Current Protocols in Cell Biology, Bonifacino, J.S., Dasso, M., Harford, J.B., Lippincott-Schwartz, J. and Yamada, K.M. (eds.), John Wiley & Sons, Inc. (2000).

Bispecific tetravalent antibodies are expressed by transient co-transfection of the respective three expression plasmids in adherently growing HEK293-EBNA or in HEK29-F cells growing in suspension as described below.

Transient transfections in HEK293-EBNA system

Bispecific tetravalent antibodies are expressed by transient co-transfection of the respective three expression plasmids (e.g. encoding the modified heavy chain, as well as the corresponding light and modified light chain) in adherently growing HEK293-EBNA cells (human embryonic kidney cell line 293 expressing Epstein-Barr-Virus nuclear antigen; American type culture collection deposit number ATCC # CRL-10852, Lot. 959 218) cultivated in DMEM (Dulbecco's modified Eagle's medium, Gibco) supplemented with 10% Ultra Low IgG FCS (fetal calf serum, Gibco), 2 mM L-Glutamine (Gibco), and 250 µg/ml Geneticin (Gibco). For transfection FuGENE™ 6 Transfection Reagent (Roche Molecular Biochemicals) is used in a ratio of FuGENE™ reagent (µl) to DNA (µg) of 4:1 (ranging from 3:1 to 6:1). Proteins are expressed from the respective plasmids using a molar ratio of (modified and wildtype) light chain and modified heavy chain encoding plasmids of 1:1:1 (equimolar) ranging from 1:1:2 to 2:2:1, respectively. Cells are feeded at day 3 with L-Glutamine ad 4 mM, Glucose [Sigma] and NAA [Gibco]. Bispecific tetravalent antibody containing cell culture supernatants are harvested from day 5 to 11 after transfection by centrifugation and stored at -20°C. General information regarding the recombinant expression of human immunoglobulins in e.g. HEK293 cells is given in: Meissner, P., et al., Biotechnol. Bioeng. 75 (2001) 197-203.

Transient transfections in HEK293-F system

Alternatively, bispecific tetravalent antibodies are generated by transient transfection of the respective plasmids (e.g. encoding the modified heavy chain, as well as the corresponding light and modified light chain) using the HEK293-F system (Invitrogen) according to the manufacturer's instruction. Briefly, HEK293-

F cells (Invitrogen) growing in suspension either in a shake flask or in a stirred fermenter in serumfree FreeStyle 293 expression medium (Invitrogen) are transfected with a mix of the three expression plasmids as described above and 293fectin or fectin (Invitrogen). For 2 L shake flask (Corning) HEK293-F cells are seeded at a density of 1.0E*6 cells/mL in 600 mL and incubated at 120 rpm, 8% CO2. The day after the cells are transfected at a cell density of ca. 1.5E*6 cells/mL with ca. 42 mL mix of A) 20 mL Opti-MEM (Invitrogen) with 600 µg total plasmid DNA (1 µg/mL) encoding the modified heavy chain, the corresponding light chain and the corresponding modified light chain in an equimolar ratio and B) 20 ml Opti-MEM + 1.2 mL 293 fectin or fectin (2 µl/mL). According to the glucose consumption glucose solution is added during the course of the fermentation. The supernatant containing the secreted antibody is harvested after 5-10 days and antibodies are either directly purified from the supernatant or the supernatant is frozen and stored.

Protein determination

The protein concentration of purified bispecific tetravalent antibodies and derivatives is determined by determining the optical density (OD) at 280 nm, using the molar extinction coefficient calculated on the basis of the amino acid sequence according to Pace, C.N., et al., Protein Science, 1995, 4, 2411-1423.

Antibody concentration determination in supernatants

The concentration of bispecific tetravalent antibodies in cell culture supernatants is estimated by immunoprecipitation with Protein A Agarose-beads (Roche). 60 µL Protein A Agarose beads are washed three times in TBS-NP40 (50 mM Tris, pH 7.5, 150 mM NaCl, 1% Nonidet-P40). Subsequently, 1 -15 mL cell culture supernatant are applied to the Protein A Agarose beads pre-equilibrated in TBS-NP40. After incubation for at 1 h at room temperature the beads are washed on an Ultrafree-MC-filter column (Amicon] once with 0.5 mL TBS-NP40, twice with 0.5 mL 2x phosphate buffered saline (2xPBS, Roche) and briefly four times with 0.5 mL 100 mM Na-citrate pH 5,0. Bound antibody is eluted by addition of 35 µl NuPAGE® LDS Sample Buffer (Invitrogen). Half of the sample is combined with NuPAGE® Sample Reducing Agent or left unreduced, respectively, and heated for 10 min at 70°C. Consequently, 5-30 µl are applied to an 4-12% NuPAGE® Bis-Tris SDS-PAGE (Invitrogen) (with MOPS buffer for non-reduced SDS-PAGE and MES buffer with NuPAGE® Antioxidant running buffer additive (Invitrogen) for reduced SDS-PAGE) and stained with Coomassie Blue.

The concentration of bispecific tetravalent antibodies in cell culture supernatants is quantitatively measured by affinity HPLC chromatography. Briefly, cell culture supernatants containing antibodies and derivatives that bind to Protein A are applied to an Applied Biosystems Poros A/20 column in 200 mM KH2PO4, 100 mM sodium citrate, pH 7.4 and eluted from the matrix with 200 mM NaCl, 100 mM citric acid, pH 2,5 on an Agilent HPLC 1100 system. The eluted protein is quantified by UV absorbance and integration of peak areas. A purified standard IgG1 antibody served as a standard.

Alternatively, the concentration of bispecific tetravalent antibodies in cell culture supernatants is measured by Sandwich-IgG-ELISA. Briefly, StreptaWell High Bind Strepatavidin A-96 well microtiter plates (Roche) are coated with 100 µL/well biotinylated anti-human IgG capture molecule F(ab')2<h-Fcγ> BI (Dianova) at 0.1 µg/mL for 1 h at room temperature or alternatively over night at 4°C and subsequently washed three times with 200 µL/well PBS, 0.05% Tween (PBST, Sigma). 100 µL/well of a dilution series in PBS (Sigma) of the respective antibody containing cell culture supernatants is added to the wells and incubated for 1-2 h on a microtiterplate shaker at room temperature. The wells are washed three times with 200 µL/well PBST and bound antibody is detected with 100 µl F(ab')2<hFcγ>POD (Dianova) at 0.1 µg/mL as detection antibody for 1-2 h on a microtiterplate shaker at room temperature. Unbound detection antibody is washed away three times with 200 µL/well PBST and the bound detection antibody is detected by addition of 100 µL ABTS/well. Determination of absorbance is performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

Protein purification

Proteins are purified from filtered cell culture supernatants referring to standard protocols. In brief, bispecific tetravalent antibodies are applied to a Protein A Sepharose column (GE healthcare) and washed with PBS. Elution of bispecific tetravalent antibodies is achieved at pH 2.8 followed by immediate neutralization of the sample. Aggregated protein is separated from monomeric antibodies by size exclusion chromatography (Superdex 200, GE Healthcare) in PBS or in 20 mM Histidine, 150 mM NaCl pH 6.0. Monomeric fractions are pooled, concentrated if required using e.g. a MILLIPORE Amicon Ultra (30 MWCO) centrifugal concentrator, frozen and stored at -20°C or -80°C. Part of the samples are provided

for subsequent protein analytics and analytical characterization e.g. by SDS-PAGE, size exclusion chromatography or mass spectrometry.

SDS-PAGE

The NuPAGE® Pre-Cast gel system (Invitrogen) is used according to the manufacturer's instruction. In particular, 10% or 4-12% NuPAGE® Novex® Bis-TRIS Pre-Cast gels (pH 6.4) and a NuPAGE® MES (reduced gels, with NuPAGE® Antioxidant running buffer additive) or MOPS (non-reduced gels) running buffer is used.

Analytical size exclusion chromatography

Size exclusion chromatography for the determination of the aggregation and oligomeric state of bispecific tetravalent antibodies is performed by HPLC chromatography. Briefly, Protein A purified antibodies are applied to a Tosoh TSKgel G3000SW column in 300 mM NaCl, 50 mM KH2PO4/K2HPO4, pH 7.5 on an Agilent HPLC 1100 system or to a Superdex 200 column (GE Healthcare) in 2 x PBS on a Dionex HPLC-System. The eluted protein is quantified by UV absorbance and integration of peak areas. BioRad Gel Filtration Standard 151–1901 served as a standard.

Mass spectrometry

The total deglycosylated mass of the bispecific tetravalent antibodies is determined and confirmed via electrospray ionization mass spectrometry (ESI-MS). Briefly, 100 µg purified antibodies are deglycosylated with 50 mU N-Glycosidase F (PNGaseF, ProZyme) in 100 mM KH2PO4/K2HPO4, pH 7 at 37°C for 12-24 h at a protein concentration of up to 2 mg/ml and subsequently desalted via HPLC on a Sephadex G25 column (GE Healthcare). The mass of the respective modified heavy, light chain and modified light chain is determined by ESI-MS after deglycosylation and reduction. In brief, 50 µg bispecific tetravalent antibody in 115 µl are incubated with 60 µl 1M TCEP and 50 µl 8 M Guanidine-hydrochloride subsequently desalted. The total mass and the mass of the reduced heavy and light chains is determined via ESI-MS on a Q-Star Elite MS system equipped with a NanoMate source.

VEGF binding ELISA

The binding properties of the bispecific tetravalent antibodies is evaluated in an ELISA assay with full-length VEGF165-His protein (R&D Systems). For this sake Falcon polystyrene clear enhanced microtiter plates are coated with 100 µl 2

µg/mL recombinant human VEGF165 (R&D Systems) in PBS for 2 h at room temperature or over night at 4°C. The wells are washed three times with 300µl PBST (0,2% Tween 20) and blocked with 200 µl 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300µl PBST. 100 µL/well of a dilution series of the purified bispecific tetravalent antibodies in PBS (Sigma) is added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells are washed three times with 300µl PBST (0,2% Tween 20) and bound antibody is detected with 100 µL/well 0.1 µg/ml F(ab') <hFcgamma>POD (Immuno research) in 2% BSA 0,1% Tween 20 as detection antibody for 1 h on a microtiterplate shaker at room temperature. Unbound detection antibody is washed away three times with 300 µL/well PBST and the bound detection antibody is detected by addition of 100 µL ABTS/well. Determination of absorbance is performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

VEGF binding: Kinetic characterization of VEGF binding at 37°C by surface plasmon resonance (Biacore)

In order to further corroborate the ELISA findings the binding of the bispecific tetravalent antibodies to VEGF is quantitatively analyzed using surface plasmon resonance technology on a Biacore T100 instrument according to the following protocol and analyzed using the T100 software package: Briefly, bispecific tetravalent antibodies are captured on a CM5-Chip via binding to a Goat Anti Human IgG (JIR 109-005-098). The capture antibody is immobilized by amino coupling using standard amino coupling as follows: HBS-N buffer served as running buffer, activation is done by mixture of EDC/NHS with the aim for a ligand density of 700 RU. The Capture-Antibody is diluted in coupling buffer NaAc, pH 5.0, c = 2 µg/mL, finally still activated carboxyl groups are blocked by injection of 1 M Ethanolamine. Capturing of bispecific tetravalent <VEGF> antibodies is done at a flow of 5 µL/min and c = 10 nM, diluted with running buffer + 1 mg/mL BSA; a capture level of approx. 30 RU should be reached. rhVEGF (rhVEGF, R&D-Systems Cat.-No, 293-VE) is used as analyte. The kinetic characterization of VEGF binding to bispecific tetravalent <VEGF> antibodies is performed at 25°C or 37°C in PBS + 0.005 % (v/v) Tween20 as running buffer. The sample is injected with a flow of 50 µL/min and an association of time 80 sec. and a dissociation time of 1200 sec with a concentration series of rhVEGF from 300 - 0.29 nM. Regeneration of free capture antibody surface is performed with 10 mM Glycin pH 1.5 and a contact time of 60 sec after each analyte cycle. Kinetic

constants are calculated by using the usual double referencing method (control reference: binding of rhVEGF to capture molecule Goat Anti Human IgG, blanks on the measuring flow cell, rhVEGF concentration "0", Model: Langmuir binding 1:1, (Rmax set to local because of capture molecule binding).

Ang-2 binding ELISA

The binding properties of the bispecific tetravalent antibodies is evaluated in an ELISA assay with full-length Ang-2-His protein (R&D Systems). For this sake Falcon polystyrene clear enhanced microtiter plates are coated with 100 µl 1 µg/mL recombinant human Ang-2 (R&D Systems, carrier-free) in PBS for 2 h at room temperature or over night at 4°C. The wells are washed three times with 300µl PBST (0,2% Tween 20) and blocked with 200 µl 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300µl PBST. 100 µL/well of a dilution series of the purified bispecific tetravalent antibodies in PBS (Sigma) is added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells are washed three times with 300µl PBST (0,2% Tween 20) and bound antibody is detected with 100 µL/well 0.1 µg/ml F(ab') <hk>POD (Biozol Cat.No. 206005) in 2% BSA 0,1% Tween 20 as detection antibody for 1 h on a microtiterplate shaker at room temperature. Unbound detection antibody is washed away three times with 300 µL/well PBST and the bound detection antibody is detected by addition of 100 µL ABTS/well. Determination of absorbance is performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

Ang-2 binding BIACORE

Binding of the bispecific tetravalent antibodies to human Ang-2 is investigated by surface plasmon resonance using a BIACORE T100 instrument (GE Healthcare Biosciences AB, Uppsala, Sweden). Briefly, for affinity measurements goat<hIgG-Fcγ> polyclonal antibodies are immobilized on a CM5 chip via amine coupling for presentation of the bispecific tetravalent antibodies against human Ang-2. Binding is measured in HBS buffer (HBS-P (10 mM HEPES, 150 mM NaCl, 0.005% Tween 20, ph 7.4), 25°C. Purified Ang-2-His (R&D systems or in house purified) is added in various concentrations in solution. Association is measured by an Ang-2-injection of 3 minutes; dissociation is measured by washing the chip surface with HBS buffer for 3 minutes and a KD value is estimated using a 1:1 Langmuir binding model. Due to heterogenity of the Ang-2 preparation no 1:1 binding can be observed; KD values are thus only relative estimations. Negative control data (e.g.

buffer curves) are subtracted from sample curves for correction of system intrinsic baseline drift and for noise signal reduction. Biacore T100 Evaluation Software version 1.1.1 is used for analysis of sensorgrams and for calculation of affinity data. Alternatively, Ang-2 could be captured with a capture level of 2000-1700 RU via a PentaHisAntibody (PentaHis-Ab BSA-free, Qiagen No. 34660) that is immobilized on a CM5 chip via amine coupling (BSA-free) (see below).

Ang-2-VEGF bridging ELISA

The binding properties of the bispecific tetravalent antibodies is evaluated in an ELISA assay with immobilized full-length VEGF165-His protein (R&D Systems) and human Ang-2-His protein (R&D Systems) for detection of bound bispecific antibody. Only a bispecific tetravalent <VEGF-Ang-2> antibody is able to o bind simultaneously to VEGF and Ang-2 and thus bridge the two antigens whereas monospecific "standard" IgG1 antibodies is not be capable of simultaneously binding to VEGF and Ang-2 (Figure 7).

For this sake Falcon polystyrene clear enhanced microtiter plates are coated with 100 µl 2 µg/mL recombinant human VEGF165 (R&D Systems) in PBS for 2 h at room temperature or over night at 4°C. The wells are washed three times with 300µl PBST (0,2% Tween 20) and blocked with 200 µl 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300µl PBST. 100 µL/well of a dilution series of purified bispecific tetravalent antibodies in PBS (Sigma) is added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells are washed three times with 300µl PBST (0,2% Tween 20) and bound antibody is detected by addition of 100 µl 0.5 µg/ml human Ang-2-His (R&D Systems) in PBS. The wells are washed three times with 300µl PBST (0,2% Tween 20) and bound Ang-2 is detected with 100 µl 0.5 µg/mL <Ang-2>mIgG1-Biotin antibody (BAM0981, R&D Systems) for 1 h at room temperature. Unbound detection antibody is washed away with three times 300µl PBST (0,2% Tween 20) and bound antibody is detected by addition of 100 µl 1:2000 Streptavidin-POD conjugate (Roche Diagnostics GmbH, Cat. No.11089153) 1:4 diluted in blocking buffer for 1h at room temperature. Unbound Streptavidin-POD conjugate is washed away with three-six times 300µl PBST (0,2% Tween 20) and bound Strepatavidin-POD conjugate is detected by addition of 100 µL ABTS/well. Determination of absorbance is performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

Demonstration of simultaneous binding of bispecific tetravalent antibody <VEGF-Ang-2> to VEGF-A and Ang-2 by Biacore

In order to further corroborate the data from the bridging ELISA an additional assay is established to confirm simultaneous binding to VEGF and Ang-2 using surface plasmon resonance technology on a Biacore T100 instrument according to the following protocol and analyzed using the T100 software package (T100 Control, Version 2.01, T100 Evaluation, Version 2.01, T100 Kinetics Summary, Version 1.01): Ang-2 is captured with a capture level of 2000-1700 RU in PBS, 0.005 % (v/v) Tween20 running buffer via a PentaHisAntibody (PentaHis-Ab BSA-free, Qiagen No. 34660) that is immobilized on a CM5 chip via amine coupling (BSA-free). HBS-N buffer served as running buffer during coupling, activation is done by mixture of EDC/NHS. The PentaHis-Ab BSA-free Capture-Antibody is diluted in coupling buffer NaAc, pH 4.5, c = 30 µg/mL, finally still activated carboxyl groups are blocked by injection of 1 M Ethanolamine; ligand densities of 5000 and 17000 RU are tested. Ang-2 with a concentration of 500 nM is captured by the PentaHis-Ab at a flow of 5 µL/min diluted with running buffer + 1 mg/mL BSA. Subsequently, <Ang-2, VEGF> bispecific tetravalent antibody binding to Ang-2 and to VEGF is demonstrated by incubation with rhVEGF and formation of a sandwich complex. For this sake, the bispecific tetravalent <VEGF-Ang-2> antibody is bound to Ang-2 at a flow of 50 µL/min and a concentration of 100 nM, diluted with running buffer + 1 mg/mL BSA and simultaneous binding is detected by incubation with VEGF (rhVEGF, R&D-Systems Cat.-No, 293-VE) in PBS + 0.005 % (v/v) Tween20 running buffer at a flow of 50 µL/min and a VEGF concentration of 150 nM. Association time 120 sec, dissociation time 1200 sec. Regeneration is done after each cycle at a flow of 50 µL/min with 2 x 10 mM Glycin pH 2.0 and a contact time of 60 sec. Sensorgrams are corrected using the usual double referencing (control reference: binding of bispecific antibody and rhVEGF to capture molecule PentaHisAb). Blanks for each Ab are measured with rhVEGF concentration "0".

Generation of HEK293-Tie2 cell line

In order to determine the interference of <Ang-2, VEGF> bispecific tetravalent antibodies with Ang-2 stimulated Tie2 phosphorylation and binding of Ang-2 to Tie2 on cells a recombinant HEK293-Tie cell line was generated. Briefly, a pcDNA3 based plasmid (RB22-pcDNA3 Topo hTie2) coding for full-length human Tie2 under control of a CMV promoter and a Neomycin resistance marker was transfected using Fugene (Roche Applied Science) as transfection reagent into

HEK293 cells (ATCC) and resistant cells were selected in DMEM 10 % FCS, 500µg/ml G418. Individual clones were isolated via a cloning cylinder, and subsequently analyzed for Tie2 expression by FACS. Clone 22 was identified as clone with high and stable Tie2 expression even in the absence of G418 (HEK293-Tie2 clone22). HEK293-Tie2 clone22 is subsequently used for cellular assays: Ang-2 induced Tie2 phosphorylation and Ang-2 cellular ligand binding assay.

Ang-2 induced Tie2 phosphorylation assay

Inhibition of Ang-2 induced Tie2 phosphorylation by <Ang-2, VEGF> bispecific tetravalent antibodies is measured according to the following assay principle. HEK293-Tie2 clone22 is stimulated with Ang-2 for 5 minutes in the absence or presence of Ang-2 antibody and P-Tie2 is quantified by a sandwich ELISA. Briefly, 2x105 HEK293-Tie2 clone 22 cells per well are grown over night on a Poly-D-Lysine coated 96 well- microtiter plate in 100µl DMEM, 10% FCS, 500 µg/ml Geneticin. The next day a titration row of <Ang-2, VEGF> bispecific tetravalent antibodies is prepared in a microtiter plate (4-fold concentrated, 75µl final volume/well, duplicates) and mixed with 75µl of an Ang-2 (R&D systems # 623-AN] dilution (3.2 µg/ml as 4-fold concentrated solution). Antibodies and Ang-2 are pre-incubated for 15 min at room temperature. 100 µl of the mix are added to the HEK293-Tie2 clone 22 cells (pre-incubated for 5 min with 1 mM NaV3O4, Sigma #S6508) and incubated for 5 min at 37°C. Subsequently, cells are washed with 200µl ice-cold PBS + 1mM NaV3O4 per well and lysed by addition of 120µl lysis buffer (20 mM Tris, pH 8.0, 137 mM NaCl, 1% NP-40, 10% glycerol, 2mM EDTA, 1 mM NaV3O4, 1 mM PMSF and 10 µg/ml Aprotinin) per well on ice. Cells are lysed for 30 min at 4°C on a microtiter plate shaker and 100 µl lysate are transferred directly into a p-Tie2 ELISA microtiter plate (R&D Systems, R&D #DY990) without previous centrifugation and without total protein determination. P-Tie2 amounts are quantified according to the manufacturer's instructions and IC50 values for inhibition are determined using XLfit4 analysis plug-in for Excel (Dose-response one site, model 205). IC50 values can be compared within on experiment but might vary from experiment to experiment.

VEGF induced HUVEC proliferation assay

VEGF induced HUVEC (Human Umbilical Vein Endothelial Cells, Promocell #C-12200) proliferation is chosen to measure the cellular function of <Ang-2, VEGF> bispecific tetravalent antibodies. Briefly, 5000 HUVEC cells (low passage number, ≤ passages) per 96 well are incubated in 100µl starvation medium (EBM-2

Endothelial basal medium 2, Promocell # C-22211, 0.5% FCS, Penicilline/Streptomycine) in a collagen I-coated BD Biocoat Collagen I 96-well microtiter plate (BD #354407 / 35640 over night. Varying concentrations of <Ang-2, VEGF> bispecific tetravalent antibody are mixed with rhVEGF (30 ngl/ml final concentration, BD # 354107) and pre-incubated for 15 minutes at room temperature. Subsequently, the mix is added to the HUVEC cells and they are incubated for 72 h at 37°C, 5% CO2. On the day of analysis the plate is equilibrated to room temperature for 30 min and cell viability/proliferation is determined using the CellTiter-GloTM Luminescent Cell Viability Assay kit according to the manual (Promega, # G7571/2/3). Luminescence is determined in a spectrophotometer.

Example 1

Production, expression, purification and characterization of a bispecific, tetravalent antigen binding protein recognizing Ang-2 and VEGF-A

In a first example a bispecific, tetravalent antigen binding protein recognizing Ang-2 and VEGF-A is made by fusing via a (G4S)4-connector a VH-CH1 domain fusion of an antibody recognizing Ang-2 to the C-terminus of the heavy chain of said antibody recognizing Ang-2 (SEQ1); and by fusing via a (G4S)4-connector a VH-CL domain fusion of an antibody recognizing VEGF-A to the C-terminus of the heavy chain of a CH1-CL exchange antibody recognizing VEGF (SEQ3). In order to induce heterodimerization of the two respective heavy chains SEQ 1 contains e.g. the knob sequence (T366W) and SEQ2 contains e.g. the hole sequences T366S, L368A and Y407V as well as two introduced Cysteine residues S354C/Y349'C respectively to form a stabilizing disulfide bridge upon heterodimerization. In order to obtain the bispecific, tetravalent antigen binding protein according to the invention this heavy chain constructs are co-expressed with plasmids coding for the respective light chain of the Ang-2 antibody (SEQ2) and a VL-CH1 domain fusion recognizing VEGF-A (SEQ4). A general scheme of the respective bispecific, tetravalent antigen binding protein with knobs-into-holes modification is given in Fig. 4.

The bispecific, tetravalent antigen binding protein was generated as described in the general methods section by classical molecular biology techniques and is expressed transiently in HEK293F cells as described above. Subsequently, it is purified from the supernatant by a combination of Protein A affinity chromatography and size exclusion chromatography. The obtained product was

characterized for identity by mass spectrometry and analytical properties such as purity by SDS-PAGE, monomer content and stability.

expression	**purification**	
Titer [µg/ml]	yield final product	homogeneity (final product)
9,8	16.7 mg/L	29 %

These data show that the bispecific, tetravalent antigen binding protein can be produced in good yields and is stable.

Subsequently binding to Ang-2 and VEGF-A as well as simultaneous binding was studied by ELISA and Biacore assays described above and functional properties such as inhibition of Tie2 phosphorylation and inhibition of VEGF induced HUVEC proliferation are analyzed showing that the generated bispecific tetravalent antibody is able to bind to Ang-2 and VEGF-A and block their activity simultaneously.

Patent Claims

1. A bispecific, tetravalent antigen binding protein, comprising:

a) a modified heavy chain of a first antibody,
which specifically binds to a first antigen,
and to which C-terminus of said heavy chain additionally the VH-CH1 domains of said first antibody are fused via their N-terminus;

b) two light chains of said first antibody of a);

c) a modified heavy chain of a second antibody,
which specifically binds to a second antigen,
wherein the CH1 domain is replaced by the CL domain of said second antibody and to which C-terminus of said heavy chain additionally the VH-CL domains of said second antibody are fused via their N-terminus; and

d) two modified light chains of said second antibody of c),
wherein the CL domain is replaced by the CH1 domain of said second antibody.

2. The antigen binding protein according to claim 1, characterized in that the CH3 domain of the modified heavy chain of the antibody of a) and the CH3 domain of the modified heavy chain of the antibody of c) each meet at an interface which comprises an original interface between the antibody CH3 domains;

wherein said interface is altered to promote the formation of the bispecific, tetravalent antigen binding protein, wherein the alteration is characterized in that:

i) the CH3 domain of one heavy chain is altered,

so that within the original interface the CH3 domain of one heavy chain that meets the original interface of the CH3 domain of the other heavy chain within the bispecific, tetravalent antigen binding protein,

an amino acid residue is replaced with an amino acid residue having a larger side chain volume, thereby generating a protuberance within the interface of the CH3 domain of one heavy chain which is

positionable in a cavity within the interface of the CH3 domain of the other heavy chain

and
ii) the CH3 domain of the other heavy chain is altered,

so that within the original interface of the second CH3 domain that meets the original interface of the first CH3 domain within the bispecific, tetravalent antigen binding protein,

an amino acid residue is replaced with an amino acid residue having a smaller side chain volume, thereby generating a cavity within the interface of the second CH3 domain within which a protuberance within the interface of the first CH3 domain is positionable.

3. The antigen binding protein according to claim 2, characterized in that the said amino acid residue having a larger side chain volume is selected from the group consisting of arginine (R), phenylalanine (F), tyrosine (Y), tryptophan (W) and
said amino acid residue having a smaller side chain volume is selected from the group consisting of alanine (A), serine (S), threonine (T), valine (V).

4. The antigen binding protein according to claims 2 or 3, characterized in that both CH3 domains are further altered by the introduction of cysteine (C) as amino acid in the corresponding positions of each CH3 domain such that a disulfide bridge between both CH3 domains can be formed.

5. A method for the preparation of a bispecific, tetravalent antigen binding protein according to claims 1 to 4, comprising the steps of

a) transforming a host cell with vectors comprising nucleic acid molecules encoding
a bispecific, tetravalent antigen binding protein according to claims 1 to 4
b) culturing the host cell under conditions that allow synthesis of said antigen binding protein molecule; and
c) recovering said antigen binding protein molecule from said culture.

6. A host cell comprising the vectors according to claim 5.

7. A pharmaceutical composition comprising the bispecific, tetravalent antigen binding protein according to claims 1 to 4 and at least one pharmaceutically acceptable excipient.

8. The bispecific, tetravalent antigen binding protein according to claims 1 to 4 for the treatment of cancer.

9. Use of the bispecific, tetravalent antigen binding protein according to claims 1 to 4 for the manufacture of a medicament for the treatment of cancer.

10. A method for the treatment of a patient in need of therapy, characterized by administering to the patient a therapeutically effective amount of a bispecific, tetravalent antigen binding protein according to claims 1 to 4.