Bispecific, bivalent anti-VEGF/anti-ANG-2 antibodies

The present invention relates to bispecific, bivalent antibodies against human vascular endothelial growth factor (VEGF/VEGF-A) and against human angiopoietin-2 (ANG-2), methods for their production, pharmaceutical compositions containing said antibodies, and uses thereof.

Background of the Invention

Angiogenesis is implicated in the pathogenesis of a variety of disorders which include solid tumors, intraocular neovascular syndromes such as proliferative retinopathies or age-related macular degeneration (AMD), rheumatoid arthritis, and psoriasis (Folkman, J., et al., J. Biol. Chem. 267 (1992) 10931-10934; Klagsbrun, M., et al., Annu. Rev. Physiol. 53 (1991) 217-239; and Garner, A., Vascular diseases, in: Pathobiology of ocular disease, A dynamic approach, Garner, A., and Klintworth, G. K. (eds.), 2nd edition, Marcel Dekker, New York (1994), pp. 1625-1710). In the case of solid tumors, the neovascularization allows the tumor cells to acquire a growth advantage and proliferative autonomy compared to the normal cells. Accordingly, a correlation has been observed between density of microvessels in tumor sections and patient survival in breast cancer as well as in several other tumors (Weidner, N., et al., N Engl J Med. 324 (1991) 1-8; Horak, E.R., et al., Lancet 340 (1992) 1120-1124; and Macchiarini, P., et al., Lancet 340 (1992) 145-146).

VEGF and anti-VEGF antibodies

Human vascular endothelial growth factor (VEGF/VEGF-A) (SEQ ID No: 105) is described in e.g. Leung, D.W., et al., Science 246 (1989) 1306-9; Keck, P.J., et al., Science 246 (1989) 1309-12 and Connolly, D.T., et al., J. Biol. Chem. 264 (1989) 20017-24. VEGF is involved in the regulation of normal and abnormal angiogenesis and neovascularization associated with tumors and intraocular disorders (Ferrara, N., et al., Endocr. Rev. 18 (1997) 4-25; Berkman, R.A., et al., J. Clin. Invest. 91 (1993) 153-159; Brown, L.F., et al., Human Pathol. 26 (1995) 86-91; Brown, L.F., et al., Cancer Res. 53 (1993) 4727-4735; Mattern, J., et al., Brit. J. Cancer. 73 (1996) 931-934; and Dvorak, H.F., et al., Am. J. Pathol. 146 (1995) 1029-1039). VEGF is a homodimeric glycoprotein that has been isolated from several sources. VEGF shows highly specific mitogenic activity for endothelial cells. VEGF has important regulatory functions in the formation of new blood

vessels during embryonic vasculogenesis and in angiogenesis during adult life (Carmeliet, P., et al., Nature, 380 (1996) 435-439; Ferrara, N., et al., Nature, 380 (1996) 439-442; reviewed in Ferrara, N., et al., Endocr. Rev. 18 (1997) 4-25. The significance of the role played by VEGF has been demonstrated in studies showing that inactivation of a single VEGF allele results in embryonic lethality due to failed development of the vasculature (Carmeliet, P., et al., Nature, 380 (1996) 435-439; Ferrara, N., et al., Nature, 380 (1996) 439-442. In addition VEGF has strong chemoattractant activity towards monocytes, can induce the plasminogen activator and the plasminogen activator inhibitor in endothelial cells, and can also induce microvascular permeability. Because of the latter activity, it is sometimes referred to as vascular permeability factor (VPF). The isolation and properties of VEGF have been reviewed; see Ferrara, N., et al., J. Cellular Biochem., 47 (1991) 211-218 and Connolly, D.T., J. Cellular Biochem., 47 (1991) 219-223. Alternative mRNA splicing of a single VEGF gene gives rise to five isoforms of VEGF.

Anti-VEGF neutralizing antibodies suppress the growth of a variety of human tumor cell lines in mice (Kim, K.J., et al., Nature 362 (1993) 841-844; Warren, S.R., et al., J. Clin. Invest. 95 (1995) 1789-1797; Borgstrom, P., et al., Cancer Res. 56 (1996) 4032-4039; and Melnyk, O., et al., Cancer Res. 56 (1996) 921-924). WO 94/10202, WO 98/45332, WO 2005/00900 and WO 00/35956 refer to antibodies against VEGF. Humanized monoclonal antibody bevacizumab (sold under the trade name Avastin®) is an anti-VEGF antibody used in tumor therapy WO 98/45331).

Ranibizumab (trade name Lucentis®) is a monoclonal antibody fragment derived from the same parent murine antibody as bevacizumab (Avastin). It is much smaller than the parent molecule and has been affinity matured to provide stronger binding to VEGF-A (WO 98/45331). It is an anti-angiogenic that has been approved to treat the "wet" type of age-related macular degeneration (ARMD), a common form of age-related vision loss. Another anti-VEGF antibody is e.g. HuMab G6-31 described e.g. in US 2007/0141065.

ANG-2 and anti-ANG-2 antibodies

Human angiopoietin-2 (ANG-2) (alternatively abbreviated with ANGPT2 or ANG2) (SEQ ID No: 106) is described in Maisonpierre, P.C., et al, Science 277 (1997) 55-60 and Cheung,A.H., et al., Genomics 48 (1998) 389-91. The angiopoietins-1 and -2 (ANG-1 (SEQ ID No: 107) and ANG-2 (SEQ ID No: 106))

were discovered as ligands for the Ties, a family of tyrosine kinases that is selectively expressed within the vascular endothelium. Yancopoulos, G.D., et al., Nature 407 (2000) 242-48. There are now four definitive members of the angiopoietin family. Angiopoietin-3 and -4 (Ang-3 and Ang-4) may represent widely diverged counterparts of the same gene locus in mouse and man. Kim, I., et al., FEBS Let, 443 (1999) 353-56; Kim, I., et al., J Biol Chem 274 (1999) 26523-28. ANG-1 and ANG-2 were originally identified in tissue culture experiments as agonist and antagonist, respectively (see for ANG-1: Davis, S., et al., Cell 87 (1996) 1161-69; and for ANG-2: Maisonpierre, P.C., et al., Science 277 (1997) 55-60) All of the known angiopoietins bind primarily to Tie2, and both Ang-1 and -2 bind to Tie2 with an affinity of 3 nM (Kd). Maisonpierre, P.C., et al., Science 277 (1997) 55-60. Ang-1 was shown to support EC survival and to promote endothelium integrity, Davis, S., et al., Cell 87 (1996) 1161-69; Kwak, H.J., et al., FEBS Lett 448 (1999) 249-53; Suri, C., et al., Science 282 (1998) 468-71; Thurston, G., et al., Science 286 (1999) 2511-2514; Thurston, G., et al., Nat. Med. 6 (2000) 460-63, whereas ANG-2 had the opposite effect and promoted blood vessel destabilization and regression in the absence of the survival factors VEGF or basic fibroblast growth factor. Maisonpierre, P.C., et al., Science 277 (1997) 55-60. However, many studies of ANG-2 function have suggested a more complex situation. ANG-2 might be a complex regulator of vascular remodeling that plays a role in both vessel sprouting and vessel regression. Supporting such roles for ANG-2, expression analyses reveal that ANG-2 is rapidly induced, together with VEGF, in adult settings of angiogenic sprouting, whereas ANG-2 is induced in the absence of VEGF in settings of vascular regression. Holash, J., et al., Science 284 (1999) 1994-98; Holash, J., et al., Oncogene 18 (1999) 5356-62. Consistent with a context-dependent role, ANG-2 specifically binds to the same endothelial-specific receptor, Tie-2, which is activated by Ang-1, but has context-dependent effects on its activation. Maisonpierre, P.C., et al., Science 277 (1997) 55-60.

Corneal angiogenesis assays have shown that both ANG-1 and ANG-2 had similar effects, acting synergistically with VEGF to promote growth of new blood vessels. Asahara, T., et al., Circ. Res. 83 (1998) 233-40. The possibility that there was a dose-dependent endothelial response was raised by the observation that in vitro at high concentration, ANG-2 can also be pro-angiogenic. Kim, I., et al., Oncogene 19 (2000) 4549-52. At high concentration, ANG-2 acts as an apoptosis survival factor for endothelial cells during serum deprivation apoptosis through activation

of Tie2 via PI-3 Kinase and Akt pathway. Kim, I., et al., Oncogene 19 (2000) 4549-52.

Other in vitro experiments suggested that during sustained exposure, the effects of ANG-2 may progressively shift from that of an antagonist to an agonist of Tie2, and at later time points, it may contribute directly to vascular tube formation and neovessel stabilization. Teichert-Kuliszewska, K., et al., Cardiovasc. Res. 49 (2001) 659-70. Furthermore, if ECs were cultivated on fibrin gel, activation of Tie2 with ANG-2 was also observed, perhaps suggesting that the action of ANG-2 could depend on EC differentiation state. Teichert-Kuliszewska, K., et al., Cardiovasc. Res. 49 (2001) 659-70. In microvascular EC cultured in a three-dimensional collagen gel, ANG-2 can also induce Tie2 activation and promote formation of capillary-like structures. Mochizuki, Y., et al., J. Cell. Sci. 115 (2002) 175-83. Use of a 3-D spheroidal coculture as an in-vitro model of vessel maturation demonstrated that direct contact between ECs and mesenchymal cells abrogates responsiveness to VEGF, whereas the presence of VEGF and ANG-2 induced sprouting. Korff, T., et al., Faseb J. 15 (2001) 447-57 . Etoh, T.H. et al. demonstrated that ECs that constitutively express Tie2, the expression of MMP-1, -9 and u-PA were strongly upregulated by ANG-2 in the presence of VEGF. Etoh, T., et al., Cancer Res. 61 (2001) 2145-53. With an in vivo pupillary membrane model, Lobov, I.B. et al. showed that ANG-2 in the presence of endogenous VEGF promotes a rapid increase in capillary diameter, remodeling of the basal lamina, proliferation and migration of endothelial cells, and stimulates sprouting of new blood vessels. Lobov, I.B., et al., Proc. Natl. Acad. Sci. USA 99 (2002) 11205-10. By contrast, ANG-2 promotes endothelial cell death and vessel regression without endogenous VEGF. Lobov, I.B., et al., Proc. Natl. Acad. Sci. USA 99 (2002) 11205-10. Similarly, with an in vivo tumor model, Vajkoczy, P., et al. demonstrated that multicellular aggregates initiate vascular growth by angiogenic sprouting via the simultaneous expression of VEGFR-2 and ANG-2 by host and tumor endothelium. Vajkoczy, P., et al., J. Clin. Invest. 109 (2002) 777-85. This model illustrated that the established microvasculature of growing tumors is characterized by a continuous remodeling, putatively mediated by the expression of VEGF and ANG-2 (Vajkoczy, P., et al., J. Clin. Invest. 109 (2002) 777-85).

Knock-out mouse studies of Tie-2 and Angiopoietin-1 show similar phenotypes and suggest that Angiopoietin-1 stimulated Tie-2 phosphorylation mediates remodeling and stabilization of developing vessel, promoting blood vessel maturation during angiogenesis and maintenance of endothelial cell-support cell

adhesion (Dumont, D.J., et al., Genes & Development, 8 (1994) 1897-1909; Sato, T.N., Nature, 376 (1995) 70-74; (Thurston, G., et al., Nature Medicine 6 (2000) 460-463). The role of Angiopoietin-1 is thought to be conserved in the adult, where it is expressed widely and constitutively (Hanahan, D., Science, 277 (1997) 48-50; Zagzag, D., et al., Exp Neurology 159 (1999) 391-400). In contrast, Angiopoietin-2 expression is primarily limited to sites of vascular remodeling where it is thought to block the constitutive stabilizing or maturing function of Angiopoietin-1, allowing vessels to revert to, and remain in, a plastic state which may be more responsive to sprouting signals (Hanahan, D., 1997; Holash, J., et al., Oncogene 18 (199) 5356-62; Maisonpierre, P.C., 1997). Studies of Angiopoietin-2 expression in pathological angiogenesis have found many tumor types to show vascular Angiopoietin-2 expression (Maisonpierre, P.C., et al., Science 277 (1997) 55-60). Functional studies suggest Angiopoietin-2 is involved in tumor angiogenesis and associate Angiopoietin-2 overexpression with increased tumor growth in a mouse xenograft model (Ahmad, S.A., et al., Cancer Res., 61 (2001) 1255-1259). Other studies have associated Angiopoietin-2 overexpression with tumor hypervascularity (Etoh, T., et al., Cancer Res. 61 (2001) 2145-53; Tanaka, F., et al., Cancer Res. 62 (2002) 7124-7129).

In recent years Angiopoietin-1, Angiopoietin-2 and/or Tie-2 have been proposed as possible anti-cancer therapeutic targets. For example US 6,166,185, US 5,650,490 and US 5,814,464 each disclose anti-Tie-2 ligand and receptor antibodies. Studies using soluble Tie-2 were reported to decrease the number and size of tumors in rodents (Lin, 1997; Lin 1998). Siemeister, G., et al., Cancer Res. 59:3 (1999) 3185-91 generated human melanoma cell lines expressing the extracellular domain of Tie-2, injected these into nude mice and reported soluble Tie-2 to result in significant inhibition of tumor growth and tumor angiogenesis. Given both Angiopoietin-1 and Angiopoietin-2 bind to Tie-2, it is unclear from these studies whether Angiopoietin-1, Angiopoietin-2 or Tie-2 would be an attractive target for anti-cancer therapy. However, effective anti-Angiopoietin-2 therapy is thought to be of benefit in treating diseases such as cancer, in which progression is dependant on aberrant angiogenesis where blocking the process can lead to prevention of disease advancement (Folkman, J., Nature Medicine. 1 (1995) 27-31).

In addition some groups have reported the use of antibodies and peptides that bind to Angiopoietin-2. See, for example, US 6,166,185 and US 2003/10124129. WO 03/030833, WO 2006/068953, WO 03/057134 or US 2006/0122370.

Study of the effect of focal expression of Angiopoietin-2 has shown that antagonizing the Angiopoietin-1/Tie-2 signal loosens the tight vascular structure thereby exposing ECs to activating signals from angiogenesis inducers, e.g. VEGF (Hanahan, D., Science, 277 (1997) 48-50). This pro-angiogenic effect resulting from inhibition of Angiopoietin-1 indicates that anti-Angiopoietin-1 therapy would not be an effective anti-cancer treatment.

ANG-2 is expressed during development at sites where blood vessel remodeling is occurring. Maisonpierre, P.C., et al., Science 277 (1997) 55-60. In adult individuals, ANG-2 expression is restricted to sites of vascular remodeling as well as in highly vascularized tumors, including glioma, Osada, H., et al., Int. J. Oncol. 18 (2001) 305-09); Koga, K., et al., Cancer Res. 61 (2001) 6248-54, hepatocellular carcinoma, Tanaka, S., et al., J. Clin. Invest. 103 (1999) 341-45, gastric carcinoma, Etoh, T., et al., Cancer Res. 61 (2001) 2145-53; Lee, J.H., et al., Int. J. Oncol. 18 (2001) 355-61, thyroid tumor, Bunone, G., et al., Am J Pathol 155 (1999) 1967-76 non-small cell lung cancer, Wong, M.P., et al., Lung Cancer 29 (2000) 11-22, and cancer of colon, Ahmad, S.A., et al., Cancer 92 (2001) 1138-43, and prostate Wurmbach, J.H., et al., Anticancer Res. 20 (2000) 5217-20. Some tumor cells are found to express ANG-2. For example, Tanaka, S., et al., J. Clin. Invest. 103 (1999) 341-45 detected ANG-2 mRNA in 10 out of 12 specimens of human hepatocellular carcinoma (HCC). Ellis' group reported that ANG-2 is expressed ubiquitously in tumor epithelium. Ahmad, S.A., et al., Cancer 92 (2001) 1138-43. Other investigators reported similar findings. Chen, L., et al., J. Tongji Med. Univ. 21 (2001) 228-35. By detecting ANG-2 mRNA levels in archived human breast cancer specimens, Sfiligoi, C., et al., Int. J. Cancer 103 (2003) 466-74 reported that ANG-2 mRNA is significantly associated with auxiliary lymph node invasion, short disease-free time and poor overall survival. Tanaka, F., et al., Cancer Res. 62 (2002) 7124-29 reviewed a total of 236 patients of non-small cell lung cancer (NSCLC) with pathological stage-I to -IIIA, respectively. Using immunohistochemistry, they found that 16.9% of the NSCLC patients were ANG-2 positive. The microvessel density for ANG-2 positive tumor is significantly higher than that of ANG-2 negative. Such an angiogenic effect of ANG-2 was seen only when VEGF expression was high. Moreover, positive expression of ANG-2 was a significant factor to predict a poor postoperative survival. Tanaka, F., et al., Cancer Res. 62 (2002) 7124-7129. However, they found no significant correlation between Ang-1 expression and the microvessel density. Tanaka, F., et al., Cancer Res. 62

(2002) 7124-7129. These results suggest that ANG-2 is an indicator of poor prognosis patients with several types of cancer.

Recently, using an ANG-2 knockout mouse model, Yancopoulos' group reported that ANG-2 is required for postnatal angiogenesis. Gale, N.W., et al., Dev. Cell 3 (2002) 411-23. They showed that the developmentally programmed regression of the hyaloid vasculature in the eye does not occur in the ANG-2 knockout mice and their retinal blood vessels fail to sprout out from the central retinal artery. Gale, N.W., et al., Dev. Cell 3 (2002) 411-23. They also found that deletion of ANG-2 results in profound defects in the patterning and function of the lymphatic vasculature. Gale, N.W., et al., Dev. Cell 3 (2002) 411-23. Genetic rescue with Ang-1 corrects the lymphatic, but not the angiogenesis defects. Gale, N.W., et al., Dev. Cell 3 (2002) 411-23.

Peters and his colleagues reported that soluble Tie2, when delivered either as recombinant protein or in a viral expression vector, inhibited in vivo growth of murine mammary carcinoma and melanoma in mouse models. Lin, P., et al., Proc. Natl. Acad. Sci. USA 95 (1998) 8829-34; Lin, P., et al., J. Clin. Invest. 100 (1997) 2072-78. Vascular densities in the tumor tissues so treated were greatly reduced. In addition, soluble Tie2 blocked angiogenesis in the rat corneal stimulated by tumor cell conditioned media. Lin, P., et al., J. Clin. Invest. 100 (1997) 2072-78. Furthermore, Isner and his team demonstrated that addition of ANG-2 to VEGF promoted significantly longer and more circumferential neovascularity than VEGF alone. Asahara, T., et al., Circ. Res. 83 (1998) 233-40. Excess soluble Tie2 receptor precluded modulation of VEGF-induced neovascularization by ANG-2. Asahara, T., et al., Circ. Res. 83 (1998) 233-40. Siemeister, G., et al., Cancer Res. 59:3 (1999) 3185-91 showed with nude mouse xenografts that overexpression of the extracellular ligand-binding domains of either Flt-1 or Tie2 in the xenografts results in significant inhibition of pathway could not be compensated by the other one, suggesting that the VEGF receptor pathway and the Tie2 pathway should be considered as two independent mediators essential for the process of in vivo angiogenesis. Siemeister, G., et al., Cancer Res. 59:3 (1999) 3185-91. This is proven by a more recent publication by White, R., R., et al., , Proc. Natl. Acad. Sci. USA 100 (2003) 5028-33. In their study, it was demonstrated that a nuclease-resistant RNA aptamer that specifically binds and inhibits ANG-2 significantly inhibited neovascularization induced by bFGF in the rat corneal micropocket angiogenesis model.

Bispecific antibodies

A wide variety of recombinant 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., Léger, O., Pathobiology 74 (2007) 3-14; Shen, J., et al., Journal of Immunological 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 scFvs (Fischer, N., Léger, O., Pathobiology 74 (2007) 3-14). It has to be kept in mind that 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 receptor binding, by maintaining a high degree of similarity to naturally occurring antibodies.

In WO 2007/024715 are reported dual variable domain immunoglobulins as engineered multivalent and multispecific binding proteins. A process for the preparation of biologically active antibody dimers is reported in US 6,897,044. Multivalent F_V antibody construct having at least four variable domains which are linked with each over via peptide linkers are reported in US 7,129,330. Dimeric and multimeric antigen binding structures are reported in US 2005/0079170. Tri- or tetra-valent monospecific antigen-binding protein comprising three or four Fab fragments bound to each other covalently by a connecting structure, which protein is not a natural immunoglobulin are reported in US 6,511,663. In WO 2006/020258 tetravalent bispecific antibodies are reported that can be efficiently expressed in prokaryotic and eukaryotic cells, and are useful in therapeutic and diagnostic methods. A method of separating or preferentially synthesizing dimers which are linked via at least one interchain disulfide linkage from dimers which are not linked via at least one interchain disulfide linkage from a mixture comprising the two

types of polypeptide dimers is reported in US 2005/0163782. Bispecific tetravalent receptors are reported in US 5,959,083. Engineered antibodies with three or more functional antigen binding sites are reported in WO 2001/077342.

Multispecific and multivalent antigen-binding polypeptides are reported in WO 1997/001580. WO 1992/004053 reports homoconjugates, typically prepared from monoclonal antibodies of the IgG class which bind to the same antigenic determinant are covalently linked by synthetic cross-linking. Oligomeric monoclonal antibodies with high avidity for antigen are reported in WO 1991/06305 whereby the oligomers, typically of the IgG class, are secreted having two or more immunoglobulin monomers associated together to form tetravalent or hexavalent IgG molecules. Sheep-derived antibodies and engineered antibody constructs are reported in US 6,350,860, which can be used to treat diseases wherein interferon gamma activity is pathogenic. In US 2005/0100543 are reported targetable constructs that are multivalent carriers of bi-specific antibodies, i.e., each molecule of a targetable construct can serve as a carrier of two or more bi-specific antibodies. Genetically engineered bispecific tetravalent antibodies are reported in WO 1995/009917. In WO 2007/109254 stabilized binding molecules that consist of or comprise a stabilized scFv are reported.

Combination of VEGF and ANG-2 Inhibitors

WO 2007/068895 refers to a combination of an ANG-2 antagonist and a VEGF, KDR and/or FLTL antagonists. WO 2007/089445 refers to ANG-2 and VEGF inhibitor combinations.

WO 2003/106501 refers to fusion proteins binding to Angiopoietin and containing a multimerization domain. WO 2008/132568 relates to fusion proteins binding to Angiopoietin and VEGF. WO 2003/020906 relates to multivalent protein conjugates with multiple ligand-binding domains of receptors.

WO 2009/136352 relates to anti-angiogenic compounds.

Summary

The disclosure is directed to a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1, and as light chain variable domain (VL) the SEQ ID NO: 2; and

ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3, and as light chain variable domain (VL) the SEQ ID NO: 4.

The bispecific antibody according to the disclosure may be characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF; and

b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other.

In one aspect of the disclosure, there is provided a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1, and as light chain variable domain (VL) the SEQ ID NO: 2; and

ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3, and as light chain variable domain (VL) the SEQ ID NO: 4;and further

characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;

b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 7, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 5, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 8, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 6.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 11, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 9, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 12, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 10.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 15, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 13, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 16, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 14.

The disclosure also relates to a pharmaceutical composition comprising said bispecific antibody, said composition for the treatment of cancer, the use of said bispecific antibody for the manufacture of a medicament for the treatment of cancer, a method of treatment of patient suffering from cancer by administering said bispecific antibody. to a patient in the need of such treatment.

In a second aspect, there is provided a pharmaceutical composition comprising an antibody as defined above.

In a third aspect, there is provided the bispecific antibody as defined above for the treatment of cancer.

In a fourth aspect, there is provided the use of the bispecific antibody as defined above for the manufacture of a medicament for the treatment of cancer.

The disclosure also relates to a pharmaceutical composition comprising said bispecific antibody, said composition for the treatment of vascular diseases, the use of said bispecific antibody for the manufacture of a medicament for the treatment of vascular diseases, a method of treatment of patient suffering from vascular diseases by administering said bispecific antibody. to a patient in the need of such treatment.

In a fifth aspect, there is provided the bispecific antibody as defined above for use in the treatment of a condition selected from intraocular neovascular syndromes, rheumatoid arthritis or psoriasis.

In a sixth aspect, there is provided the use of the bispecific antibody as defined above for the manufacture of a medicament for the treatment of a condition selected from intraocular neovascular syndromes, rheumatoid arthritis or psoriasis.

The disclosure further provides a nucleic acid molecule encoding a chain of a bispecific antibody according to the disclosure.

In a seventh aspect, there is provided a nucleic acid encoding a bispecific antibody as defined above.

The disclosure further provides expression vectors containing said nucleic acid according to the disclosure capable of expressing said nucleic acid in a prokaryotic or eukaryotic host cell, and host cells containing such vectors for the recombinant production of a bispecific antibody according to the disclosure.

In an eighth aspect, there is provided an expression vector containing said nucleic acid as defined above capable of expressing said nucleic acid in a prokaryotic or eukaryotic host cell.

In a ninth aspect, there is provided a prokaryotic or eukaryotic host cell comprising a vector according to the disclosure.

The disclosure further comprises a method for the production of a bispecific antibody according to the disclosure, characterized by expressing a nucleic acid according to the disclosure in a prokaryotic or eukaryotic host cell and recovering said bispecific antibody from said cell or the cell culture supernatant. The disclosure further comprises the antibody obtained by such method for the production of a bispecific antibody.

Accordingly one embodiment of the disclosure is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 5, of SEQ ID NO: 6, of SEQ ID NO: 7, and of SEQ ID NO: 8.

Accordingly one embodiment of the disclosure is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 9, of SEQ ID NO: 10, of SEQ ID NO: 11, and of SEQ ID NO: 12.

Accordingly one embodiment of the disclosure is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 13, of SEQ ID NO: 14, of SEQ ID NO: 15, and of SEQ ID NO: 16.

The bispecific, bivalent antibodies according to the disclosure show benefits for human patients in need of a VEGF and ANG-2 targeting therapy. The antibodies according to the disclosure have highly valuable properties causing a benefit for a patient suffering from such a disease, especially suffering from cancer. The bispecific antibodies according to the disclosure are highly effective in tumor growth and/or inhibition of tumor angiogenesis or vascular diseases. The bispecific, bivalent antibodies according to the disclosure The bispecific, bivalent <VEGF-ANG-2> antibodies according to the disclosure show valuable pharmacokinetic/-dynamic properties like e.g. stability, good (i.e. slow) clearance (e.g. at low doses).

The bispecific antibodies according to the disclosure are highly effective in

a) tumor growth inhibition (e.g. with the bispecific antibodies according to the invention tumor stasis could be achieved already at lower concentrations compared to the combination of the two monospecific antibodies (e.g. in the Colo205 and the KPL-4 tumor models of Example 9 and 10, tumor stasis was already achieved with 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of ANG2i-LC06 + 10 mg/kg of Avastin), and/or

b) inhibition of tumor angiogenesis or vascular diseases (e.g. maximal antiangiogenic effects with the bispecific antibodies according to the invention could already be achieved at lower concentrations compared to the combination of the two monospecific antibodies (e.g. in the mouse corneal angiogenesis assay of Example 8, the maximal antiangiogenic effect was already achieved with 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of ANG2i-LC06 + 10 mg/kg of Avastin).

Description of the Figures

Figure 1 Exemplary bivalent bispecific antibody format for XMab examples including Knobs-into-Holes modified CH3 domains

Figure 2a Exemplary bivalent bispecific antibody format for OAscFab examples including Knobs-into-Holes modified CH3 domains

Figure 2b Exemplary bivalent bispecific antibody format for example OAscXFab1 including Knobs-into-Holes modified CH3 domains

Figure 2c Exemplary bivalent bispecific antibody format for examples OAscXFab2 and OAscXFab3 including Knobs-into-Holes modified CH3 domains

Figure 3 Simultaneous binding of <VEGF-Ang-2> XMab1 to VEGF (1. Step) followed by binding to hAng-2 (second step)

Figure 4 ELISA principle for quantification of binding active mAb<Ang2/VEGF> antibodies

Figure 5 Calibration curve of ELISA for quantification of binding active <Ang2/VEGF> XMab1 antibodies

Figure 6 Mouse corneal angiogenesis assay – inhibition of vessel outgrowth from the limbus towards the VEGF gradient by administration of a bispecific antibody according to the invention.

Figure 7 Mouse corneal angiogenesis assay – inhibition of angiogenesis/vessel outgrowth from the limbus towards the VEGF gradient by administration of a bispecific antibody according to the invention- Comparison of the bispecific <Ang2/VEGF> antibody XMab1, the <Ang2> Mab ANG2i-LC06 (LC06), the <VEGF> Mab bevacizumab (Avastin) and the combination ANG2i-LC06 and <VEGF> Mab bevacizumab (Avastin).

Figure 8 In vivo tumor growth inhibition in mouse xenograft of human colorectal cancer Colo205 (small tumors) by a bispecific antibody according to the invention - Comparison of the bispecific <Ang2/VEGF> antibody XMab1, the <Ang2> Mab ANG2i-LC06 (LC06), the <VEGF> Mab bevacizumab (Avastin) and the combination ANG2i-LC06 and <VEGF> Mab bevacizumab (Avastin).

Figure 9 In vivo tumor growth inhibition in mouse xenograft of human colorectal cancer Colo205 (large tumors) by a bispecific antibody according to the invention - Comparison of the bispecific <Ang2/VEGF> antibody XMab1, the <Ang2> Mab ANG2i-LC06 (LC06), the <VEGF> Mab bevacizumab (Avastin) and the combination ANG2i-LC06 and <VEGF> Mab bevacizumab (Avastin).

Figure 10 In vivo tumor growth inhibition in mouse xenograft of human breast cancer KPL-4 (small tumors) by a bispecific antibody according to the invention - Comparison of the bispecific <Ang2/VEGF> antibody XMab1, the <Ang2> Mab ANG2i-LC06 (LC06), the <VEGF> Mab bevacizumab (Avastin) and the combination ANG2i-LC06 and <VEGF> Mab bevacizumab (Avastin).

Figure 11 In vivo tumor growth inhibition in mouse xenograft of human breast cancer KPL-4 (large tumors) by a bispecific antibody according to the invention - Comparison of the bispecific <Ang2/VEGF> antibody XMab1, the <Ang2> Mab ANG2i-LC06 (LC06), the <VEGF> Mab bevacizumab (Avastin) and the combination ANG2i-LC06 and <VEGF> Mab bevacizumab (Avastin).

Figure 12 In vivo tumor growth inhibition in mouse xenograft of gastric cancer N87 by a bispecific antibody according to the invention - Comparison of the bispecific <Ang2/VEGF> antibody XMab1, the <Ang2> Mab ANG2i-LC06 (LC06), the <VEGF> Mab bevacizumab (Avastin) and the combination ANG2i-LC06 and <VEGF> Mab bevacizumab (Avastin).

Detailed Description of the Invention

The invention is directed to a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2. characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1, and as light chain variable domain (VL) the SEQ ID NO: 2; and
ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3, and as light chain variable domain (VL) the SEQ ID NO: 4.

In one aspect of the invention the bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;
b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other.

This bispecific, bivalent antibody format for the bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) is described in WO 2009/080253 (see exemplary scheme in including Knobs-into-Holes modified CH3 domains in Figure 1). The antibodies based on this bispecific, bivalent antibody format are named XMab in the examples of the current invention.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 7, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 5, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 8, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 6.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 11, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 9, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 12, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 10.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 15, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 13, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 16, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 14.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 19, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 17, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 20, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 18.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 23, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 21, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 24, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 22.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 27, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 25, and
b) as modified heavy chain of the second full length antibody the amino acid sequence of SEQ ID NO: 28, and as modified light chain of the second full length antibody the amino acid sequence of SEQ ID NO: 26.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 5, of SEQ ID NO: 6, of SEQ ID NO: 7, and of SEQ ID NO: 8.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 9, of SEQ ID NO: 10, of SEQ ID NO: 11, and of SEQ ID NO: 12.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 13, of SEQ ID NO: 14, of SEQ ID NO: 15, and of SEQ ID NO: 16.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 17, of SEQ ID NO: 18, of SEQ ID NO: 19, and of SEQ ID NO: 20.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 21, of SEQ ID NO: 22, of SEQ ID NO: 23, and of SEQ ID NO: 24.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 25, of SEQ ID NO: 26, of SEQ ID NO: 27, and of SEQ ID NO: 28.

In another aspect of the invention the bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;
b) the heavy chain and the light chain of a second full length antibody that specifically binds to ANG-2, wherein the N-terminus of the heavy chain is connected to the C-terminus of the light chain via a peptide linker.

An exemplary scheme of this bispecific, bivalent antibody format for this bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) is shown in Figure 2a including Knobs-into-Holes modified CH3 domains. The antibodies based on this bispecific, bivalent antibody format are named OAscFab in the examples of the current invention.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 30, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 31, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the amino acid sequence of SEQ ID NO: 29.

In one embodiment such bispecific, bivalent antibody is characterized in comprising

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 33, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 34, and

b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the amino acid sequence of SEQ ID NO: 32.

In one embodiment the antibody heavy chain variable domain (VH) and the antibody light chain variable domain (VL) of the heavy and light chain of the second full length antibody are disulfide stabilized by introduction of a disulfide bond between the following positions: heavy chain variable domain position 44 to light chain variable domain position 100 (numbering always according to EU index of Kabat; (Kabat, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991))). Such further disulfide stabilization is achieved by the introduction of a disulfide bond between the variable domains VH and VL of the second full length antibody heavy and light chain. Techniques to introduce unnatural disulfide bridges for stabilization are described e.g. in WO 94/029350, Rajagopal, V., et al, Prot. Engin. 10 (1997) 1453-59; Kobayashi, et al., Nuclear Medicine & Biology, Vol. 25 (1998) 387-393; or Schmidt, M., et al., Oncogene 18 (1999) 1711-1721.

Thus in one embodiment such bispecific, bivalent antibody is characterized in comprising a disulfide bond between the variable domains of the second full length antibody heavy and light chain is between heavy chain variable domain position 44 and light chain variable domain position 100, and comprises

a) as heavy chain of the first full length antibody the amino acid sequence of SEQ ID NO: 36, and as light chain of the first full length antibody the amino acid sequence of SEQ ID NO: 37, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the amino acid sequence of SEQ ID NO: 35.

In another aspect of the invention the bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;

b) the heavy chain and the light chain of a second full length antibody that specifically binds to ANG-2,
wherein the N-terminus of the heavy chain is connected to the C-terminus of

the light chain via a peptide linker; and
wherein the variable domains VL and VH are replaced by each other.

An exemplary scheme of this bispecific, bivalent antibody format for this bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) is shown in Figure 2b including Knobs-into-Holes modified CH3 domains. The antibodies based on this bispecific, bivalent antibody format are named in the examples OAscXFab1.

In one embodiment such bispecific antibody is characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 39, and as light chain of the first full length antibody the SEQ ID NO: 40, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the SEQ ID NO: 38.

In another aspect of the invention the bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;
b) the heavy chain and the light chain of a second full length antibody that specifically binds to ANG-2,
wherein the N-terminus of the heavy chain is connected to the C-terminus of the light chain via a peptide linker; and
wherein the constant domains CL and CH1 are replaced by each other.

An exemplary scheme of this bispecific, bivalent antibody format for this bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) is shown in Figure 2c including Knobs-into-Holes modified CH3 domains. The antibodies based on this bispecific, bivalent antibody format are named in the examples OAscXFab2 and OAscXFab3.

In one embodiment such bispecific antibody is characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 42, and as light chain of the first full length antibody the SEQ ID NO: 43, and

b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the SEQ ID NO: 41.

In one embodiment such bispecific antibody is characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 45, and as light chain of the first full length antibody the SEQ ID NO: 46, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the SEQ ID NO: 44.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 29, of SEQ ID NO: 30, and of SEQ ID NO: 31.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 32, of SEQ ID NO: 33, and of SEQ ID NO: 34.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 35, of SEQ ID NO: 36, and of SEQ ID NO: 37.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 38, of SEQ ID NO: 39, and of SEQ ID NO: 40.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2,

characterized in comprising the amino acid sequences of SEQ ID NO: 41, of SEQ ID NO: 42, and of SEQ ID NO: 43.

Accordingly one embodiment of the invention is a bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in comprising the amino acid sequences of SEQ ID NO: 44, of SEQ ID NO: 45, and of SEQ ID NO: 46.

Preferably the CH3 domains of the bispecific, bivalent antibody according to the invention is 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 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.

In a preferred aspect of the invention all bispecific antibodies according to the invention are characterized in that

the CH3 domain of one heavy chain and the CH3 domain of the other heavy chain 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 antibody, wherein the alteration is characterized in that:

a) 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 antibody,

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

b) 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 antibody

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.

Thus the antibody according to invention is preferably characterized in that

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

wherein i) in the CH3 domain of one heavy chain

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 wherein

ii) in the CH3 domain of the other heavy chain

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 embodiment, the bispecific 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". 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 chain" and a E356C mutation or a S354C mutation into the CH3 domain of the "hole chain".

In another embodiment, the bispecific antibody according to the invention 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. In a another preferred embodiment the bispecific 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 (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; (Kabat, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991))). But also other knobs-in-holes technologies as described by EP 1 870 459 A1, can be used alternatively or additionally. Thus another example for the bispecific 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; (Kabat, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991))).

In another embodiment the bispecific 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 embodiment the bispecific 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 trivalent, bispecific 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".

In one embodiment of the invention the bispecific antibody according to the invention is characterized in having one or more of the following properties (determined in assays as described in Examples 3 to 7):

- the bispecific, bivalent antibody binds to VEGF with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody binds to ANG-2 with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody inhibits ANG-2-induced Tie2 phosphorylation in HEK293 cells transfected with Tie2 with an IC50 of 15 nM or less, (in one embodiment with an IC50 of 10 nM or less);
- the bispecific, bivalent antibody inhibits ANG-2 binding to Tie2 with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF binding to VEGF receptor with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF-induced proliferation of HUVEC cells with an with an IC50 of 10 nM or less, (in one embodiment with an IC50 of 5 nM or less).

In one embodiment the bispecific, bivalent antibody is characterized in comprising

a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1, and as light chain variable domain (VL) the SEQ ID NO: 2; and

ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3, and as light chain variable domain (VL) the SEQ ID NO: 4;

and having one or more of the following properties (determined in assays as described in Examples 3 to 7):

- the bispecific, bivalent antibody binds to VEGF with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody binds to ANG-2 with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody inhibits ANG-2-induced Tie2 phosphorylation in HEK293 cells transfected with Tie2 with an IC50 of 15 nM or less, (in one embodiment with an IC50 of 10 nM or less);
- the bispecific, bivalent antibody inhibits ANG-2 binding to Tie2 with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF binding to VEGF receptor with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF-induced proliferation of HUVEC cells with an with an IC50 of 10 nM or less, (in one embodiment with an IC50 of 5 nM or less).

In one aspect of the invention such bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;
b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other;

and having one or more of the following properties (determined in assays as described in Examples 3 to 7):

- the bispecific, bivalent antibody binds to VEGF with a KD value of the binding affinity of 5 nM or less;

- the bispecific, bivalent antibody binds to ANG-2 with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody inhibits ANG-2-induced Tie2 phosphorylation in HEK293 cells transfected with Tie2 with an IC50 of 15 nM or less, (in one embodiment with an IC50 of 10 nM or less);
- the bispecific, bivalent antibody inhibits ANG-2 binding to Tie2 with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF binding to VEGF receptor with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF-induced proliferation of HUVEC cells with an with an IC50 of 10 nM or less, (in one embodiment with an IC50 of 5 nM or less).

In one embodiment the bispecific, bivalent antibody is characterized in comprising

a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1 with no more than 1 amino acid residue substitutions in the CDRs, and as light chain variable domain (VL) the SEQ ID NO: 2 with no more than 1 amino acid residue substitutions in the CDRs; and

ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3 with no more than 1 amino acid residue substitutions in the CDRs, and as light chain variable domain (VL) the SEQ ID NO: 4 with no more than 1 amino acid residue substitutions in the CDRs.

In one embodiment the bispecific, bivalent antibody is characterized in comprising

a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1 with no more than 1 amino acid residue

substitutions in the CDRs, and as light chain variable domain (VL) the SEQ ID NO: 2 with no more than 1 amino acid residue substitutions in the CDRs; and

ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3 with no more than 1 amino acid residue substitutions in the CDRs, and as light chain variable domain (VL) the SEQ ID NO: 4 with no more than 1 amino acid residue substitutions in the CDRs;

and having one or more of the following properties (determined in assays as described in Examples 3 to 7):

- the bispecific, bivalent antibody binds to VEGF with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody binds to ANG-2 with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody inhibits ANG-2-induced Tie2 phosphorylation in HEK293 cells transfected with Tie2 with an IC50 of 15 nM or less, (in one embodiment with an IC50 of 10 nM or less);
- the bispecific, bivalent antibody inhibits ANG-2 binding to Tie2 with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF binding to VEGF receptor with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF-induced proliferation of HUVEC cells with an with an IC50 of 10 nM or less, (in one embodiment with an IC50 of 5 nM or less).

In one aspect of the invention the bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF,

and wherein the heavy chain of the first full length antibody comprises the amino acid sequence of SEQ ID NO:7 with no more than 1 amino acid residue substitutions in the CDRs, and the light chain of the first full

length antibody comprises the amino acid sequence of SEQ ID NO: 5 with no more than 1 amino acid residue substitutions in the CDRs, and

b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other ,

and wherein the modified heavy chain of the second full length antibody comprises the amino acid sequence of SEQ ID NO: 8 with no more than 1 amino acid residue substitutions in the CDRs, and the modified light chain of the second full length antibody comprises the amino acid sequence of SEQ ID NO: 6 with no more than 1 amino acid residue substitutions in the CDRs.

In one aspect of the invention the bispecific antibody according to the invention is characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF,

and wherein the heavy chain of the first full length antibody comprises the amino acid sequence of SEQ ID NO:7 with no more than 1 amino acid residue substitutions in the CDRs, and the light chain of the first full length antibody comprises the amino acid sequence of SEQ ID NO: 5 with no more than 1 amino acid residue substitutions in the CDRs, and

b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other ,

and wherein the modified heavy chain of the second full length antibody comprises the amino acid sequence of SEQ ID NO: 8 with no more than 1 amino acid residue substitutions in the CDRs, and the modified light chain of the second full length antibody comprises the amino acid sequence of SEQ ID NO: 6 with no more than 1 amino acid residue substitutions in the CDRs;

and having one or more of the following properties (determined in assays as described in Examples 3 to 7):

- the bispecific, bivalent antibody binds to VEGF with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody binds to ANG-2 with a KD value of the binding affinity of 5 nM or less;
- the bispecific, bivalent antibody inhibits ANG-2-induced Tie2 phosphorylation in HEK293 cells transfected with Tie2 with an IC50 of 15 nM or less, (in one embodiment with an IC50 of 10 nM or less);
- the bispecific, bivalent antibody inhibits ANG-2 binding to Tie2 with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF binding to VEGF receptor with an IC50 of 20 nM or less, (in one embodiment with an IC50 of 15 nM or less);
- the bispecific, bivalent antibody inhibits VEGF-induced proliferation of HUVEC cells with an with an IC50 of 10 nM or less, (in one embodiment with an IC50 of 5 nM or less).

As used herein, "antibody" refers to a binding protein that comprises antigen-binding sites. The terms “binding site” or “antigen-binding site” as used herein denotes the region(s) of an antibody molecule to which a ligand actually binds. The term “antigen-binding site” comprises an antibody heavy chain variable domains (VH) and an antibody light chain variable domains (VL) (pair of VH/VL).).

Antibody specificity refers to selective recognition of the antibody for a particular epitope of an antigen. Natural antibodies, for example, are monospecific.

“Bispecific antibodies” according to the invention are antibodies which have two different antigen-binding specificities. Antibodies of the present invention are specific for two different antigens, VEGF as first antigen and ANG-2 as second antigen.

The term “monospecific” antibody as used herein denotes an antibody 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. As such, the terms “bivalent”, “tetravalent”, and “hexavalent” denote the presence of two binding site, four binding sites, and six binding sites, respectively, in an antibody molecule. The bispecific antibodies according to the invention are “bivalent”.

The term "VEGF" as used herein refers to human vascular endothelial growth factor (VEGF/VEGF-A) (SEQ ID NO: 47) which is described e.g. in Leung, D.W., et al., Science 246 (1989) 1306-9; Keck, P.J., et al., Science 246 (1989) 1309-12 and Connolly, D.T., et al., J. Biol. Chem. 264 (1989) 20017-24. VEGF is involved in the regulation of normal and abnormal angiogenesis and neovascularization associated with tumors and intraocular disorders (Ferrara, N., et al., Endocr. Rev. 18 (1997) 4-25; Berkman, R.A.,et al., J. Clin. Invest. 91 (1993) 153-159; Brown, L.F., et al., Human Pathol. 26 (1995) 86-91; Brown, L.F., et al., Cancer Res. 53 (1993) 4727-4735; Mattern, J., et al., Brit. J. Cancer. 73 (1996) 931-934; and Dvorak, H.F., et al., Am. J. Pathol. 146 (1995) 1029-1039). VEGF is a homodimeric glycoprotein that has been isolated from several sources. VEGF shows highly specific mitogenic activity for endothelial cells.

The term "ANG-2" as used herein refers to human angiopoietin-2 (ANG-2) (alternatively abbreviated with ANGPT2 or ANG2) (SEQ ID NO: 48) which is described e.g. in Maisonpierre, P.C., et al, Science 277 (1997) 55-60 and Cheung, A.H., et al., Genomics 48 (1998) 389-91. The angiopoietins-1 and -2 were discovered as ligands for the Ties, a family of tyrosine kinases that is selectively expressed within the vascular endothelium. Yancopoulos, G.D., et al., Nature 407 (2000) 242-48. There are now four definitive members of the angiopoietin family. Angiopoietin-3 and -4 (Ang-3 and Ang-4) may represent widely diverged counterparts of the same gene locus in mouse and man. Kim, I., et al., FEBS Let, 443 (1999) 353-56; Kim, I., et al., J Biol Chem 274 (1999) 26523-28. ANG-1 and ANG-2 were originally identified in tissue culture experiments as agonist and antagonist, respectively (see for ANG-1: Davis, S., et al., Cell 87 (1996) 1161-69; and for ANG-2: Maisonpierre, P.C., et al., Science 277 (1997) 55-60) All of the known angiopoietins bind primarily to Tie2, and both Ang-1 and -2 bind to Tie2 with an affinity of 3 nM (Kd). Maisonpierre, P.C., et al., Science 277 (1997) 55-60.

An antigen-binding sites of the bispecific antibody of the invention contain 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. Also included within the scope of the invention are functional antigen binding sites comprised of fewer CDRs (i.e., where binding specificity is

determined by three, four or five CDRs). For example, less than a complete set of 6 CDRs may be sufficient for binding. In some cases, a VH or a VL domain will be sufficient.

The antibodies of the invention further 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.

The terms "monoclonal antibody" or "monoclonal antibody composition" as used herein refer to a preparation of antibody 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, A., et al. and Boerner, P., et al. are also available for the preparation of human monoclonal antibodies (Cole, A., et al., Monoclonal Antibodies and Cancer Therapy, Liss, A.L., 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 domain 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, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991) (includes the numbering according to the EU Index of Kabat, (abbreviated as numbering according to Kabat herein below)).

As used herein, the term "binding" or "specifically binding" refers to the binding of the antibody to an epitope of the antigen (either human VEGF or human ANG-2) in an in vitro assay, preferably in an plasmon resonance assay (BIAcore, GE-Healthcare Uppsala, Sweden) (Example 3) with purified wild-type antigen. 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). In one embodiment 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.

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.

The term "full length antibody" denotes an antibody consisting of two "full length antibody heavy chains" and two "full length antibody light chains" (see Fig. 1). A "full length antibody heavy chain" 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 "full length antibody heavy chain" is a polypeptide consisting in N-terminal to C-terminal direction of VH, CH1, HR, CH2 and CH3. A "full length antibody light chain" 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 two full length antibody chains are linked together via inter-polypeptide disulfide bonds between the CL domain and the CH1 domain 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 full length 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 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. The N-terminus of the

heavy or light chain of said full length antibody denotes the last amino acid at the N- terminus of said heavy or light chain.

The term "peptide linker" as used within the invention denotes a peptide with amino acid sequences, which is preferably of synthetic origin. These peptides according to invention are used to connect the C-terminus of the light chain to the N-terminus of heavy chain of the second full length antibody (that specifically binds to a second antigen) via a peptide linker. The peptide linker within the second full length antibody heavy and light chain is a peptide with an amino acid sequence with a length of at least 30 amino acids, preferably with a length of 32 to 50 amino acids. In one the peptide linker is a peptide with an amino acid sequence with a length of 32 to 40 amino acids. In one embodiment said linker is (GxS)n with G = glycine, S = serine, (x =3, n= 8, 9 or 10 and m= 0, 1, 2 or 3) or (x = 4 and n= 6, 7 or 8 and m= 0, 1, 2 or 3), preferably with x = 4, n= 6 or 7 and m= 0, 1, 2 or 3, more preferably with x = 4, n= 7 and m= 2. In one embodiment said linker is $(G_4S)_6G_2$.

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 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).

Preferably the bispecific, bivalent antibodies according to the invention have a constant region of human IgG1 subclass.

While antibodies of the IgG4 subclass show reduced Fc receptor (FcγRIIIa) binding, antibodies of other IgG subclasses show 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 antibody according to the invention has a reduced FcR binding compared to an IgG1 antibody and the bispecific, bivalent antibody is in regard to FcR binding of IgG4 subclass or of IgG1 subclass with a mutation in S228, L234, L235 and/or D265, and/ or contains the PVA236 mutation. In one embodiment the mutations in the bispecific bivalent antibody are in IgG4 S228P and L235E and in IgG1 L234A and L235A.

Another aspect of the invention a bispecific, bivalent antibody characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to a first antigen;

b) the heavy chain and the light chain of a second full length antibody that specifically binds to a second antigen ,
wherein the N-terminus of the heavy chain is connected to the C-terminus of the light chain via a peptide linker; and
wherein the variable domains VL and VH or the constant domains CL and CH1 are replaced by each other.

Preferably the CH3 domains of this bispecific, bivalent antibody format is 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 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. For further details and embodiments see above.

Another aspect of the invention a bispecific, bivalent antibody characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to a first antigen;

b) the heavy chain and the light chain of a second full length antibody that specifically binds to a second antigen ,
wherein the N-terminus of the heavy chain is connected to the C-terminus of the light chain via a peptide linker; and
wherein the variable domains VL and VH are replaced by each other.

An exemplary scheme of this bispecific, bivalent antibody format is shown in Figure 2b including Knobs-into-Holes modified CH3 domains. The antibodies based on this bispecific, bivalent antibody format are named in the examples OAscXFab1.

In one embodiment such bispecific antibody is characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 39, and as light chain of the first full length antibody the SEQ ID NO: 40, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the SEQ ID NO: 38.

Another aspect of the invention a bispecific, bivalent antibody characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to a first antigen;
b) the heavy chain and the light chain of a second full length antibody that specifically binds to a second antigen,
wherein the N-terminus of the heavy chain is connected to the C-terminus of the light chain via a peptide linker; and
wherein the constant domains CL and CH1 are replaced by each other.

An exemplary scheme of this bispecific, bivalent antibody format is shown in Figure 2c including Knobs-into-Holes modified CH3 domains. The antibodies

based on this bispecific, bivalent antibody format are named in the examples OAscXFab2 and OAscXFab3.

In one embodiment such bispecific antibody is characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 42, and as light chain of the first full length antibody the SEQ ID NO: 43, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the SEQ ID NO: 41.

In one embodiment such bispecific antibody is characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 45, and as light chain of the first full length antibody the SEQ ID NO: 46, and
b) as heavy chain of the second full length antibody connected to the light chain of the second full length antibody via a peptide linker the SEQ ID NO: 44.

The antibody according to the invention is produced by recombinant means. Thus, one aspect of the current invention is a nucleic acid encoding the antibody according to the invention and a further aspect is a cell comprising said nucleic acid encoding an antibody 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 antibody 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 antibody 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) 151-160; Werner, R.G., Drug Res. 48 (1998) 870-880.

Accordingly one embodiment of the invention is a method for the preparation of a bispecific antibody according to the invention, comprising the steps of

a) transforming a host cell with vectors comprising nucleic acid molecules encoding said antibody;

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

c) recovering said antibody molecule from said culture.

The bispecific antibodies 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 and 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 antibody are prepared by introducing appropriate nucleotide changes into the antibody DNA, or by nucleotide synthesis. Such modifications can be performed, however, only in a very limited range. 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).

It has now been found that the bispecific antibodies against human VEGF and human ANG-2 according to the current invention have valuable characteristics such as high stability and valuable pharmacokinetic/pharmacodynamic properties like e.g. good (i.e. slow) clearance (e.g. at low doses).

The bispecific, bivalent antibodies according to the invention show benefits for human patients in need of a VEGF and ANG-2 targeting therapy.

Furthermore they have biological or pharmacological activity and show in vivo tumor growth inhibition and/or inhibition of tumor angiogenesis.

The bispecific antibodies according to the invention are highly effective in

a) tumor growth inhibition (e.g. with the bispecific antibodies according to the invention tumor stasis could be achieved already at lower concentrations compared to the combination of the two monospecific antibodies (e.g in the COLO205 and the KPL4 tumor models of Example 9 and 10, tumor stasis was already achieved with 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of ANG2i-LC06 + 10 mg/kg of Avastin), and/or

b) inhibition of tumor angiogenesis or vascular diseases (e.g. maximal antiangiogenic effects with the bispecific antibodies according to the invention could already be achieved at lower concentrations compared to the combination of the two monospecific antibodies (e.g. in the mouse corneal angiogenesis assay of Example 8, the maximal antiangiogenic effect was already achieved with 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of ANG2i-LC06 + 10 mg/kg of Avastin).

Finally the bivalent bispecific against human VEGF and human ANG-2 according to the current invention may have a valuable efficacy/toxicity profile and may provide benefits for a patient in the need of an anti-VEGF and anti-ANG-2 therapy.

One aspect of the invention is a pharmaceutical composition comprising an antibody according to the invention. Another aspect of the invention is the use of

an antibody 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 antibody according to the invention. In another aspect, the present invention provides a composition, e.g. a pharmaceutical composition, containing an antibody according to the present invention, formulated together with a pharmaceutical carrier.

One embodiment of the invention is the bispecific antibody according to the invention for the treatment of cancer.

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

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

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

Another aspect of the invention is said pharmaceutical composition for the prevention of metastasis.

The invention comprises the bispecific antibody according to the invention for the prevention of metastasis.

Another aspect of the invention is the use of a bispecific antibody according to the invention for the manufacture of a medicament for the prevention of metastasis.

Another aspect of the invention is a method of prevention metastasis in patient suffering from primary cancer by administering a bispecific according to the invention to a patient in the need of such preventative treatment.

We could show highly efficient prevention of spontaneous metastasis/secondary tumors in vivo in a orthotopic and a subcutaneous cancer model (see Example 9) (in contrast to experimental model where the tumor cells are injected i.v. This is similar to the clinical situation wherein cells disseminate from a primary tumor and metastase to secondary organ like lung or liver (where secondary tumors).

The term "metastasis" according to the invention refers to the transmission of cancerous cells from the primary tumor to one or more sites elsewhere in a patient where then secondary tumors develop. Means to determine if a cancer has metastasized are known in the art and include bone scan, chest X-ray, CAT scan, MRI scan, and tumor marker tests.

The term "prevention of metastasis" or "prevention of secondary tumors" as used herein have the same meaning and refers a prophylactic agent against metastasis in patient suffering from cancer in this way inhibiting or reducing a further transmission of cancerous cells from the primary tumor to one or more sites elsewhere in a patient. This means that the metastasis of the primary, tumor or cancer is prevented, delayed, or reduced and thus the development of secondary tumors is prevented, delayed, or reduced. Preferably the metastasis i.e. secondary tumors of the lung are prevented or reduced, which means that metastatic transmission of cancerous cells from the primary tumor to the lung is prevented or reduced.

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.

Another aspect of the invention is the bispecific antibody according to the invention or said pharmaceutical composition as anti-angiogenic agent. Such anti-angiogenic agent can be used for the treatment of cancer, especially solid tumors, and other vascular diseases.

One embodiment of the invention is the bispecific antibody according to the invention for the treatment of vascular diseases.

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

Another aspect of the invention is the use of an antibody according to the invention for the manufacture of a medicament for the treatment of vascular diseases.

Another aspect of the invention is method of treatment of patient suffering from vascular diseases by administering an antibody according to the invention to a patient in the need of such treatment.

The term "vascular diseases" includes Cancer, Inflammatory diseases, Atherosclerosis, Ischemia, Trauma, Sepsis, COPD, Asthma, Diabetes, AMD, Retinopathy, Stroke, Adipositas, Acute lung injury, Hemorrhage, Vascular leak e.g. Cytokine induced, Allergy, Graves' Disease, Hashimoto's Autoimmune Thyroiditis, Idiopathic Thrombocytopenic Purpura, Giant Cell Arteritis, Rheumatoid Arthritis, Systemic Lupus Erythematosus (SLE), Lupus Nephritis, Crohn's Disease, Multiple Sclerosis, Ulcerative Colitis, especially to solid tumors, intraocular neovascular syndromes such as proliferative retinopathies or age-related macular degeneration (AMD), rheumatoid arthritis, and psoriasis (Folkman, J., et al., J. Biol. Chem. 267 (1992) 10931-10934; Klagsbrun, M., et al., Annu. Rev. Physiol. 53 (1991) 217-239; and Garner, A., Vascular diseases, In: Pathobiology of ocular disease, A dynamic approach, Garner, A., and Klintworth, G.K., (eds.), 2nd edition, Marcel Dekker, New York (1994), pp 1625-1710).

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, F.L., van der Eb, A.J., Virology 52 (1973) 546-467. 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 (Amino acid sequences)

SEQ ID NO:1	variable heavy chain domain VH of <VEGF> bevacizumab
SEQ ID NO:2	variable light chain domain VL of <VEGF> bevacizumab
SEQ ID NO:3	variable heavy chain domain VH of <ANG-2> E6Q
SEQ ID NO:4	variable light chain domain VL of < ANG-2> E6Q
SEQ ID NO: 5	XMab1 –<VEGF> light chain
SEQ ID NO: 6	XMab1 –<ANG2> light chain
SEQ ID NO: 7	XMab1 –<VEGF> heavy chain
SEQ ID NO: 8	XMab1 –<ANG2> heavy chain
SEQ ID NO: 9	XMab2 –<VEGF> light chain
SEQ ID NO: 10	XMab2 –<ANG2> light chain
SEQ ID NO: 11	XMab2 –<VEGF> heavy chain
SEQ ID NO: 12	XMab2 –<ANG2> heavy chain

SEQ ID NO: 13	XMab3 –<VEGF> light chain
SEQ ID NO: 14	XMab3–<ANG2> light chain
SEQ ID NO: 15	XMab3 –<VEGF> heavy chain
SEQ ID NO: 16	XMab3 –<ANG2> heavy chain
SEQ ID NO: 17	XMab4 –<VEGF> light chain
SEQ ID NO: 18	XMab4–<ANG2> light chain
SEQ ID NO: 19	XMab4 –<VEGF> heavy chain
SEQ ID NO: 20	XMab4 –<ANG2> heavy chain
SEQ ID NO: 21	XMab5 –<VEGF> light chain
SEQ ID NO: 22	XMab5 –<ANG2> light chain
SEQ ID NO: 23	XMab5 –<VEGF> heavy chain
SEQ ID NO: 24	XMab5 –<ANG2> heavy chain
SEQ ID NO: 25	XMab6 –<VEGF> light chain
SEQ ID NO: 26	XMab6 –<ANG2> light chain
SEQ ID NO: 27	XMab6 –<VEGF> heavy chain
SEQ ID NO: 28	XMab6 –<ANG2> heavy chain
SEQ ID NO: 29	OAscFab1 –<ANG2> peptide connected heavy chain and light chain
SEQ ID NO: 30	OAscFab1 –<VEGF> heavy chain
SEQ ID NO: 31	OAscFab1 –<VEGF> light chain
SEQ ID NO: 32	OAscFab2 –<ANG2> peptide connected heavy chain and light chain
SEQ ID NO: 33	OAscFab2 –<VEGF> heavy chain
SEQ ID NO: 34	OAscFab2 –<VEGF> light chain
SEQ ID NO: 35	OAscFab3 –<ANG2> peptide connected heavy chain and light chain
SEQ ID NO: 36	OAscFab3 –<VEGF> heavy chain
SEQ ID NO: 37	OAscFab3 –<VEGF> light chain
SEQ ID NO:38	OAscXFab1 –<ANG2> peptide connected heavy chain and light chain
SEQ ID NO: 39	OAscXFab1 –<VEGF> heavy chain
SEQ ID NO: 40	OAscXFab1 –<VEGF> light chain
SEQ ID NO: 41	OAscXFab2 –<ANG2> peptide connected heavy chain and light chain
SEQ ID NO: 42	OAscXFab2 –<VEGF> heavy chain
SEQ ID NO: 43	OAscXFab2 –<VEGF> light chain

SEQ ID NO: 44	OAscXFab3 –<ANG2> peptide connected heavy chain and light chain
SEQ ID NO: 45	OAscXFab3 –<VEGF> heavy chain
SEQ ID NO: 46	OAscXFab3 –<VEGF> light chain
SEQ ID NO: 47	Human vascular endothelial growth factor (VEGF)
SEQ ID NO: 48	Human angiopoietin-2 (ANG-2)

Experimental procedures

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 were 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 were used according to the manufacturer's instructions.

Gene synthesis

Desired gene segments can be prepared from oligonucleotides made by chemical synthesis. The gene segments, which are flanked by singular restriction endonuclease cleavage sites, were 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 were confirmed by DNA sequencing.

Gene synthesis fragments were ordered according to given specifications at Geneart (Regensburg, Germany). All gene segments encoding light and heavy

chains of Ang-2/VEGF bispecific antibodies were synthesized with a 5'-end DNA sequence coding for a leader peptide (MGWSCIILFLVATATGVHS), which targets proteins for secretion in eukaryotic cells, and unique restriction sites at the 5' and 3' ends of the synthesized gene. DNA sequences carrying disulfide stabilized "knobs-into-hole" modified heavy chains were designed with S354C and T366W mutations in the "knobs" heavy chain and Y349C, T366S, L368A and Y407V mutations in the "hole" heavy chain.

DNA sequence determination

DNA sequences were 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 was used for sequence creation, mapping, analysis, annotation and illustration.

Expression vectors

For the expression of the described antibodies variants of expression plasmids for transient expression (e.g. in HEK293 EBNA or HEK293-F) cells or for stable expression (e.g. in CHO cells) based either on a cDNA organization with a CMV-Intron A promoter or on a genomic organization with a CMV promoter (e.g. Figure 2B) were 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 antibody chain (heavy chain, modified heavy chain or light chain) 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.

For transient and stable transfections larger quantities of the plasmids were prepared by plasmid preparation from transformed E. coli cultures (Nucleobond AX, Macherey-Nagel).

Cell culture techniques

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

Transient transfections in HEK293-F system

Recombinant immunoglobulin variants were expressed by transient transfection of human embryonic kidney 293-F cells using the FreeStyle™ 293 Expression System according to the manufacturer's instruction (Invitrogen, USA). Briefly, suspension FreeStyle™ 293-F cells were cultivated in FreeStyle™ 293 Expression medium at 37°C/8 % CO_2 and the cells were seeded in fresh medium at a density of 1-2x10^6 viable cells/ml on the day of transfection. DNA-293fectin™ complexes were prepared in Opti-MEM® I medium (Invitrogen, USA) using 325 µl of 293fectin™ (Invitrogen, Germany) and 250 µg of heavy and light chain plasmid DNA in a 1:1 molar ratio for a 250 ml final transfection volume for monospecific parent antibodies. "Knobs-into-hole" DNA-293fectin complexes with two heavy chains and one light chain were prepared in Opti-MEM® I medium (Invitrogen, USA) using 325 µl of 293fectin™ (Invitrogen, Germany) and 250 µg of "Knobs-into-hole" heavy chain 1 and 2 and light chain plasmid DNA generally in a 1:1:1 molar ratio for a 250 ml final transfection volume (OAscFab and OAscXFab). For expression yield optimization the ratio can be varied. XMab DNA-293fectin complexes were prepared in Opti-MEM® I medium (Invitrogen, USA) using 325 µl of 293fectin™ (Invitrogen, Germany) and 250 µg of "Knobs-into-hole" heavy chain 1 and 2 and light chain plasmid DNA in a 1:1:1:1 molar ratio for a 250 ml final transfection volume. For expression yield optimization the ratio can be varied. Antibody containing cell culture supernatants were harvested 7 days after transfection by centrifugation at 14000 g for 30 minutes and filtered through a sterile filter (0.22 µm). Supernatants were stored at -20° C until purification.

Protein determination

The protein concentration of purified antibodies and derivatives was 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 4 (1995) 2411-1423.

Antibody concentration determination in supernatants

The concentration of antibodies and derivatives in cell culture supernatants was 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, 20 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 antibodies and derivatives in cell culture supernatants was measured by Protein A-HPLC chromatography. Briefly, cell culture supernatants containing antibodies and derivatives that bind to Protein A were applied to a HiTrap Protein A column (GE Healthcare) in 50 mM K2HPO4, 300 mM NaCl, pH 7.3 and eluted from the matrix with 550 mM acetic acid, pH 2.5 on a Dionex HPLC-System. The eluted protein was quantified by UV absorbance and integration of peak areas. A purified standard IgG1 antibody served as a standard.

Alternatively, the concentration of antibodies and derivatives in cell culture supernatants was measured by Sandwich-IgG-ELISA. Briefly, StreptaWell High Bind Strepatavidin A-96 well microtiter plates (Roche) were coated with 100 µL/well biotinylated anti-human IgG capture molecule F(ab')2<h-Fcgamma> 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 was added to the wells and incubated for 1-2 h on a microtiterplate shaker at room temperature. The wells were washed three times with 200 µL/well PBST and bound antibody was detected with 100 µl F(ab')2<hFcgamma>POD (Dianova) at 0.1 µg/mL as detection antibody for 1-2 h on a microtiterplate shaker at room temperature. Unbound detection antibody was washed away three times with 200 µL/well PBST and the bound detection antibody was detected by addition of 100 µL ABTS/well. Determination of absorbance was performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

Purification of bispecific antibodies

Bispecific antibodies were purified from cell culture supernatants by affinity chromatography using Protein A-Sepharose™ (GE Healthcare, Sweden) and Superdex200 size exclusion chromatography. Briefly, sterile filtered cell culture supernatants were applied on a HiTrap ProteinA HP (5 ml) column equilibrated with PBS buffer (10 mM Na_2HPO_4, 1 mM KH_2PO_4, 137 mM NaCl and 2.7 mM KCl, pH 7.4). Unbound proteins were washed out with equilibration buffer. Antibody and antibody variants were eluted with 0.1 M citrate buffer, pH 2.8, and the protein containing fractions were neutralized with 0.1 ml 1 M Tris, pH 8.5. Then, the eluted protein fractions were pooled, concentrated with an Amicon Ultra centrifugal filter device (MWCO: 30 K, Millipore) to a volume of 3 ml and loaded on a Superdex200 HiLoad 120 ml 16/60 gel filtration column (GE Healthcare, Sweden) equilibrated with 20mM Histidin, 140 mM NaCl, pH 6.0. Fractions containing purified bispecific antibodies with less than 5 % high molecular weight aggregates were pooled and stored as 1.0 mg/ml aliquots at -80°C.

SDS-PAGE

The NuPAGE® Pre-Cast gel system (Invitrogen) was used according to the manufacturer's instruction. In particular, 4-20 % NuPAGE® Novex® TRIS-Glycine Pre-Cast gels and a Novex® TRIS-Glycine SDS running buffer were used. (see e.g. Figure 3). Reducing of samples was achieved by adding NuPAGE® sample reducing agent prior to running the gel.

Analytical size exclusion chromatography

Size exclusion chromatography for the determination of the aggregation and oligomeric state of antibodies was performed by HPLC chromatography. Briefly, Protein A purified antibodies were 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 was quantified by UV absorbance and integration of peak areas. BioRad Gel Filtration Standard 151–1901 served as a standard. (see e.g. Figure 4).

Mass spectrometry

The total deglycosylated mass of crossover antibodies was determined and confirmed via electrospray ionization mass spectrometry (ESI-MS). Briefly, 100 µg purified antibodies were 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 heavy and light chains was determined by ESI-MS after deglycosylation and reduction. In brief, 50 µg antibody in 115 µl were 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 was determined via ESI-MS on a Q-Star Elite MS system equipped with a NanoMate source.

Generation of HEK293-Tie2 cell line

In order to determine the interference of Angiopoietin-2 antibodies with ANGPT2 stimulated Tie2 phosphorylation and binding of ANGPT2 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 (SEQ ID 108) 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 was subsequently used for cellular assays: ANGPT2 induced Tie2 phosphorylation and ANGPT2 cellular ligand binding assay.

ANGPT2 induced Tie2 phosphorylation assay

Inhibition of ANGPT2 induced Tie2 phosphorylation by ANGPT2 antibodies was measured according to the following assay principle. HEK293-Tie2 clone22 was stimulated with ANGPT2 for 5 minutes in the absence or presence of ANGPT2 antibody and P-Tie2 was quantified by a sandwich ELISA. Briefly, 2x105

HEK293-Tie2 clone 22 cells per well were 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 ANGPT2 antibodies was prepared in a microtiter plate (4-fold concentrated, 75µl final volume/well, duplicates) and mixed with 75µl of an ANGPT2 (R&D systems # 623-AN] dilution (3.2 µg/ml as 4-fold concentrated solution). Antibodies and ANGPT2 were pre-incubated for 15 min at room temperature. 100 µl of the mix were 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 were 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 were lysed for 30 min at 4°C on a microtiter plate shaker and 100 µl lysate were 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 were quantified according to the manufacturer's instructions and IC50 values for inhibition were 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 was chosen to measure the cellular function of VEGF antibodies. Briefly, 5000 HUVEC cells (low passage number, ≤5 passages) per 96 well were 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 antibody were mixed with rhVEGF (30 ngl/ml final concentration, BD # 354107) and pre-incubated for 15 minutes at room temperature. Subsequently, the mix was added to the HUVEC cells and they were incubated for 72 h at 37°C, 5% CO2. On the day of analysis the plate was equilibrated to room temperature for 30 min and cell viability/proliferation was determined using the CellTiter-GloTM Luminescent Cell Viability Assay kit according to the manual (Promega, # G7571/2/3). Luminescence was determined in a spectrophotometer.

Example 1a

Expression & Purification of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules XMab

According the procedures described in the materials and methods above, the bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules XMab1, XMab1 and XMab3 were expressed and purified. The VH and VL of <VEGF> part (SEQ ID NO:1 and SEQ ID NO:2) are based on bevacizumab. The VH of <ANG2> part (SEQ ID NO:3) was derived by a E6Q mutation (the original amino acid glutamic acid (E) at position 6 was replaced by glutamine (Q)) of the VH sequence of ANG2i-LC06 (which is described in the PCT application No. PCT/EP2009/007182 (WO2010/040508) – and which is further maturated fragment of a sequence obtained via phage display). The VL of <ANG2> part (SEQ ID NO:4) was derived from the VL sequences ANG2i-LC06 (see PCT application No. PCT/EP2009/007182 (WO2010/040508)). The bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules XMab1, XMab2 and XMab3 were expressed and purified. The relevant light and heavy chain amino acid sequences of these bispecific, bivalent antibodies are given in SEQ ID NO: 5 - 8 (XMab1), in SEQ ID NO: 9 -12 (XMab2), and in SEQ ID NO: 13-16 (XMab3). For an exemplary structure see Figure 1.

Key data	XMab1	XMab2	XMab3
Expression (Yield)	32 µg/mL	10 µg/mL	39 µg/mL
Purification (Yield, Prot. A. homog.)	31 mg/L, 64%	8 µg/mL, 80 %	-

The bispecific, bivalent <VEGF-ANG-2> antibodies XMab4, XMab5 and XMab6 (with the relevant light and heavy chain amino acid sequences given in SEQ ID NO: 17-20 (XMab4), in SEQ ID NO: 21-24 (XMab5), and in SEQ ID NO: 25-28 (XMab6)) are expressed and purified analogously.

Binding affinities and other properties were or are determined as described.

Example 1b

Expression & Purification bispecific, bivalent <VEGF-ANG-2> antibody molecules OAscFab

According to the procedures described in the materials and methods above, the bispecific, bivalent <VEGF-ANG-2> antibody molecules OAscFab1, OAscFab2, OAscFab3 were expressed and purified. The VH and VL of <VEGF> part (SEQ ID NO:1 and SEQ ID NO:2) are based on bevacizumab. The VH of <ANG2>E6Q part (SEQ ID NO:3) was derived by a E6Q mutation (the original amino acid glutamic acid (E) at position 6 was replaced by glutamine (Q)) of the VH sequences ANG2i-LC06 (which is described in the PCT application No. PCT/EP2009/007182 (WO2010/040508) – and which is further maturated fragment of a sequence obtained via phage display). The VL of <ANG2>E6Q part (SEQ ID NO:4) was derived from the VL sequence of ANG2i-LC06 (see PCT application No. PCT/EP2009/007182 (WO2010/040508) (WO2010/040508)). The relevant light and heavy chain amino acid sequences of these bispecific, bivalent antibodies are given in SEQ ID NO: 29 -31 (OAscFab1), in SEQ ID NO: 32 -34 (OAscFab2), and in SEQ ID NO: 35-37 (OAscFab3). For an exemplary structure see Figure 2a. Expression of OAscFab1, OAscFab1, OAscFab2 and OAscFab3 was confirmed by Western blot. Purification of OAscFab2 and OAscFab3 led to the following yields.

Antibody	**Supernatant**	**Protein A**		**SEC**	
		Yield	**Mono.**	**Yield**	**Monomer**
OAscFab2	0.5 L	36.0 mg	86 %	21.7 mg	> 95 %
OAscFab3	0.5 L	29.3 mg	85 %	17.7 mg	> 95 %

Binding affinities and other properties are determined as described.

Example 1c

Expression & Purification bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules OAscXFab

According the procedures described in the materials and methods above, the bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules

OAscXFab1, OAscXFab2, OAscXFab3, were expressed and purified. The VH and VL of <VEGF> part (SEQ ID NO:1 and SEQ ID NO:2) are based on bevacizumab. The VH of <ANG2>E6Q part (SEQ ID NO:3) was derived by a E6Q mutation (the original amino acid glutamic acid (E) at position 6 was replaced by glutamine (Q)) of the VH sequences ANG2i-LC06 (which is described in the PCT application No. PCT/EP2009/007182 (WO2010/040508) – and which is further maturated fragment of a sequence obtained via phage display). The VL of <ANG2>E6Q part (SEQ ID NO:4) was derived from the VL sequence of ANG2i-LC06 (see PCT application No. PCT/EP2009/007182 (WO2010/040508)). The relevant light and heavy chain amino acid sequences of these bispecific, bivalent antibodies are given in SEQ ID NO: 38 -40 (OAscXFab1), in SEQ ID NO: 41 -43 (OAscXFab2), and in SEQ ID NO: 44-46 (OAscXFab3). For an exemplary structure see Figure 2b (OAscXFab1) and Figure 2c (OAscXFab2, OAscXFab3). Expression was confirmed by Western blot.

Key data	OAscXFab1	OAscXFab2	OAscXFab3
Expression (Yield)	23 µg/mL	23 µg/mL	26 µg/mL

Binding affinities and other properties are determined as described.

Example 2

Stability of bispecific antibodies

Denaturation temperature (SYPRO orange method)

To determine the temperature at which protein denaturation (i.e. temperature-induced loss of protein structure) occurs, a method was used that relies a hydrophobic fluorescent dye (SYPRO orange, Invitrogen) that exhibits strong fluorescence in hydrophobic environments. Upon protein denaturation, hydrophobic patches become exposed to the solvent, leading to an increased fluorescence. At temperatures above the denaturation temperature, fluorescence intensities decrease again, hence the temperature at which a maximum intensity is reached is defined as the denaturation temperature. The method is described by Ericsson, U.B., et al., Anal Biochem 357 (2006) 289-298 and He, F., et al., Journal of Pharmaceutical Sciences 99 (2010) 1707-1720.

Proteins samples at a concentration of approx. 1 mg/mL in 20 mM His/HisCl, 140 mM NaCl, pH 6.0 were mixed with SYPRO orange (5000x stock solution) to reach

a final dilution of 1:5000. A volume of 20 µL was transferred into a 384 well-plate and temperature-dependent fluorescence was recorded in a LightCycler ® 480 Real-Time PCR System (Roche Applied Sciences) at a heat rate of 0.36 °C/min.

Aggregation temperature by Dynamic Light Scattering (DLS)

The temperature at which thermally induced protein aggregation occurs was determined by dynamic light scattering (DLS). DLS yields information on the size distribution of macromolecules in solution, derived from fluctuations of scattered light intensities on a microsecond scale. When samples are heated up gradually, aggregation starts at a certain temperature, giving rise to growing particle sizes. The temperature at which particle sizes begin to increase is defined as the aggregation temperature. Aggregation and denaturation temperatures need not necessarily be identical since denaturation may not necessarily be a prerequisite for aggregation.

For aggregation temperature measurements, a DynaPro DLS platereader (Wyatt technologies) was used. Preceding the measurement, samples were filtered via 384-well filter plates (Millipore MultiScreen 384-well Filtration System, 0.45 µm) into optical 384 well plates (Corning #3540). A sample volume of 35 µL was used at a protein concentration of approx. 1 mg/mL in formulation buffer (20 mM citrate, 180 mM sucrose, 20 mM arginine, 0.02 % polysorbate 20). Each well was covered with 20 µL paraffin oil (Sigma) to avoid evaporation. Samples were heated from 25 °C to 80 °C at a rate of 0.05 °C/min and DLS data were acquired continuously for a maximum number of 15 samples per run.

Aggregation rate per DLS

DLS is a sensitive method for detecting aggregates of macromolecules in solution, since aggregates give rise to strong light scattering signals. Hence, the tendency of a molecule to aggregate can be followed over time by repeated acquisition of DLS data. To accelerate potential aggregation to practical rates, measurements were conducted at 50 °C.

Sample preparation was performed as described above. DLS data were recorded for up to 100 hours. Aggregation rates (nm/day) were calculated as the slope of a linear fit of average diameters over time.

Stability in formulation buffer

To assess bispecific molecules for their stability with regard to aggregation/fragmentation, samples were incubated for 3 weeks at 40 °C in

formulation buffer (20 mM citrate, 180 mM sucrose, 20 mM arginine, 0.02 % polysorbate 20) at a protein concentration of approximately 1 mg/mL. A control sample was stored for 3 weeks at -80 °C.

Size exclusion chromatography for the quantification of aggregates and low-molecular weight (LMW) species was performed by HPLC. An amount of 25-100 µg of protein was applied to a Tosoh TSKgel G3000SWXL column in 300 mM NaCl, 50 mM potassium phosphate, pH 7.5 on an Ultimate3000 HPLC system (Dionex). The eluted protein was quantified by UV absorbance at 280 nm.

Results:

Method	**Stability of XMab1 (SEQ ID NO: 5-8)**
Denaturation temperature (SYPRO orange method)	71 °C
Aggregation temperature by Dynamic Light Scattering (DLS)	65 °C
Aggregation rate per DLS	0.04 nm/day
Stability in formulation buffer (difference between 40°C and -80°C after 3 weeks storage)	ΔHMW: 0.6 area% ΔLMW: 0.5 area% ΔMonomer: -1.2 area%

Example 3:

Binding properties of bispecific antibody <VEGF-Ang-2>

A) Binding properties characterized by Surface Plasmon Resonance (SPR) Analysis

Simultaneous binding of both antigens was confirmed by applying Surface Plasmon Resonance (SPR) using a BIAcore T100 instrument (GE Healthcare Biosciences AB, Uppsala, Sweden). VEGF was immobilized to a CM5 Sensorchip using standard amine coupling chemistry. In a first step, <VEGF-Ang-2> XMAb was injected at a concentration of 10 µg/ml in HBS buffer (10 mM HEPES, 150 mM NaCl, 0.05% Tween 20, pH 7.4) at 25°C. After binding of the antibody to the immobilized VEGF, hAng-2 was injected at 10 µg/ml in a second step (Figure 3)

In a further experiment the affinity and binding kinetics of <VEGF-Ang-2> XMab were determined. Briefly, goat<hIgG-Fcgamma> polyclonal antibodies were immobilized on a CM4 chip via amine coupling for presentation of the bispecific

antibody against Ang-2 and VEGF. Binding was measured in HBS buffer at 25°C or 37°C. Purified Ang-2-His (R&D systems or in house purified) or VEGF (R&D systems or in house purified) was added in various concentrations between 0.37 nM and 30 nM or between 3.7 nM and 200 nM in solution. Association was measured by an injection of 3 minutes; dissociation was measured by washing the chip surface with HBS buffer for 10 minutes and a KD value was estimated using a 1:1 Langmuir binding model. Due to heterogenity of the Ang-2 preparation no 1:1 binding could be observed. Therefore KD values are apparent values. The determined affinity of <VEGF-Ang-2> XMab to VEGF was extremely high, the calculated off-rate was out of Biacore specifications even at 37°C. In Table 1 the binding constants for both antigens are summarized.

Table 1: Kinetic parameters of <VEGF-Ang-2> XMab1 binding to Ang-2 and VEGF

Analyte	**Apparent ka (1/Ms)**	**Apparent kd (1/s)**	**Apparent KD (M)**
Ang-2	2.7E+06	6.3E-04	2.4E-10
VEGF	1.2E+05	< 1E-06	< 1E-10

B) Assay for quantification of binding active bispecific <Ang2/VEGF> XMab1

Additionally to the SPR analysis, an ELISA was established to quantify the amount of binding active bispecific mAb<Ang2/VEGF>antibodies. In this assay, hAng2 is directly coated to the wells of a maxisorp microtiter plate (MTP) in the first step. Meanwhile, the samples / reference standards (mAb<Ang2/VEGF>) were pre-incubated in the wells of another MTP with digoxigenylated VEGF. After pre-incubation and coating, excess of unbound Ang2 was removed by washing the Ang2 coated MTP. The pre-incubated mixture of <Ang2/VEGF> and VEGF-Dig was then transferred to the hAng2 coated MTP and incubated. After incubation, the excess of pre-incubation solution was removed by washing followed by incubation with a horse-radish peroxidase labeled anti-digoxigenin antibody. The antibody-enzyme conjugate catalyzes the color reaction of the ABTS® substrate. The signal was measured by ELISA reader at 405 nm wavelength (reference wavelength: 490 nm ([405/490] nm)). Absorbance values of each sample were determined in duplicates. (A scheme exemplifying this test system is shown in Figure 4 and Calibration curve of ELISA for quantification is shown in Figure 5)

Example 4

Tie2 phosphorylation

In order to confirm that the anti-ANGPT2 related activities are retained in the bispecific bivalent <VEGF-ANGPT2> antibody XMAb1 Tie2 phosphorylation assay was performed. The efficacy of XMAb1 was determined in the ANGPT2 stimulated Tie2 phosphorylation assay as described above.

It was shown that XMAb1 interferes with ANGPT2 stimulated Tie2 phosphorylation in the ANGPT2 stimulated Tie2 phosphorylation assay as described above. IC50 for XMAb1 was 7.4 nM +/- 2.3.

Example 5

Inhibition of huANG-2 binding to Tie-2 (ELISA)

The interaction ELISA was performed on 384 well microtiter plates (MicroCoat, DE, Cat.No. 464718) at RT. After each incubation step plates were washed 3 times with PBST. ELISA plates were coated with 5 µg/ml Tie-2 protein for 1 hour (h). Thereafter the wells were blocked with PBS supplemented with 0.2% Tween-20 and 2% BSA (Roche Diagnostics GmbH, DE) for 1 h. Dilutions of purified bispecific Xmab antibodies in PBS were incubated together with 0.2 µg/ml huAngiopoietin-2 (R&D Systems, UK, Cat.No. 623-AN) for 1 h at RT. After washing a mixture of 0.5 µg/ml biotinylated anti-Angiopoietin-2 clone BAM0981 (R&D Systems, UK) and 1:3000 diluted streptavidin HRP (Roche Diagnostics GmbH, DE, Cat.No.11089153001) was added for 1 h. Thereafter the plates were washed 3 times with PBST. Plates are developed with freshly prepared ABTS reagent (Roche Diagnostics GmbH, DE, buffer #204 530 001, tablets #11 112 422 001) for 30 minutes at RT. Absorbance was measured at 405 nm and the IC50 was determined. XMab1 showed an inhibition of ANG-2 binding to Tie-2 with an IC50 of 12 nM.

Example 6

Inhibition of hVEGF binding to hVEGF Receptor (ELISA)

The test was performed on 384 well microtiter plates (MicroCoat, DE, Cat.No. 464718) at RT. After each incubation step plates were washed 3 times with PBST. At the beginning, plates were coated with 1 µg/ml hVEGF-R protein (R&D Systems, UK, Cat.No.321-FL) for 1 hour (h). Thereafter the wells were blocked with PBS supplemented with 0.2% Tween-20 and 2% BSA (Roche Diagnostics

GmbH, DE) for 1 h. Dilutions of purified bispecific XMab antibodies in PBS were incubated together with 0.15 µg/ml huVEGF121 (R&D Systems, UK, Cat.No. 298-VS) for 1 h at RT. After washing a mixture of 0.5 µg/ml anti VEGF clone Mab923 (R&D Systems, UK) and 1:2000 horse radish peroxidase (HRP)-conjugated F(ab')2 anti mouse IgG (GE Healthcare, UK, Cat.No.NA9310V) was added for 1 h. Thereafter the plates were washed 6 times with PBST. Plates were developed with freshly prepared ABTS reagent (Roche Diagnostics GmbH, DE, buffer #204 530 001, tablets #11 112 422 001) for 30 minutes at RT. Absorbance was measured at 405 nm and the IC50 was determined. XMab1 showed an inhibition of Inhibition of VEGF binding to VEGF Receptor with an IC50 of 10 nM.

Example 7

HUVEC proliferation

In order to confirm that the anti-VEGF related activities are retained in the bispecific bivalent <VEGF-ANG2> antibody XMAb1 VEGF-induced HUVEC proliferation assay was performed. It was shown that XMAb1 interferes with VEGF-induced HUVEC proliferation in a comparable manner as bevacizumab in the VEGF-induced HUVEC proliferation assay as described above. XMAb1 interferes in a concentration dependent manner with VEGF-induced HUVEC proliferation comparable to the parental antibody bevacizumab (Avastin). IC50 was 1.1 nM for bevacizumab and 2.3 nM for XMAb.

Example 8

Mouse cornea micropocket angiogenesis assay

8 to 10 weeks old female Balb/c mice were purchased from Charles River, Sulzfeld, Germany. The protocol was modified according to the method described by Rogers, M.S., et al., Nat Protoc 2 (2007) 2545-2550. Briefly, micropockets with a width of about 500 µm were prepared under a microscope at approximately 1 mm from the limbus to the top of the cornea using a surgical blade and sharp tweezers in the anesthetized mouse. The disc (Nylaflo®, Pall Corporation, Michigan) with a diameter of 0.6 mm was implanted and the surface of the implantation area was smoothened. Discs were incubated in corresponding growth factor or in vehicle for at least 30 min. After 3, 5 and 7 days (or alternatively only after 3 days) , eyes were photographed and vascular response was measured. The assay was quantified by calculating the percentage of the area of new vessels per total area of the cornea.

The discs were loaded with 300 ng VEGF or with PBS as a control and implanted for 7 days. The outgrowth of vessels from the limbus to the disc was monitored over time on day 3, 5 and 7. One day prior to disc implantation the antibodies (<Ang-2/VEGF> XMAb1, <hVEGF> Avastin (bevacizumab)) were administered intravenously at a dose of 10 mg/kg for Avastin and XMAb1. Animals in the control group received vehicle. The application volume was 10 ml/kg.

To test the effect of XMAb1 on VEGF-induced angiogenesis *in vivo*, we performed the mouse corneal angiogenesis assay. In this assay a VEGF soaked Nylaflo disc is implanted into a pocket of the avascular cornea at a fixed distance to the limbal vessels. Vessels immediately grow into the cornea towards the developing VEGF gradient. Our results demonstrate that systemic administration of the XMAb1 (10 mg/kg) almost completely inhibited the outgrowth of the vessel from the limbus towards the VEGF gradient from study day 3 to 5 (**Fig. 6**). In a further experiment, direct comparison studies were performed. The discs were loaded with 300 ng VEGF or with PBS as a control and implanted for 3 days. The outgrowth of vessels from the limbus to the disc was monitored over time on day 3. One day prior to disc implantation the antibodies (bispecific <Ang-2/VEGF> antibody XMAb1, parent <VEGF> antibody bevacizumab (Avastin), parent <Ang-2> antibody ANG2i-LC06, and the combination of <VEGF> antibody bevacizumab (Avastin) and <Ang-2> antibody ANG2i-LC06) were administered intravenously at a dose of 10 mg/kg for bevacizumab (Avastin), 10 mg/kg for XMAb1, 10 mg/kg for bevacizumab (Avastin), and 10 mg/kg for ANG2i-LC06. The combination of bevacizumab (Avastin) and ANG2i-LC06 was administered with 10mg/kg for bevacizumab (Avastin) and 10mg/kg for ANG2i-LC06. Animals in the control group received vehicle. The application volume was 10 ml/kg.

Our results (see Fig. 7 and Table below) demonstrate that systemic administration of the XMAb1 (10 mg/kg) almost completely inhibited the outgrowth of the vessel from the limbus towards the VEGF gradient at study day 3 comparable to the combination of bevacizumab and ANG2i-LC06. Anti-Ang-2 monotherapy in contrast only slightly inhibited VEGF-induced angiogenesis (**Fig.7**). The maximum effect could already be achieved at lower concentrations of 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of ANG2i-LC06+ 10 mg/kg of bevacizumab (Avastin).

Table: Percent inhibition of VEGF-induced angiogenesis on day 3 in a Mouse cornea micropocket angiogenesis assay

		% inhibition of VEGF-induced angiogenesis
day 3	VEGF (300ng)	0
	ANG2i-LC06 (10mg/kg)	38
	Bevacizumab (Avastin) (10mg/kg)	83
	XMab1 (10mg/kg)	96
	Ang2i-LC06 (10mg/kg) + bevacizumab (Avastin) (10mg/kg)	95

Example 9

In vivo efficacy of bispecific antibody <VEGF-ANG-2> antibody in Colo205 xenograft model in Scid beige mice

Cell lines and culture conditions:

Colo205 human colorectal cancer cells (ATCC No. CCL-222). Tumor cell line were routinely cultured in RPMI 1640 medium (PAA, Laboratories, Austria) supplemented with 10% fetal bovine serum (PAA Laboratories, Austria) and 2 mM L-glutamine, at 37°C in a water-saturated atmosphere at 5% CO_2. Passage 2-5 is used for transplantation.

Animals:

Female SCID beige mice; age 4–5 weeks at arrival (purchased from Charles River Germany) were maintained under specific-pathogen-free condition with daily cycles of 12 h light /12 h darkness according to committed guidelines (GV-Solas; Felasa; TierschG). Experimental study protocol was reviewed and approved by local government. After arrival animals were maintained in the quarantine part of the animal facility for one week to get accustomed to new environment and for observation. Continuous health monitoring is carried out on regular basis. Diet food (Provimi Kliba 3337) and water (acidified pH 2.5-3) were provided ad libitum. Age of mice at start of the study is about 10 weeks.

Tumor cell injection:

At the day of injection, tumor cells were harvested (trypsin-EDTA) from culture flasks (Greiner) and transferred into 50 ml culture medium, washed once and resuspended in PBS. After an additional washing step with PBS and filtration (cell strainer; Falcon ⌀ 100µm) the final cell titer was adjusted to 2.5 x 10^7 / ml. Tumor cell suspension was carefully mixed with transfer pipette to avoid cell aggregation. After this, cell suspension was filled into a 1.0 ml tuberculin syringe (Braun Melsungen) using a wide needle (1.10 x 40 mm); for injection needle size is changed (0.45 x 25 mm) and for every injection a new needle was used. Anesthesia was performed using a Stephens inhalation unit for small animals with preincubation chamber (plexiglas), individual mouse nose-mask (silicon) and not flammable or explosive anesthesia compound Isoflurane (cp-pharma) in a closed circulation system. Two days before injection coat of the animals was shaved and for cell injection skin of anaesthetized animals was carefully lifted up with an anatomic forceps and 100 µl cell suspension (= 2.5 x 10^6 cells) was injected subcutaneously in the right flank of the animals.

Treatment of animals

Treatment of animals started at day of randomization at a mean tumor volume of ~100 mm3, respectively. Mice were treated once weekly i.p. with the different compounds as indicated in following table .

No of animals	Compound	Dose (mg/kg)	Route/Mode of administration
10	Xolair	10	i.p. once weekly
10	<VEGF > Avastin	10	i.p. once weekly
10	< ANG-2> Ang2i-LC06	10	i.p. once weekly
10	Ang2i-LC06 + Avastin	10 10	i.p. once weekly i.p. once weekly
10	XMAb1	10	i.p. once weekly

Monitoring:

Animals were controlled 2x per week for their health status. Body weights were documented 2x per week after cell injection. The tumor dimensions were measured by caliper beginning on the staging day and subsequently 2 times per week during the whole treatment period. Tumor volume was calculated according to NCI protocol (Tumor weight = 1/2ab^2, where "a" and "b" are the long and the short

diameters of the tumor, respectively). Termination criteria were the critical tumor mass (up to 1.7 g or Ø > 1.5 cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

The results (see (**Fig. 8**) show that the bispecific bivalent <VEGF-ANG-2> antibody XMAb1 showed a higher tumor growth inhibition in xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibodies. The efficacy of the combination of ANG2i-LC06 and bevacizumab showed comparable results to the XMAb1. Maximal efficacy of XMAb1 was already reached with 10mg/kg .

In a second experiment the effect of XMAb1 on bigger tumors was analyzed.

Treatment of animals

Treatment of animals started at day of randomization at a mean tumor volume of ~400 mm3, respectively. Mice were treated once weekly i.p. with the different compounds as indicated in following table .

No of animals	Compound	Dose (mg/kg)	Route/Mode of administration
10	Xolair	10	i.p. once weekly
10	<VEGF > Avastin	10	i.p. once weekly
10	< ANG-2> Ang2i-LC06	10	i.p. once weekly
10	Ang2i-LC06 + Avastin	10 10	i.p. once weekly i.p. once weekly
10	XMAb1	10	i.p. once weekly

Monitoring:

Animals were controlled 2x per week for their health status. Body weights were documented 2x per week after cell injection. The tumor dimensions were measured by caliper beginning on the staging day and subsequently 2 times per week during the whole treatment period. Tumor volume is calculated according to NCI protocol (Tumor weight = $1/2ab^2$, where "a" and "b" are the long and the short diameters of the tumor, respectively). Termination criteria were the critical tumor mass (up to 1.7 g or Ø > 1.5 cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

The results (see Fig. 9) show that the bispecific bivalent <VEGF-ANG-2> antibody XMAb1 showed a higher tumor growth inhibition in xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibodies which showed no efficacy in big tumors compared to the control. The efficacy of the combination of ANG2i-LC06 and bevacizumab showed comparable results to the XMAb1. Maximal efficacy of XMAb1 was already reached with 10mg/kg.

Taken together the results demonstrate that independent of the tumor size XMAb1 shows superior efficacy compared to the treatment with monospecific antibodies.

Tumor stasis in these models could already be achieved at lower concentrations of 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of ANG2i-LC06+ 10 mg/kg of Avastin.

Example 10

In vivo efficacy of bispecific antibody <VEGF-ANG-2> antibody in orthotopic KPL-4 xenograft model in Scid beige mice

Tumor cell line

The human breast cancer cell line KPL-4 ((Kurebayashi, J., et al., Br. J. Cancer 79 (1999) 707-17)) has been established from the malignant pleural effusion of a breast cancer patient with an inflammatory skin metastasis. Tumor cells were routinely cultured in DMEM medium (PAN Biotech, Germany) supplemented with 10 % fetal bovine serum (PAN Biotech, Germany) and 2 mM L-glutamine (PAN Biotech, Germany) at 37 °C in a water-saturated atmosphere at 5 % CO_2. Culture passage was performed with trypsin / EDTA 1x (PAN) splitting three times / week.

Mice

After arrival, female SCID beige mice (age 10-12 weeks; body weight 18-20 g) Charles River, Sulzfeld, Germany) were maintained in the quarantine part of the AALAAC approved animal facility for one week to get them accustomed to the new environment and for observation. Continuous health monitoring was carried out. The mice were kept under SPF-conditions according to the international guidelines (GV-Solas; Felasa; TierschG) with daily cycles of 12 h light /12 h darkness. Diet food (Kliba Provimi 3347) and water (filtered) were provided ad libitum. Experimental study protocol was reviewed and approved by the local government (Regierung von Oberbayern; registration no. 211.2531.2-22/2003).

Tumor cell injection

At the day of injection tumor cells were harvested (trypsin-EDTA) from culture flasks (Greiner TriFlask) and transferred into 50 ml culture medium, washed once and resuspended in PBS. After an additional washing step with PBS and filtration (cell strainer; Falcon ∅ 100µm) the final cell titer was adjusted to 1.5 x 10^8 / ml. Tumor cell suspension was carefully mixed with transfer pipette to avoid cell aggregation. Anesthesia is performed using a Stephens inhalation unit for small animals with preincubation chamber (plexiglas), individual mouse nose-mask (silicon) and not flammable or explosive anesthesia compound Isoflurane (Pharmacia-Upjohn, Germany) in a closed circulation system. Two days before injection coat of the animals were shaved. For i.m.f.p. injection cells were injected orthotopically at a volume of 20 µl into the right penultimate inguinal mammary fat pad of each anesthetized mouse. For the orthotopic implantation, the cell suspension was injected through the skin under the nipple using a using a Hamilton microliter syringe and a 30Gx1/2" needle.

Treatment of animals

Treatment of animals started at day of randomization at a mean tumor volume of ~80 mm3, respectively. Mice were treated once weekly i.p. with the different compounds as indicated in following table .

No of animals	Compound	Dose (mg/kg)	Route/Mode of administration
10	Xolair	10	i.p. once weekly
10	<VEGF > Avastin	10	i.p. once weekly
10	< ANG-2> Ang2i-LC06	10	i.p. once weekly
10	Ang2i-LC06 + Avastin	10 10	i.p. once weekly i.p. once weekly
10	XMAb1	10	i.p. once weekly

Monitoring of tumor growth

Animals were controlled 2x per week for their health status. Body weights were documented 2x per week after cell injection. The tumor dimensions were measured by caliper on the staging day, at beginning of treatment period 2 times per week. Tumor volume was calculated according to NCI protocol (B. Teicher; Anticancer drug development guide, Humana Press, 1997, Chapter 5, page 92) (Tumor weight

= $1/2ab^2$, where "a" and "b" are the long and the short diameters of the tumor, respectively).

Termination criteria were the critical tumor mass (up to 1.7 g or Ø > 1.5 cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

The results (see Fig.10) show that the bispecific bivalent <VEGF-ANG-2> antibody XMAb1 showed a higher tumor growth inhibition in xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibodies. The efficacy of the combination of ANG2i-LC06 and bevacizumab showed comparable results to the XMAb1. Maximal efficacy of XMAb1 was already reached with 10mg/kg.

In a second experiment the effect of XMAb1 on bigger tumors was analyzed.

Treatment of animals

Treatment of animals started at day of randomization at a mean tumor volume of ~160 mm3, respectively. Mice were treated once weekly i.p. with the different compounds as indicated in following table .

No of animals	Compound	Dose (mg/kg)	Route/Mode of administration
10	Xolair	10	i.p. once weekly
10	<VEGF > Avastin	10	i.p. once weekly
10	< ANG-2> Ang2i-LC06	10	i.p. once weekly
10	Ang2i-LC06 + Avastin	10 10	i.p. once weekly i.p. once weekly
10	XMAb1	10	i.p. once weekly

Monitoring:

Animals were controlled 2x per week for their health status. Body weights were documented 2x per week after cell injection. The tumor dimensions were measured by caliper on the staging day, at beginning of treatment period 2 times per week. Tumor volume was calculated according to NCI protocol (B. Teicher; Anticancer drug development guide, Humana Press, 1997, Chapter 5, page 92) (Tumor weight = $1/2ab^2$, where "a" and "b" are the long and the short diameters of the tumor, respectively).

Termination criteria were the critical tumor mass (up to 1.7 g or Ø > 1.5 cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

The results (see Fig.11) show that the bispecific bivalent <VEGF-ANG-2> antibody XMAb1 showed a higher tumor growth inhibition in xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibodies. The efficacy of the combination of ANG2i-LC06 and bevacizumab showed comparable results to the XMAb1. Maximal efficacy of XMAb1 was already reached with 10mg/kg.

Taken together the results demonstrate that independent of the tumor size XMAb1 shows superior efficacy compared to the treatment with monospecific antibodies.

Tumor stasis in these models could be already achieved at lower concentrations of 10 mg/kg XMAb1 compared to the combination of 10 mg/kg of Ang2i-LC06 + 10 mg/kg of Avastin.

Example 11

Effect of treatment with XMAb1 on micro-vessel density in s.c. Colo205 xenograft

Vascular density is assessed by counting all vessels of a tumor slide. Vessels were labeled with fluorescent anti-mouse CD34 antibody (clone MEC14.7) on paraffin-embedded sections. Vessels were quantified and microvessel density is calculated as vessels per mm^2. All results were expressed as mean ± SEM. To define significant differences of experimental groups, Dunnetts-Method was used. $p<0.05$ was considered as statistically significant. The results show that total intratumoral MVD was decreased in treated tumors. Treatment with ANG2i-LC06 reduced MVD by 29%, bevacizumab by </=0%, bevacizumab + ANG2i-LC06 by 15% and XMAb1 by 28%.

Example 12

In vivo efficacy of bispecific antibody <VEGF-ANG-2> antibody in s.c. N87 xenograft model in Scid beige mice

Tumor cell line

The human gastric cancer cell line N87 cancer cells (NCI-N87 (ATCC No.CRL 5822)). Tumor cells were routinely cultured in RPMI1640 supplemented with 10 %

fetal bovine serum (PAN Biotech, Germany) and 2 mM L-glutamine (PAN Biotech, Germany) at 37 °C in a water-saturated atmosphere at 5 % CO_2. Culture passage was performed with trypsin / EDTA 1x (PAN) splitting three times / week.

Mice

After arrival, female SCID beige mice (age 10-12 weeks; body weight 18-20 g) Charles River, Sulzfeld, Germany) were maintained in the quarantine part of the AALAAC approved animal facility for one week to get them accustomed to the new environment and for observation. Continuous health monitoring was carried out. The mice were kept under SPF-conditions according to the international guidelines (GV-Solas; Felasa; TierschG) with daily cycles of 12 h light /12 h darkness. Diet food (Kliba Provimi 3347) and water (filtered) were provided ad libitum. Experimental study protocol was reviewed and approved by the local government (Regierung von Oberbayern; registration no. 211.2531.2-22/2003).

Tumor cell injection

At the day of cell injection, cells were harvested from culture flasks (Greiner T 75), transferred into 50 ml culture medium, washed once and resuspended in PBS. After an additional washing with PBS the cell concentration was measured with a Vi-Cell™ (Cell Viability Analyzer, Beckman Coulter, Madison, Wisconsin, U.S.A.). The tumor cell suspension (PBS) was mixed carefully (to reduce cell aggregation) and kept on ice. The cell suspension was filled into a 1.0 ml syringe. For injection, a needle size of 0.45 x 25 mm was used. To generate primary tumors, 5 x 10^6 N87 tumor cells in a volume of 100 µl PBS were injected subcutaneously into the right flank of each mouse.

Treatment of animals

Treatment of animals started at day of randomization at a mean tumor volume of ~130 mm3, respectively. Mice are treated once weekly i.p. with the different compounds as indicated in following table.

No of animals	Compound	Dose (mg/kg)	Route/Mode of administration
10	Xolair	10	i.p. once weekly
10	<VEGF > Avastin	10	i.p. once weekly
10	< ANG-2> Ang2i-LC06	10	i.p. once weekly
10	XMAb1	10	i.p. once weekly

Monitoring of tumor growth

Animals were controlled 1x per week for their health status. Body weights were documented 1x per week after cell injection. The tumor dimensions were measured by caliper on the staging day, at beginning of treatment period once per week. Tumor volume was calculated according to NCI protocol (B. Teicher; Anticancer drug development guide, Humana Press, 1997, Chapter 5, page 92) (Tumor weight = $1/2ab^2$, where "a" and "b" are the long and the short diameters of the tumor, respectively).

Termination criteria were the critical tumor mass (up to 1.7 g or Ø > 1.5 cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

The results show that the bispecific bivalent <VEGF-ANG-2> antibody XMAb1 showed a higher tumor growth inhibition in xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibodies (**Fig. 12**).

Patent Claims

1. A bispecific, bivalent antibody comprising a first antigen-binding site that specifically binds to human VEGF and a second antigen-binding site that specifically binds to human ANG-2, characterized in that

i) said first antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 1, and as light chain variable domain (VL) the SEQ ID NO: 2; and

ii) said second antigen-binding site comprises as heavy chain variable domain (VH) the SEQ ID NO: 3, and as light chain variable domain (VL) the SEQ ID NO: 4;and further

characterized in comprising

a) the heavy chain and the light chain of a first full length antibody that specifically binds to VEGF;

b) the modified heavy chain and modified light chain of a full length antibody that specifically binds to ANG-2, wherein the constant domains CL and CH1 are replaced by each other.

2. The bispecific antibody according to claim 1, characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 7, and as light chain of the first full length antibody the SEQ ID NO: 5, and

b) as modified heavy chain of the second full length antibody the SEQ ID NO: 8, and as modified light chain of the second full length antibody the SEQ ID NO: 6.

3. The bispecific antibody according to claim 1, characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 11, and as light chain of the first full length antibody the SEQ ID NO: 9, and

b) as modified heavy chain of the second full length antibody the SEQ ID NO: 12, and as modified light chain of the second full length antibody the SEQ ID NO: 10.

4. The bispecific antibody according to claim 1, characterized in comprising

a) as heavy chain of the first full length antibody the SEQ ID NO: 15, and as light chain of the first full length antibody the SEQ ID NO: 13, and

b) as modified heavy chain of the second full length antibody the SEQ ID NO: 16, and as modified light chain of the second full length antibody the SEQ ID NO: 14.

5. A pharmaceutical composition comprising an antibody according to claims 1 to 4.

6. The bispecific antibody according to any one of claims 1 to 4 for the treatment of cancer.

7. Use of the bispecific antibody according to any one of claims 1 to 4 for the manufacture of a medicament for the treatment of cancer.

8. The bispecific antibody according to any one of claims 1 to 4 for use in the treatment of a condition selected from intraocular neovascular syndromes, rheumatoid arthritis or psoriasis.

9. The bispecific antibody for use according to claim 8, which is for use in the treatment of proliferative retinopathy or age-related macular degeneration

10. Use of the bispecific antibody according to any one of claims 1 to 4 for the manufacture of a medicament for the treatment of a condition selected from intraocular neovascular syndromes, rheumatoid arthritis or psoriasis.

11. Use according to claim 10, wherein the medicament is for the treatment of proliferative retinopathy or age-related macular degeneration.

12. A nucleic acid encoding a bispecific antibody according to any one of claims 1 to 4 .

13. Expression vector containing said nucleic acid according to claim 12 capable of expressing said nucleic acid in a prokaryotic or eukaryotic host cell.

14. A prokaryotic or eukaryotic host cell comprising a vector according to claim 13.

15. A method for the preparation of a bispecific antibody according to claims 1 to 4

comprising the steps of

a) transforming a host cell with vectors comprising nucleic acid molecules encoding said antibody;

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

c) recovering said antibody molecule from said culture.

16. A bispecific antibody obtained by the method of claim 15.