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FISCHER et al., "Bispecific Antibodies: Molecules That Enable Novel Therapeutic Strategies" Pathobiology, 1 May 2007, Vol. 74, No. 1, pages 3-14
JENDREYKO N. et al., "Simultaneous, Phenotypic Knockout of VEGF-R2 and Tie-2 with an Intradiabody Enhances Antiangiogenic Effects In Vivo", KLINISCHE PADIATRIE, May 2006, Vol. 218, No. 3, pages 143-151
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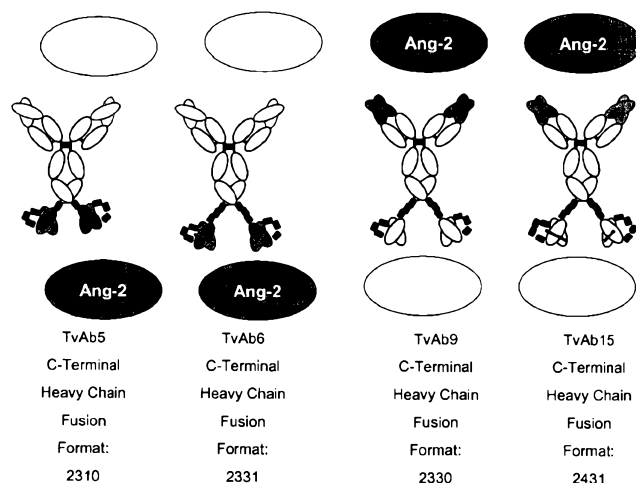
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(54) Title: BISPECIFIC ANTI-VEGF/ANTI-ANG-2 ANTIBODIES

Figure 1B



(57) Abstract: The present invention relates to bispecific antibodies against human VEGF and against human ANG-2, methods for their production, pharmaceutical compositions containing said antibodies, and uses thereof.



GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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Bispecific anti-VEGF/anti-ANG-2 antibodies

The present invention relates to bispecific 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., 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 and Davis-Smyth, Endocrine 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, 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, I., 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 Lett, 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) 251 1-14; 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.* 09 (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, 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
5 it is expressed widely and constitutively (Hanahan, D., *Science*, 277 (1997) 48-50; Zagzag, D., et al., *Exp Neurology*, 159:391-400 (1999)). 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
10 responsive to sprouting signals (Hanahan, D., 1997; Holash, J., et al., *Orzcogerze* 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
15 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) 124-29).

20 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). Siemester, G., et al. Siemeister, G., et al., *Cancer*
25 *Res.* 59 (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
30 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 (Follunan, 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.

- 5 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.
- 10 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
- 15 Wurbach, 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.
- 20 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
- 25 when VEGF expression was high. Moreover, positive expression of ANG-2 was a
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- 35

significant factor to predict a poor postoperative survival. Tanaka, F., et al., Cancer Res. 62 (2002) 7124-29. However, they found no significant correlation between Ang-1 expression and the microvessel density. Tanaka, F., et al., Cancer Res. 62 (2002) 7124-29. 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 (200) 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 (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

5 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).

10 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.,
15 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
20 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
25 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 other via peptide linkers are reported in US 7,129,330. Dimeric and multimeric antigen binding structures are reported in US 2005/0079170. Tri- or
30 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
5 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
10 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
15 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
20 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,
25 KDR and/or FLT1 antagonists. WO 2007/089445 refers to ANG-2 and VEGF inhibitor combinations.

WO 2003/106501 refers to fusion proteins binding to Angiopoetin and containing a multimerization domain. WO 2008/132568 fusion proteins binding to Angiopoetin and VEGF.

30 Summary of the Invention

A first aspect of the current invention is a bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoetin-2

(ANG-2) 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.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 5 i) said antigen-binding sites are each a pair of an antibody heavy chain variable domain and an antibody light chain variable domain;
- ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, SEQ ID NO: 9, SEQ ID NO: 17, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, SEQ ID NO: 10, SEQ ID NO: 18, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO: 3, SEQ ID NO: 11, SEQ ID NO: 19, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, SEQ ID NO: 12, SEQ ID NO: 20, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO: 5, SEQ ID NO: 13, SEQ ID NO: 21, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO: 6, SEQ ID NO: 14, SEQ ID NO: 22, or SEQ ID NO: 99;
- iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 25, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO: 70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 26, SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 27, SEQ ID NO: 40, SEQ ID NO: 48, SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 28, SEQ ID NO: 28 with the mutations T92L, H93Q and W94T, SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 29, SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 51, SEQ ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 83, or SEQ ID NO: 91.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- i) said antigen-binding sites are each a pair of an antibody heavy chain variable domain and an antibody light chain variable domain;
- 5 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6;
- 10 or said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 9, a CDR2 region of SEQ ID NO: 10, and a CDR1 region of SEQ ID NO:11, and in the light chain variable domain a CDR3 region of SEQ ID NO: 12, a CDR2 region of SEQ ID NO:13, and a CDR1 region of SEQ ID
- 15 NO:14;
- or said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 17, a CDR2 region of SEQ ID NO: 18, and a CDR1 region of SEQ ID NO:19, and in the light chain variable domain a CDR3 region of SEQ ID NO: 20, a CDR2 region of SEQ ID NO:21, and a CDR1 region of SEQ ID
- 20 NO:22; and
- iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 25, a CDR2 region of SEQ ID NO: 26, and a CDR1 region of SEQ
- 25 ID NO:27, and in the light chain variable domain a CDR3 region of SEQ ID NO: 28 or SEQ ID NO: 28 with the mutations T92L, H93Q and W94T, a CDR2 region of SEQ ID NO:29, and a CDR1 region of SEQ ID NO:30.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- i) said antigen-binding sites are each a pair of an antibody heavy chain variable domain and an antibody light chain variable domain;

- ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, SEQ ID NO: 15, SEQ ID NO: 23, or SEQ ID NO: 100, and as light chain variable domain SEQ ID NO: 8, SEQ ID NO: 16, SEQ ID NO: 24, or SEQ ID NO: 101, and
- 5 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 31, SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 84 or SEQ ID NO: 92, and as light chain variable domain a SEQ ID NO: 32, SEQ ID NO: 32 with the mutations T92L, H93Q and W94T SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 69, SEQ ID NO: 77, SEQ ID NO: 85 or SEQ ID NO: 93.
- 10

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO: 3, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO: 5, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO: 6, or SEQ ID NO: 99;
- 15
- iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO: 70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 40, SEQ ID NO: 48, SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 43, SEQ ID NO: 51, SEQ
- 20
- 25
- 30

ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 83, or SEQ ID NO: 91.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 5 ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, or SEQ ID NO: 100, and as light chain variable domain SEQ ID NO: 8 or SEQ ID NO: 101, and
- iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 84
10 or SEQ ID NO: 92, and as light chain variable domain a SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 69, SEQ ID NO: 77, SEQ ID NO: 85 or SEQ ID NO: 93.

15 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO: 70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 40, SEQ ID NO: 48, SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 43, SEQ ID NO: 51, SEQ ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 83, or SEQ ID NO: 91.
30

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

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- 5 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 84 or SEQ ID NO: 92, and as light chain variable domain a SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 69, SEQ ID NO: 77, SEQ ID NO: 85 or SEQ ID NO: 93.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 10 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6; and
- 15 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 46, a CDR2 region of, SEQ ID NO: 47, and a CDR1 region of SEQ ID NO: 48, and in the light chain variable domain a CDR3 region of SEQ ID NO: 49, a CDR2 region of SEQ ID NO: 50, and a CDR1 region of
- 20 SEQ ID NO: 51.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 25 ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8, and
- iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 52, and as light chain variable domain a SEQ ID NO: 53.

30 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

5 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO:3, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO:5, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO:6, or SEQ ID NO: 99;

10 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 62, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 63, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 64, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 65, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 66, or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 67, or SEQ ID NO: 91.

15 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

 ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, or SEQ ID NO: 100, and as light chain variable domain SEQ ID NO: 8 or SEQ ID NO: 101, and

20 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 68, or SEQ ID NO: 92, and as light chain variable domain a SEQ ID NO: 69, or SEQ ID NO: 93.

25 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

30 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6;

 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID

NO: 62, a CDR2 region of SEQ ID NO: 63, and a CDR1 region of SEQ ID NO: 64, and in the light chain variable domain a CDR3 region of SEQ ID NO: 65, a CDR2 region of SEQ ID NO: 66, and a CDR1 region of SEQ ID NO: 67,.

5 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8; and

10 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 68, and as light chain variable domain a SEQ ID NO: 69.

Said bispecific antibodies are at least bivalent and may be trivalent, tetravalent or multivalent. Preferably the bispecific antibody according to the invention is
15 bivalent, trivalent or tetravalent.

A further aspect of the invention is a nucleic acid molecule encoding a chain of said bispecific antibody.

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

The invention further comprises a prokaryotic or eukaryotic host cell comprising a vector according to the invention.

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

30 Still further aspects of the invention are 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.

The bispecific antibodies according to the invention show benefits for human patients in need of a VEGF and ANG-2 targeting therapy. The antibodies according to the invention have new and inventive properties causing a benefit for a patient suffering from such a disease, especially suffering from cancer. Surprisingly it has found out that the bispecific antibodies according to the invention are more effective in tumor growth and/or inhibition of tumor angiogenesis compared to combination of the respective monospecific parent antibodies.

Detailed Description of the Invention

One embodiment of the invention is a bispecific antibody specifically binding to human VEGF and human ANG-2 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 antigen-binding sites are each a pair of an antibody heavy chain variable domain and an antibody light chain variable domain;
- ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, SEQ ID NO: 9, SEQ ID NO: 17, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, SEQ ID NO: 10, SEQ ID NO: 18, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO: 3, SEQ ID NO: 11, SEQ ID NO: 19, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, SEQ ID NO: 12, SEQ ID NO: 20, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO: 5, SEQ ID NO: 13, SEQ ID NO: 21, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO: 6, SEQ ID NO: 14, SEQ ID NO: 22, or SEQ ID NO: 99;
- iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 25, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO: 70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 26, SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 27, SEQ ID NO: 40, SEQ ID NO: 48,

SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or
 SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of
 SEQ ID NO: 28, SEQ ID NO: 28 with the mutations T92L, H93Q
 and W94T, SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID
 5 NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2
 region of SEQ ID NO: 29, SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID
 NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID
 NO: 90, and a CDR1 region of SEQ ID NO: 30, SEQ ID NO: 43, SEQ
 ID NO: 51, SEQ ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID
 10 NO: 83, or SEQ ID NO: 91.

In one embodiment of the invention the bispecific antibody according to the
 invention is characterized in that

- i) said antigen-binding sites are each a pair of an antibody heavy chain
 variable domain and an antibody light chain variable domain;
- 15 ii) said first antigen-binding site specifically binding to VEGF comprises in
 the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a
 CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO: 3,
 and in the light chain variable domain a CDR3 region of SEQ ID NO: 4,
 a CDR2 region of SEQ ID NO: 5, and a CDR1 region of SEQ ID NO: 6;
- 20 or said first antigen-binding site specifically binding to VEGF comprises
 in the heavy chain variable domain a CDR3 region of SEQ ID NO: 9, a
 CDR2 region of SEQ ID NO: 10, and a CDR1 region of SEQ ID NO: 11,
 and in the light chain variable domain a CDR3 region of SEQ ID NO: 12,
 a CDR2 region of SEQ ID NO: 13, and a CDR1 region of SEQ ID
 25 NO: 14;
- or said first antigen-binding site specifically binding to VEGF comprises
 in the heavy chain variable domain a CDR3 region of SEQ ID NO: 17, a
 CDR2 region of SEQ ID NO: 18, and a CDR1 region of SEQ ID NO: 19,
 and in the light chain variable domain a CDR3 region of SEQ ID NO: 20,
 30 a CDR2 region of SEQ ID NO: 21, and a CDR1 region of SEQ ID
 NO: 22; and
- iii) said second antigen-binding site specifically binding to ANG-2
 comprises in the heavy chain variable domain a CDR3 region of SEQ ID

5 NO: 25, a CDR2 region of SEQ ID NO: 26, and a CDR1 region of SEQ ID NO:27, and in the light chain variable domain a CDR3 region of SEQ ID NO: 28 or SEQ ID NO: 28 with the mutations T92L, H93Q and W94T, a CDR2 region of SEQ ID NO:29, and a CDR1 region of SEQ ID NO:30.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- i) said antigen-binding sites are each a pair of an antibody heavy chain variable domain and an antibody light chain variable domain;
- 10 ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, SEQ ID NO: 15, SEQ ID NO: 23, or SEQ ID NO: 100, and as light chain variable domain SEQ ID NO: 8, SEQ ID NO: 16, SEQ ID NO: 24, or SEQ ID NO: 101, and
- 15 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 31, SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 84 or SEQ ID NO: 92, and as light chain variable domain SEQ ID NO: 32, SEQ ID NO: 32 with the mutations T92L, H93Q and W94T SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 20 69, SEQ ID NO: 77, SEQ ID NO: 85 or SEQ ID NO: 93.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 25 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO:3, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO:5, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO:6, or SEQ ID NO: 99;
- 30 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO:

70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 40, SEQ ID NO: 48, SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 43, SEQ ID NO: 51, SEQ ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 83, or SEQ ID NO: 91.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, or SEQ ID NO: 100, and as light chain variable domain SEQ ID NO: 8 or SEQ ID NO: 101, and
- iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 84 or SEQ ID NO: 92, and as light chain variable domain SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 69, SEQ ID NO: 77, SEQ ID NO: 85 or SEQ ID NO: 93.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- ii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO: 70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 40, SEQ ID NO: 48, SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or SEQ ID NO: 88, and in the light chain variable domain a

5 CDR3 region of SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 43, SEQ ID NO: 51, SEQ ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 83, or SEQ ID NO: 91.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

10 ii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 84 or SEQ ID NO: 92, and as light chain variable domain a SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 69, SEQ ID NO: 77, SEQ ID NO: 85 or SEQ ID NO: 93.

15 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

20 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6; and

25 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 46, a CDR2 region of SEQ ID NO: 47, and a CDR1 region of SEQ ID NO: 48, and in the light chain variable domain a CDR3 region of SEQ ID NO: 49, a CDR2 region of SEQ ID NO: 50, and a CDR1 region of SEQ ID NO: 51.

30 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8, and
- 5 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 52, and as light chain variable domain SEQ ID NO: 53.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 10 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO:3, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO:5, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO:6, or SEQ ID NO: 99;
- 15 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 62, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 63, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 64, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 65, or SEQ ID NO: 89, a CDR2 region of SEQ ID NO: 66, or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO: 67, or SEQ ID NO: 91.
- 20

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 25 ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, or SEQ ID NO: 100, and as light chain variable domain SEQ ID NO: 8 or SEQ ID NO: 101, and
- 30 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 68, or SEQ ID NO: 92, and as light chain variable domain SEQ ID NO: 69, or SEQ ID NO: 93.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 5 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6;
- 10 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 62, a CDR2 region of SEQ ID NO: 63, and a CDR1 region of SEQ ID NO: 64, and in the light chain variable domain a CDR3 region of SEQ ID NO: 65, a CDR2 region of SEQ ID NO: 66, and a CDR1 region of SEQ ID NO: 67.

15 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8; and
- 20 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 68, and as light chain variable domain SEQ ID NO: 69.

In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

- 25 ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6; and
- 30 iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 78, a

- 24 -

CDR2 region of SEQ ID NO: 79, and a CDR1 region of SEQ ID NO: 80, and in the light chain variable domain a CDR3 region of SEQ ID NO: 81, a CDR2 region of SEQ ID NO: 82, and a CDR1 region of SEQ ID NO: 83.

5 In one embodiment of the invention the bispecific antibody according to the invention is characterized in that

ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8, and

10 iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 84, and as light chain variable domain SEQ ID NO: 85.

Another embodiment of the invention is a bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) characterized in that the parent anti-ANG-2 antibody is not specifically binding to human Angiopoietin 1 (ANG-1). Typical parent antibodies which specifically bind to human ANG-2, but not to human ANG-1 are e.g. Ang2s_R3_LC03, Ang2s_LC09, Ang2i_LC06, Ang2i_LC07, and preferably Ang2i_LC10 or antibodies binding to the same epitope as Ang2s_R3_LC03, Ang2s_LC09, Ang2i_LC06, Ang2i_LC07, Ang2i_LC10, preferably antibodies binding to the same epitope as Ang2i_LC06, or Ang2i_LC10. Therefore in one embodiment of the invention the bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) but not to human ANG-1 (or wherein the parent anti-ANG-2 antibody is not specifically binding to human Angiopoietin 1 (ANG-1)) binds to the same epitope as Ang2s_R3_LC03, Ang2s_LC09, Ang2i_LC06, Ang2i_LC07, Ang2i_LC10, preferably to the same epitope as Ang2i_LC06 or Ang2i_LC10. Such bispecific antibodies specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) but not to human ANG-1 (or wherein the parent anti-ANG-2 antibody is not specifically binding to human Angiopoietin 1 (ANG-1)) can have improved properties such as e.g. biological or pharmacological activity, less toxicity, or pharmacokinetic profile, compared to bispecific antibodies specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) as well as to human ANG-1.

Thus a preferred embodiment is a bispecific antibody specifically binding to human VEGF and human ANG-2 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 the second antigen-binding site that is not specifically binding to human Angiopoietin 1 (ANG-1).

One embodiment of the invention is a bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) 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 the ratio of the binding affinities K_D (antigen-binding site specific for VEGF)/ K_D (antigen-binding site specific for ANG-2) is 1.0 - 10.0, preferably 1.5 - 8.0 (In one embodiment 5.0-8.0) and preferably the absolute K_D value is in the range of 10^{-8} - 10^{-13} mol/l. K_D values are determined in a ANG-2/VEGF binding BIACORE (see Example 2, and Fig 15A). As both proteins human VEGF and human ANG-2 are both present as soluble receptor ligands in human serum at approximately same concentrations, blocking of the said both receptor ligands by a bispecific characterized in that the ratio of the binding affinities K_D (antigen-binding site specific for VEGF)/ K_D (antigen-binding site specific for ANG-2) is 1.0- 10.0, preferably 1.5 -8.0, and in one embodiment 5.0-8.0 can lead to improved properties with respect to the anti-angiogenic effects, tumor growth inhibition or resistance mechanism during the treatment of cancer or vascular diseases with such a bispecific antibody. Preferably said bispecific antibody characterized in that the ratio of the binding affinities K_D (antigen-binding site specific for VEGF)/ K_D (antigen-binding site specific for ANG-2) is 1.0 - 10.0, preferably 1.5 -8.0 (In one embodiment 5.0-8.0) and said bispecific antibody comprises as first antigen-binding site specifically binding to VEGF a heavy chain variable domain of SEQ ID NO: 7, and a light chain variable domain of SEQ ID NO: 8, as said second antigen-binding site specifically binding to ANG-2 a) either a heavy chain variable domain of SEQ ID NO: 52, and a light chain variable domain of SEQ ID NO: 53 or b) a heavy chain variable domain of SEQ ID NO: 84, and a light chain variable domain of SEQ ID NO: 85.

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" include antibody heavy chain variable domains (VH)

and/or an antibody light chain variable domains (VL), or pairs of VH/VL, and can be derived from whole antibodies or antibody fragments such as single chain Fv, a VH domain and/or a VL domain, Fab, or (Fab)₂. In one embodiment of the current invention each of the antigen-binding sites comprises an antibody heavy chain variable domain (VH) and/or an antibody light chain variable domain (VL), and preferably is formed by a pair consisting of an antibody light chain variable domain (VL) and an antibody heavy chain variable domain (VH).

The antigen-binding site, and especially heavy chain variable domains (VH) and/or antibody light chain variable domains (VL), that specifically bind to human vascular endothelial growth factor (VEGF) can be derived a) from known anti-VEGF antibodies such as Kim et al., Nature 362 (1993) 841-844; Warren, R.S., et al., J. Clin. Invest. 95 (1995) 1789-1797; Borgstrom, P., et al., Cancer Res. 56 (1996) 4032-4039; Melnyk, O., et al., Cancer Res. 56 (1996) 921-924). WO 94/10202, WO 98/45332, WO 2005/00900, WO 00/35956 and US 2007/0141065 or b) from new anti-VEGF antibodies obtained by de novo immunization methods using inter alia either the human VEGF protein or nucleic acid or fragments thereof or by phage display.

The antigen-binding site, and especially heavy chain variable domains (VH) and/or antibody light chain variable domains (VL), that specifically bind to human angiopoietin-2 (ANG-2) can be derived a) from known anti-ANG-2 antibodies such as WO 03/030833, WO 2006/068953, WO 2006/045049 or US 6,166,185; or b) from new anti-ANG-2 antibodies obtained e.g. by de novo immunization methods using inter alia either the human ANG-2 protein or nucleic acid or fragments thereof or by phage display.

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. Where an antibody has more than one specificity, the recognized epitopes may be associated with a single antigen or with more than one antigen. Antibodies of the present invention are specific for two different antigens, i.e. 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 at least “bivalent” and may be “trivalent” or “multivalent” (e.g. (“tetravalent” or “hexavalent”). Preferably the bispecific antibody according to the invention is bivalent, trivalent or tetravalent. In one embodiment said bispecific antibody is bivalent. In one embodiment said bispecific antibody is trivalent. In one embodiment said bispecific antibody is tetravalent.

Antibodies of the present invention have two or more binding sites and are bispecific. That is, the antibodies may be bispecific even in cases where there are more than two binding sites (i.e. that the antibody is trivalent or multivalent). Bispecific antibodies of the invention include, for example, multivalent single chain antibodies, diabodies and triabodies, as well as antibodies having the constant domain structure of full length antibodies to which further antigen-binding sites (e.g., single chain Fv, a VH domain and/or a VL domain, Fab, or (Fab)₂), are linked via one or more peptide-linkers. The antibodies can be full length from a single species, or be chimerized or humanized. For an antibody with more than two antigen binding sites, some binding sites may be identical, so long as the protein has binding sites for two different antigens. That is, whereas a first binding site is specific for a VEGF, a second binding site is specific for ANG-2, and vice versa.

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., 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.

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.

An antigen-binding site of an antibody of the invention can 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.

In certain embodiments, 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. In a preferred embodiment, an antibody of the invention has a constant domain structure of an IgG type antibody, but has four antigen binding sites. This is accomplished e.g. by linking two complete antigen binding sites (e.g., a single chain Fv) specifically binding to VEGF to either to

N- or C-terminus heavy or light chain of a full antibody specifically binding to ANG-2. Alternatively this is accomplished by fusing two complete binding peptides specifically binding to ANG-2 to either to C-terminus heavy chain of a full antibody specifically binding to VEGF. The four antigen-binding sites preferably comprise two antigen-binding sites for each of two different binding specificities.

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.

5 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
10 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; Bruggemann, M., et al., *Year Immunol.* 7 (1993) 33-40). Human antibodies can also be produced
15 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
20 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
25 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
30 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
35 sequences of the VH and VL regions of the recombinant antibodies are sequences

that, while derived from and related to human germ line VH and VL sequences, may not naturally exist within the human antibody germ line repertoire in vivo.

The "variable domain" (variable domain of a light chain (VL), variable region of a heavy chain (VH) as used herein denotes each of the pair of light and heavy chains which is involved directly in binding the antibody to the antigen. The domains of variable human light and heavy chains have the same general structure and each domain comprises four framework (FR) regions whose sequences are widely conserved, connected by three "hypervariable regions" (or complementarity determining regions, CDRs). The framework regions adopt a β -sheet conformation and the CDRs may form loops connecting the β -sheet structure. The CDRs in each chain are held in their three-dimensional structure by the framework regions and form together with the CDRs from the other chain the antigen binding site. The antibody heavy and light chain CDR3 regions play a particularly important role in the binding specificity/affinity of the antibodies according to the invention and therefore provide a further object of the invention.

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

The bispecific antibodies according to the invention include, in addition, such antibodies having "conservative sequence modifications" (which is meant by "variants" of the bispecific antibodies). This means nucleotide and amino acid sequence modifications which do not affect or alter the above-mentioned characteristics of the antibody according to the invention. Modifications can be introduced by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions include ones in which the amino acid residue is replaced with an

amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g. lysine, arginine, histidine), acidic side chains (e.g. aspartic acid, glutamic acid), uncharged polar side chains (e.g. glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g. alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g. threonine, valine, isoleucine) and aromatic side chains (e.g. tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a bispecific <VEGF-ANG-2> antibody can be preferably replaced with another amino acid residue from the same side chain family. A “variant” bispecific <VEGF-ANG-2> antibody, refers therefore herein to a molecule which differs in amino acid sequence from a “parent” bispecific <VEGF-ANG-2> antibody amino acid sequence by up to ten, preferably from about two to about five, additions, deletions and/or substitutions in one or more variable region or constant region of the parent antibody. Amino acid substitutions can be performed by mutagenesis based upon molecular modeling as described by Riechmann, L., et al., Nature 332 (1988) 323-327 and Queen, C., et al., Proc. Natl. Acad. Sci. USA 86 (1989) 10029-10033. A “variant” bispecific <VEGF-ANG-2> antibody according to the invention includes also bispecific antibodies formats in which the linker (if existing) was modified, or replaced by another linker.

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 2) with purified wild-type antigen. The affinity of the binding is defined by the terms k_a (rate constant for the association of the antibody from the antibody/antigen complex), k_D (dissociation constant), and K_D (k_D/k_a). 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.

Binding of the antibody to the FcγRIII can be investigated by a BIAcore assay (GE-Healthcare Uppsala, Sweden). The affinity of the binding is defined by the terms k_a (rate constant for the association of the antibody from the antibody/antigen complex), k_D (dissociation constant), and K_D (k_D/k_a).

As used herein, the term “not binding to ANG-1” or “not specifically binding to ANG-1” denotes that the antibody has an EC50-value above 8000 ng/ml in an in-vitro ANG-1 binding ELISA assay (according to Example 9).

5 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.

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

In one embodiment of the invention the bispecific antibody comprises a full length parent antibody as scaffold.

15 The term “full length antibody” denotes an antibody consisting of two “full length antibody heavy chains” and two “full length antibody light chains” 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

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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. Thus a monospecific bivalent (= full length) antibody comprising a first antigen-binding site and consisting of two antibody light chains and two antibody heavy chains is a full length antibody. 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.

A preferred embodiment for bispecific antibody formats for the bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) according to the invention are bivalent antibodies with two different specificities as e.g. a) described in WO 2009/080251, WO 2009/080252 or WO 2009/080253 (domain exchanged antibodies- see Example 13) or b) based on a scFab-Fc fusion antibody wherein one single chain Fab fragment (eventually disulfide stabilized) is specific for VEGF and the other single chain Fab fragment (eventually disulfide stabilized) for ANG-2 (see Example 14) or c) described in Ridgway, J.B., Protein Eng. 9 (1996) 617-621; WO 96/027011; Merchant, A.M., et al., Nature Biotech 16 (1998) 677-681; Atwell, S., et al., J. Mol. Biol. 270 (1997) 26-35 and EP 1 870 459A1.

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123 and SEQ ID NO: 124 or variants thereof.

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127 and SEQ ID NO: 128 or variants thereof.

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131 and SEQ ID NO: 132 or variants thereof.

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 133, and SEQ ID NO: 134 or variants thereof.

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 135, and SEQ ID NO: 136 or variants thereof.

5 These amino acid sequences are based on the heavy chain variable domains of SEQ ID NO: 7, and the light chain variable domains of SEQ ID NO: 8 (derived from bevacizumab (Avastin)) as first antigen-binding site binding to VEGF, and on the heavy chain variable domains of SEQ ID NO: 52, and the light chain variable domains of SEQ ID NO: 53 (derived from Ang2i_LC06)) as second antigen-binding site binding to ANG-2.

10 In one embodiment said bispecific antibody is trivalent using e.g. formats based on a full length antibody specifically binding to one of the two antigens VEGF or ANG-2, to which only at one C-terminus of one heavy chain a scFab fragment is fused which specifically binds to the other of the two antigens VEGF or ANG-2, including knobs –into holes technology, as described e.g. in EP Appl.
15 No 09004909.9 (see Example 11) or e.g. formats based on a full length antibody specifically binding to one of the two antigens VEGF or ANG-2, to which at one C-terminus of one heavy chain a VH or VH-CH1 fragment and at the other C-terminus of the second heavy chain a VL or VL-CL fragment is fused which specifically binds to the other of the two antigens VEGF or ANG-2, including
20 knobs –into holes technology, as described e.g. in EP Appl. No 09005108.7 (see Example 12).

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 115, SEQ ID NO: 116, and SEQ ID NO: 117 or variants thereof.

25 In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 118, SEQ ID NO: 119, and SEQ ID NO: 120 or variants thereof.

30 These amino acid sequences are based on the heavy chain variable domains of SEQ ID NO: 7, and the light chain variable domains of SEQ ID NO: 8 (derived from bevacizumab (Avastin)) as first antigen-binding site binding to VEGF, and on the heavy chain variable domains of SEQ ID NO: 52, and the light chain variable domains of SEQ ID NO: 53 (derived from Ang2i_LC06)) as second antigen-binding site binding to ANG-2.

Preferred bispecific antibody formats for the bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) according to the invention are tetravalent antibodies (TvAb) with two different specificities as described e.g. in WO 2007/024715, or
5 WO 2007/109254 or EP Appl. No 09004909.9. Thus in one embodiment said bispecific antibody is tetravalent using formats as described e.g. in WO 2007/024715, or WO 2007/109254 or EP Appl. No 09004909.9 (see Examples 1 or 10).

10 In one embodiment of the invention the bispecific tetravalent antibody TvAb-2441-bevacizumab-LC06 is characterized in comprising a peptide of SEQ ID No: 102 and the light chain of SEQ ID No: 62 or variants thereof.

In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 109, and SEQ ID NO: 110 or variants thereof.

15 In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 111, and SEQ ID NO: 112 or variants thereof.

20 In one embodiment the bispecific antibody according to the invention is characterized in comprising as amino acid sequences of SEQ ID NO: 113, and SEQ ID NO: 114 or variants thereof.

These amino acid sequences are based on the heavy chain variable domains of SEQ ID NO: 7, and the light chain variable domains of SEQ ID NO: 8 (derived from bevacizumab (Avastin)) as first antigen-binding site binding to VEGF, and on the heavy chain variable domains of SEQ ID NO: 52, and the light chain variable
25 domains of SEQ ID NO: 53 (derived from Ang2i_LC06)) as second antigen-binding site binding to ANG-2.

In one embodiment of the invention the bispecific tetravalent antibody TvAb-2441-bevacizumab-LC08 is characterized in comprising a peptide of SEQ ID No: 103 and the light chain of SEQ ID No: 62 or variants thereof.

30 The binding sites in an antibody according to the invention may be each formed by a pair of two variable domains, i.e. of one heavy chain variable domain and one

light chain variable domain. The minimal binding site determinant in an antibody is the heavy chain CDR3 region.

In one embodiment the bispecific antibody according to the invention is tetravalent. In a further embodiment said tetravalent bispecific antibody which has the following characteristics:

- it is consisting of:

a) a monospecific bivalent parent antibody consisting of two full length antibody heavy chains and two full length antibody light chains whereby each chain is comprising only one variable domain,

b) two peptide-linkers,

c) two monospecific monovalent single chain antibodies each consisting of an antibody heavy chain variable domain, an antibody light chain variable domain, and a single-chain-linker between said antibody heavy chain variable domain and said antibody light chain variable domain;

and preferably said single chain antibodies are linked to the same terminus (C- and N-terminus) of the monospecific bivalent antibody heavy chains or, alternatively to the same terminus (preferably the C-terminus) of the monospecific bivalent antibody light chains, and more preferably to the same terminus (C- and N-terminus) of the monospecific bivalent antibody heavy chains.

In another embodiment said bispecific antibody is tetravalent, and consists of

a) a full length antibody comprising said antigen-binding site and consisting of two antibody heavy chains and two antibody light chains; and

b) two identical single chain Fab fragments comprising said second antigen-binding site,

wherein said single chain Fab fragments under b) are fused to said full length antibody under a) via a peptide connector at the C- or N- terminus of the heavy or light chain of said full length antibody.

In another embodiment said bispecific antibody is tetravalent, and consists of

a) a full length antibody comprising said second antigen-binding site and consisting of two antibody heavy chains and two antibody light chains; and

b) two identical single chain Fab fragments comprising said first antigen-binding site,

5 wherein said single chain Fab fragments under b) are fused to said full length antibody under a) via a peptide connector at the C- or N- terminus of the heavy or light chain of said full length antibody.

 Preferably said single chain Fab fragments under b) are fused to said full length antibody under a) via a peptide connector at the C-terminus of the heavy or
10 light chain of said full length antibody.

In one embodiment two identical single chain Fab fragments binding to a second antigen are fused to said full length antibody via a peptide connector at the C-terminus of each heavy or light chain of said full length antibody.

15 In one embodiment two identical single chain Fab fragments binding to a second antigen are fused to said full length antibody via a peptide connector at the C-terminus of each heavy chain of said full length antibody.

In one embodiment two identical single chain Fab fragments binding to a second antigen are fused to said full length antibody via a peptide connector at the C-terminus of each light chain of said full length antibody.

20 Such embodiments including single chain Fab fragments are described in more detail in e.g. EP Appl. No 09004909.9 which incorporated by reference.

 The term "peptide-linker" as used within the invention denotes a peptide with amino acid sequences, which is preferably of synthetic origin. These peptide-linkers according to invention are used to link the different antigen-binding sites
25 and/or antibody fragments eventually comprising the different antigen-binding sites (e.g. single chain Fv, full length antibodies, a VH domain and/or a VL domain, Fab, (Fab)₂, Fc part) together to form a bispecific antibody according to the invention. The peptide-linkers can comprise one or more of the following amino acid sequences listed in Table 1 as well as further arbitrarily selected amino acids.
30 Said peptide-linkers are peptides with an amino acid sequence with a length of at least 5 amino acids, preferably of at least 10 amino acids, more preferably with a

length between 10 and 50 amino acids. Preferably said peptide-linkers under b) are peptides with an amino acid sequence with a length of at least 10 amino acids. In one embodiment said peptide-linker is $(GxS)_n$ with G = glycine, S = serine, ($x = 3$ and $n = 3, 4, 5$ or 6) or ($x = 4$ and $n = 2, 3, 4$ or 5), preferably $x = 4$ and $n = 2$ or 3 ,
5 more preferably with $x = 4$, $n = 2$ ($(G_4S)_2$). To said $(GxS)_n$ peptide-linker also additional G = glycines can be added, e.g. GG, or GGG.

The term "single-chain-linker" as used within the invention denotes a peptide with amino acid sequences, which is preferably of synthetic origin. These single-chain-linkers according to invention are used to link a VH and a VL domain to form a
10 single chain Fv. Preferably the said single-chain-linker under c) is a peptide with an amino acid sequence with a length of at least 15 amino acids, more preferably with a length of at least 20 amino acids. In one embodiment said single-chain-linker is $(GxS)_n$ with G = glycine, S = serine, ($x = 3$ and $n = 4, 5$ or 6) or ($x = 4$ and $n = 3, 4$ or 5), preferably with $x = 4$, $n = 4$ or 5 , more preferably with $x = 4$,
15 $n = 4$.

Furthermore said single chain (single chain Fv) antibodies are preferably disulfide stabilized. Such further disulfide stabilization of single chain antibodies is achieved by the introduction of a disulfide bond between the variable domains of the single chain antibodies and is described e.g. in WO 94/029350, Rajagopal, V., et al., Prot.
20 Engin. 10 (12) (1997) 1453-59; Kobayashi, H., et al., Nuclear Medicine & Biology 25 (1998) 387-393; or Schmidt, M., et al., Oncogene 18 (1999) 1711-1721.

In one embodiment of the disulfide stabilized single chain antibodies, the disulfide bond between the variable domains of the single chain antibodies comprised in the antibody according to the invention is independently for each single chain antibody
25 selected from:

- i) heavy chain variable domain position 44 to light chain variable domain position 100,
- ii) heavy chain variable domain position 105 to light chain variable domain position 43, or
- 30 iii) heavy chain variable domain position 101 to light chain variable domain position 100.

In one embodiment the disulfide bond between the variable domains of the single chain antibodies comprised in the antibody according to the invention is between heavy chain variable domain position 44 and light chain variable domain position 100.

- 5 In one embodiment the disulfide bond between the variable domains of the single chain antibodies comprised in the antibody according to the invention is between heavy chain variable domain position 105 and light chain variable domain position 43.

10 The structure of this tetravalent embodiment of a bispecific antibody according to the invention specifically binding to VEGF and ANG-2, wherein one of the Antigens A or B is VEGF, while the other is ANG-2. The structure is based on a full length antibody specifically binding to Antigen A, to which two (optionally disulfide-stabilized) single chain Fvs specifically binding to Antigen B, are linked via the a peptide-linker is exemplified in the schemes of Figures 1 and 2.

- 15 In one embodiment said single chain (single chain Fv) antibodies without said optional disulfide stabilization between the variable domains VH and VL of the single chain antibody (single chain Fv) are preferred.

20 In a further embodiment said tetravalent bispecific antibody is characterized in that said *monospecific bivalent antibody* part under a) specifically binds to VEGF and said two monovalent monospecific single chain antibodies under c) bind to ANG-2.

In a further embodiment said tetravalent bispecific antibody is characterized in that said *monospecific bivalent antibody* part under a) specifically binds to ANG-2 and said two monovalent monospecific single chain antibodies under c) bind to VEGF

25 A "single chain Fab fragment" (see Figure 11) is a polypeptide consisting of an antibody heavy chain variable domain (VH), an antibody constant domain 1 (CH1), an antibody light chain variable domain (VL), an antibody light chain constant domain (CL) and a linker, wherein said antibody domains and said linker have one of the following orders in N-terminal to C-terminal direction: a) VH-CH1-linker-VL-CL, b) VL-CL-linker-VH-CH1, c) VH-CL-linker-VL-CH1
30 or d) VL-CH1-linker-VH-CL; and wherein said linker is a polypeptide of at least 30 amino acids, preferably between 32 and 50 amino acids. Said single chain Fab fragments a) VH-CH1-linker-VL-CL, b) VL-CL-linker-VH-CH1, c) VH-CL-linker-VL-CH1 and d) VL-CH1-linker-VH-CL, are stabilized via the natural

disulfide bond between the CL domain and the CH1 domain. The term “N-terminus” denotes the last amino acid of the N-terminus. The term “C-terminus” denotes the last amino acid of the C-terminus.

5 In a preferred embodiment said antibody domains and said linker in said single chain Fab fragment have one of the following orders in N-terminal to C-terminal direction:

a) VH-CH1-linker-VL-CL, or b) VL-CL-linker-VH-CH1, more preferably VL-CL-linker-VH-CH1.

10 In another preferred embodiment said antibody domains and said linker in said single chain Fab fragment have one of the following orders in N-terminal to C-terminal direction:

a) VH-CL-linker-VL-CH1 or b) VL-CH1-linker-VH-CL.

15 The term “peptide connector” as used within the invention denotes a peptide with amino acid sequences, which is preferably of synthetic origin. These peptide connectors according to invention are used to fuse the single chain Fab fragments to the C-or N-terminus of the full length antibody to form a multispecific antibody according to the invention. Preferably said peptide connectors under b) are peptides with an amino acid sequence with a length of at least 5 amino acids, preferably with a length of 5 to 100, more preferably of 10 to 50 amino acids. In one
20 embodiment said peptide connector is (GxS)_n or (GxS)_nG_m with G = glycine, S = serine, and (x = 3, n= 3, 4, 5 or 6, and m= 0, 1, 2 or 3) or (x = 4, n= 2, 3, 4 or 5 and m= 0, 1, 2 or 3), preferably x = 4 and n= 2 or 3, more preferably with x = 4, n= 2. In one embodiment said peptide connector is (G₄S)₂.

25 The term “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 link a) VH-CH1 to VL-CL, b) VL-CL to VH-CH1, c) VH-CL to VL-CH1 or d) VL-CH1 to VH-CL to form the following single chain Fab fragments according to the invention a) VH-CH1-linker-VL-CL, b) VL-CL-linker-VH-CH1, c) VH-CL-linker-VL-CH1 or d) VL-CH1-linker-VH-CL. Said linker
30 within the single chain Fab fragments 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 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 $(G_4S)_6G_2$.

Optionally in said single chain Fab fragment, additionally to the natural disulfide bond between the CL-domain and the CH1 domain, also the antibody heavy chain variable domain (VH) and the antibody light chain variable domain (VL) are disulfide stabilized by introduction of a disulfide bond between the following positions:

- i) heavy chain variable domain position 44 to light chain variable domain position 100,
- ii) heavy chain variable domain position 105 to light chain variable domain position 43, or
- iii) heavy chain variable domain position 101 to light chain variable domain position 100 (numbering always according to EU index of Kabat).

Such further disulfide stabilization of single chain Fab fragments is achieved by the introduction of a disulfide bond between the variable domains VH and VL of the single chain Fab fragments. Techniques to introduce unnatural disulfide bridges for stabilization for a single chain Fv are described e.g. in WO 94/029350, Rajagopal, V., et al, Prot. Engin. (1997) 1453-59; Kobayashi, H., et al; Nuclear Medicine & Biology, Vol. 25, (1998) 387-393; or Schmidt, M., et al, Oncogene (1999) 18, 1711-1721. In one embodiment the optional disulfide bond between the variable domains of the single chain Fab fragments comprised in the antibody according to the invention is between heavy chain variable domain position 44 and light chain variable domain position 100. In one embodiment the optional disulfide bond between the variable domains of the single chain Fab fragments comprised in the antibody according to the invention is between heavy chain variable domain position 105 and light chain variable domain position 43 (numbering always according to EU index of Kabat).

In an embodiment single chain Fab fragment without said optional disulfide stabilization between the variable domains VH and VL of the single chain Fab fragments are preferred.

Preferably said second embodiment of a tetravalent bispecific antibody according to the invention comprises two identical single chain Fab fragments (preferably

VL-CL-linker-VH-CH1) which are both fused to the two C-termini of the two heavy chains or to the two C-termini of the two light chains of said full length antibody under a). Such fusion results in two identical fusion peptides (either i) heavy chain and single chain Fab fragment or ii) light chain and single chain Fab
5 fragment) which are coexpressed with either i) the light chain or the heavy chain of the full length antibody to give the bispecific antibody according to the invention

In a further embodiment said bispecific antibody is characterized in that the constant region derived of human origin.

10 In a further embodiment said bispecific antibody is characterized in that the constant region of the bispecific antibody according to the invention is of human IgG1 subclass, or of human IgG1 subclass with the mutations L234A and L235A.

In a further embodiment said bispecific antibody is characterized in that the constant region of the bispecific antibody according to the invention antibody is of human IgG2 subclass.

15 In a further embodiment said bispecific antibody is characterized in that the constant region of the bispecific antibody according to the invention antibody is of human IgG3 subclass.

20 In a further embodiment said bispecific antibody is characterized in the constant region of the bispecific antibody according to the invention is of human IgG4 subclass or, of human IgG4 subclass with the additional mutation S228P.

25 It has now been found that the bispecific antibodies against human VEGF and human ANG-2 according to the current invention have improved characteristics such as biological or pharmacological activity, pharmacokinetic properties or toxicity. They show increased in vivo tumor growth inhibition and/or inhibition of tumor angiogenesis when compared to the monospecific parent antibodies against VEGF and ANG-2 (see Examples 16, 17 and 18: comparison of different bispecific <VEGF-ANG-2> antibodies bevacizumab-ANG2i-LC06 with the monospecific antibodies Avastin (bevacicimab) alone, ANG2i-LC06 alone, or both in combination).

30 Furthermore less toxic side effects (which is reflected in the improved body weight of the test animals as well as less deaths of test animals during the in vivo application) compared to the application of two corresponding individual

monospecific antibodies against VEGF and ANG-2 in combination also represent an advantage of the bispecific antibodies according to the invention.

Furthermore the bispecific antibodies according to the current invention may provide benefits such as reduced dose and/or frequency of administration and concomitantly cost savings.

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).

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

In one embodiment an antibody according to the invention has a reduced FcR binding compared to an IgG1 antibody and the monospecific bivalent (full length) parent antibody is in regard to FcR binding of IgG4 subclass or of IgG1 or IgG2 subclass with a mutation in S228, L234, L235 and/or D265, and/ or contains the

PVA236 mutation. In one embodiment the mutations in the monospecific bivalent (full length) parent antibody are S228P, L234A, L235A, L235E and/or PVA236. In another embodiment the mutations in the monospecific bivalent (full length) parent antibody are in IgG4 S228P and in IgG1 L234A and L235A. Constant heavy chain regions are shown in SEQ ID NO: 35 and 36. In one embodiment the constant heavy chain region of the monospecific bivalent (full length) parent antibody is of SEQ ID NO: 35 with mutations L234A and L235A. In another embodiment the constant heavy chain region of the monospecific bivalent (full length) parent antibody is of SEQ ID NO: 36 with mutation S228P. In another embodiment the constant light chain region of the monospecific bivalent (full length) parent antibody is a kappa light chain region of SEQ ID NO: 37 or lambda light chain region of SEQ ID NO: 34. Preferably the constant heavy chain region of the monospecific bivalent (full length) parent antibody is of SEQ ID NO: 35 or of SEQ ID NO: 36 with mutation S228P.

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

The term "antibody-dependent cellular cytotoxicity (ADCC)" refers to lysis of human target cells by an antibody according to the invention in the presence of effector cells. ADCC is measured preferably by the treatment of a preparation of CCR5 expressing cells with an antibody according to the invention in the presence of effector cells such as freshly isolated PBMC or purified effector cells from buffy coats, like monocytes or natural killer (NK) cells or a permanently growing NK cell line.

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

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) 151-161; Werner, R.G., *Drug Res.* 48 (1998) 870-880.

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
5 nucleotide synthesis. Such modifications can be performed, however, only in a very limited range, e.g. as described above. For example, the modifications do not alter the above mentioned antibody characteristics such as the IgG isotype and antigen binding, but may improve the yield of the recombinant production, protein stability or facilitate the purification.

10 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
15 "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.

20 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.
25 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.

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

A nucleic acid is "operably linked" when it is placed in a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or

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

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

One aspect of the invention is a pharmaceutical composition comprising an 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.

- 5 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.

- 10 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).

- 15 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
20 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
25 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,
30 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, schwannomas, ependymomas, 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 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.

5 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.

10 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.

15 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.

20 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 (1978) 546ff. However, other methods for introducing DNA into cells such as by nuclear injection or by protoplast fusion may also be used. If prokaryotic cells or
25 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.

30 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.

5 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.

10 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.

Description of the Amino acid Sequences

SEQ ID NO:	1	heavy chain CDR3, <VEGF>bevacizumab
SEQ ID NO:	2	heavy chain CDR2, <VEGF>bevacizumab
SEQ ID NO:	3	heavy chain CDR1, <VEGF>bevacizumab
SEQ ID NO:	4	light chain CDR3, <VEGF>bevacizumab
SEQ ID NO:	5	light chain CDR2, <VEGF>bevacizumab
SEQ ID NO:	6	light chain CDR1, <VEGF>bevacizumab
SEQ ID NO:	7	heavy chain variable domain, <VEGF>bevacizumab
SEQ ID NO:	8	light chain variable domain, <VEGF>bevacizumab
SEQ ID NO:	9	heavy chain CDR3, <VEGF>ranibizumab
SEQ ID NO:	10	heavy chain CDR2, <VEGF>ranibizumab
SEQ ID NO:	11	heavy chain CDR1, <VEGF>ranibizumab
SEQ ID NO:	12	light chain CDR3, <VEGF>ranibizumab

SEQ ID NO:	13	light chain CDR2, <VEGF>ranibizumab
SEQ ID NO:	14	light chain CDR1, <VEGF>ranibizumab
SEQ ID NO:	15	heavy chain variable domain, <VEGF>ranibizumab
SEQ ID NO:	16	light chain variable domain, <VEGF>ranibizumab
SEQ ID NO:	17	heavy chain CDR3, <VEGF>HuMab G6-31
SEQ ID NO:	18	heavy chain CDR2, <VEGF> HuMab G6-31
SEQ ID NO:	19	heavy chain CDR1, <VEGF> HuMab G6-31
SEQ ID NO:	20	light chain CDR3, <VEGF> HuMab G6-31
SEQ ID NO:	21	light chain CDR2, <VEGF> HuMab G6-31
SEQ ID NO:	22	light chain CDR1, <VEGF> HuMab G6-31
SEQ ID NO:	23	heavy chain variable domain, <VEGF> HuMab G6-31
SEQ ID NO:	24	light chain variable domain, <VEGF> HuMab G6-31
SEQ ID NO:	25	heavy chain CDR3, <ANG-2> Mab 536
SEQ ID NO:	26	heavy chain CDR2, <ANG-2> Mab 536
SEQ ID NO:	27	heavy chain CDR1, <ANG-2> Mab 536
SEQ ID NO:	28	light chain CDR3, <ANG-2> Mab 536
SEQ ID NO:	29	light chain CDR2, <ANG-2> Mab 536
SEQ ID NO:	30	light chain CDR1, <ANG-2> Mab 536
SEQ ID NO:	31	heavy chain variable domain, <ANG-2> Mab 536
SEQ ID NO:	32	light chain variable domain, <ANG-2> Mab 536

SEQ ID NO:	33	(G4S)4 linker
SEQ ID NO:	34	lambda light chain constant region
SEQ ID NO:	35	human heavy chain constant region derived from IgG1
SEQ ID NO:	36	human heavy chain constant region derived from IgG4
SEQ ID NO:	37	kappa light chain constant region
SEQ ID NO:	38	heavy chain CDR3, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	39	heavy chain CDR2, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	40	heavy chain CDR1, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	41	light chain CDR3, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	42	light chain CDR2, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	43	light chain CDR1, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	44	heavy chain variable domain, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	45	light chain variable domain, <ANG-2> Ang2s_R3_LC03
SEQ ID NO:	46	heavy chain CDR3, <ANG-2>Ang2i_LC06
SEQ ID NO:	47	heavy chain CDR2, <ANG-2> Ang2i_LC06
SEQ ID NO:	48	heavy chain CDR1, <ANG-2>Ang2i_LC06
SEQ ID NO:	49	light chain CDR3, <ANG-2>Ang2i_LC06
SEQ ID NO:	50	light chain CDR2, <ANG-2>Ang2i_LC06
SEQ ID NO:	51	light chain CDR1, <ANG-2>Ang2i_LC06
SEQ ID NO:	52	heavy chain variable domain, <ANG-2>Ang2i_LC06

SEQ ID NO:	53	light chain variable domain, <ANG-2>Ang2i_LC06
SEQ ID NO:	54	heavy chain CDR3, <ANG-2>Ang2i_LC07
SEQ ID NO:	55	heavy chain CDR2, <ANG-2>Ang2i_LC07
SEQ ID NO:	56	heavy chain CDR1, <ANG-2>Ang2i_LC07
SEQ ID NO:	57	light chain CDR3, <ANG-2>Ang2i_LC07
SEQ ID NO:	58	light chain CDR2, <ANG-2>Ang2i_LC07
SEQ ID NO:	59	light chain CDR1, <ANG-2>Ang2i_LC07
SEQ ID NO:	60	heavy chain variable domain, <ANG-2>Ang2i_LC07
SEQ ID NO:	61	light chain variable domain, <ANG-2>Ang2i_LC07
SEQ ID NO:	62	heavy chain CDR3, <ANG-2>Ang2k_LC08
SEQ ID NO:	63	heavy chain CDR2, <ANG-2> Ang2k_LC08
SEQ ID NO:	64	heavy chain CDR1, <ANG-2> Ang2k_LC08
SEQ ID NO:	65	light chain CDR3, <ANG-2> Ang2k_LC08
SEQ ID NO:	66	light chain CDR2, <ANG-2> Ang2k_LC08
SEQ ID NO:	67	light chain CDR1, <ANG-2> Ang2k_LC08
SEQ ID NO:	68	heavy chain variable domain, <ANG-2> Ang2k_LC08
SEQ ID NO:	69	light chain variable domain, <ANG-2> Ang2k_LC08
SEQ ID NO:	70	heavy chain CDR3, <ANG-2> Ang2s_LC09
SEQ ID NO:	71	heavy chain CDR2, <ANG-2> Ang2s_LC09
SEQ ID NO:	72	heavy chain CDR1, <ANG-2> Ang2s_LC09

SEQ ID NO:	73	light chain CDR3, <ANG-2> Ang2s_LC09
SEQ ID NO:	74	light chain CDR2, <ANG-2> Ang2s_LC09
SEQ ID NO:	75	light chain CDR1, <ANG-2> Ang2s_LC09
SEQ ID NO:	76	heavy chain variable domain, <ANG-2> Ang2s_LC09
SEQ ID NO:	77	light chain variable domain, <ANG-2> Ang2s_LC09
SEQ ID NO:	78	heavy chain CDR3, <ANG-2> Ang2i_LC10
SEQ ID NO:	79	heavy chain CDR2, <ANG-2> Ang2i_LC10
SEQ ID NO:	80	heavy chain CDR1, <ANG-2> Ang2i_LC10
SEQ ID NO:	81	light chain CDR3, <ANG-2> Ang2i_LC10
SEQ ID NO:	82	light chain CDR2, <ANG-2> Ang2i_LC10
SEQ ID NO:	83	light chain CDR1, <ANG-2> Ang2i_LC10
SEQ ID NO:	84	heavy chain variable domain, <ANG-2> Ang2i_LC10
SEQ ID NO:	85	light chain variable domain, <ANG-2> Ang2i_LC10
SEQ ID NO:	86	heavy chain CDR3, <ANG-2> Ang2k_LC11
SEQ ID NO:	87	heavy chain CDR2, <ANG-2> Ang2k_LC11
SEQ ID NO:	88	heavy chain CDR1, <ANG-2> Ang2k_LC11
SEQ ID NO:	89	light chain CDR3, <ANG-2> Ang2k_LC11
SEQ ID NO:	90	light chain CDR2, <ANG-2> Ang2k_LC11
SEQ ID NO:	91	light chain CDR1, <ANG-2> Ang2k_LC11
SEQ ID NO:	92	heavy chain variable domain, <ANG-2> Ang2k_LC11

SEQ ID NO:	93	light chain variable domain, <ANG-2> Ang2k_LC11
SEQ ID NO:	94	heavy chain CDR3, <VEGF>B20-4.1
SEQ ID NO:	95	heavy chain CDR2, <VEGF>B20-4.1
SEQ ID NO:	96	heavy chain CDR1, <VEGF>B20-4.1
SEQ ID NO:	97	light chain CDR3, <VEGF>B20-4.1
SEQ ID NO:	98	light chain CDR2, <VEGF>B20-4.1
SEQ ID NO:	99	light chain CDR1, <VEGF>B20-4.1
SEQ ID NO:	100	heavy chain variable domain, <VEGF>B20-4.1
SEQ ID NO:	101	light chain variable domain, <VEGF>B20-4.1
SEQ ID NO:	102	bevacizumab heavy chain Ang2i_LC06 scFv fusion peptide of <VEGF-ANG-2> TvAb-2441-bevacizumab-LC06
SEQ ID NO:	103	bevacizumab heavy chain Ang2i_LC08 scFv fusion peptide of <VEGF-ANG-2> TvAb-2441-bevacizumab-LC08
SEQ ID NO:	104	light chain of bevacizumab
SEQ ID NO:	105	Human vascular endothelial growth factor (VEGF)
SEQ ID NO:	106	Human angiopoietin-2 (ANG-2)
SEQ ID NO:	107	Human angiopoietin-1 (ANG-1)
SEQ ID NO:	108	Human Tie-2 receptor
SEQ ID NO:	109	Heavy chain 1 of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecule scFv-Avastin-LC06-2620
SEQ ID NO:	110	Light chain of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecule scFv-Avastin-LC06-2620

SEQ ID NO:	111	Heavy chain 1 of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2640
SEQ ID NO:	112	Light chain of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2640
SEQ ID NO:	113	Heavy chain 1 of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2641
SEQ ID NO:	114	Light chain of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2641
SEQ ID NO:	115	Heavy chain 1 of bispecific, trivalent single chain Fab <VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab
SEQ ID NO:	116	Heavy chain 2 of bispecific, trivalent single chain Fab <VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab
SEQ ID NO:	117	Light chain of bispecific, trivalent single chain Fab <VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab
SEQ ID NO:	118	Heavy chain 1 of bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS
SEQ ID NO:	119	Heavy chain 2 of bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS
SEQ ID NO:	120	Light chain of bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS
SEQ ID NO:	121	Heavy chain 1 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL
SEQ ID NO:	122	Heavy chain 2 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL
SEQ ID NO:	123	Light chain 1 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL
SEQ ID NO:	124	Light chain 2 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL
SEQ ID NO:	125	Heavy chain 1 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL

SEQ ID NO:	126	Heavy chain 2 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL
SEQ ID NO:	127	Light chain 1 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL
SEQ ID NO:	128	Light chain 2 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL
SEQ ID NO:	129	Heavy chain 1 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL-SS
SEQ ID NO:	130	Heavy chain 2 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL-SS
SEQ ID NO:	131	Light chain 1 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL-SS
SEQ ID NO:	132	Light chain 2 of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL-SS
SEQ ID NO:	133	Heavy chain 1 of bispecific, bivalent ScFab-Fc fusion <VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFab
SEQ ID NO:	134	Heavy chain 2 of bispecific, bivalent ScFab-Fc fusion <VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFab
SEQ ID NO:	135	Heavy chain 1 of bispecific, bivalent ScFab-Fc fusion <VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFabSS
SEQ ID NO:	136	Heavy chain 2 of bispecific, bivalent ScFab-Fc fusion <VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFabSS

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.

5

Description of the Figures

Figure 1A Schematic structure of one tetravalent embodiment of a bispecific antibody according to the invention binding to VEGF and ANG-2, wherein one of the Antigens A or B is VEGF, while the other

is ANG-2. The structure is based on a full length antibody binding to Antigen A, to which two (optionally disulfide-stabilized) single chain Fv' s binding to Antigen B, are linked via the a peptide-linker.

5

Figure 1B Schematic representation of the generated bispecific tetravalent antibodies using the TvAb nomenclature (see Examples) – either without or with disulfide stabilization of the scFv

10

Figure 2A Schematic representation of disulfide-stabilized <VEGF-ANG-2> bispecific tetravalent antibody (= <VEGF-ANG-2> TvAb6; No. 2331, see Table 3)

Figure 2B Plasmid maps of the modified heavy chain and the light vectors used for the expression of disulfide-stabilized <VEGF-ANG-2> TvAb6

15

Figure 3 SDS-PAGE of purified disulfide-stabilized <VEGF-ANG-2> TvAb6 in comparison to the “standard” human IgG1 antibody G6-31 (<VEGF> HuMab G6-31) under reducing and non-reducing conditions

20

Figure 4 Size exclusion chromatography of purified disulfide-stabilized <VEGF-ANG-2> TvAb6 in comparison to the “standard” human IgG1 antibody G6-31 shows that disulfide-stabilized TvAb6 does not form again aggregates upon purification

Figure 5 Schematic view and results from VEGF binding ELISA. disulfide-stabilized <VEGF-ANG-2> TvAb6 binds to VEGF comparable to <VEGF> G6-31. <ANG-2> Mab536 does not bind to VEGF

25

Figure 6A Schematic view and results from ANG-2 binding ELISA. disulfide-stabilized <VEGF-ANG-2> TvAb6 binds to ANG-2 comparable to <ANG-2> Mab536. <VEGF> G6-31 does not bind to ANG-2.

30

Figure 6B Schematic view and results from ANG-2 binding analysis by surface plasmon resonance (Biacore). disulfide-stabilized

<VEGF-ANG-2> TvAb6 binds to ANG-2 with comparable affinity as <ANG-2> Mab536.

5 **Figure 7** Schematic view and results from VEGF-ANG-2 bridging ELISA. disulfide-stabilized <VEGF-ANG-2> TvAb6 binds simultaneously to VEGF and ANG-2 whereas <VEGF> G6-31 and <ANG-2> Mab536 are not capable of binding simultaneously to VEGF and ANG-2.

10 **Figure 8a** Efficacy of disulfide-stabilized <VEGF-ANG-2> TvAb6 in comparison to <ANG-2> Mab536, <VEGF> G6-31 and the combination of Mab536 and G6-31 in the staged subcutaneous Colo205 xenograft model in Scid beige mice (study ANG2_Pz_Colo205_003)

15 **Figure 8b** Efficacy of disulfide-stabilized <VEGF-ANG-2> TvAb6 in comparison to <ANG-2> Mab536, <VEGF> G6-31 and the combination of Mab536 and G6-31 in the staged subcutaneous Colo205 xenograft model in Scid beige mice (study ANG2_Pz_Colo205_005)

20 **Figure 9** Blocking of VEGF-induced tube formation by the bispecific tetravalent antibody <VEGF-ANG-2> TvAb6- Results

Figure 10A + B Blocking of VEGF-induced tube formation by the b disulfide-stabilized <VEGF-ANG-2> TvAb6 -- Quantitative analysis

Figure 11 Schematic view of VEGF binding analysis by surface plasmon resonance (Biacore).

25 **Figure 12** Kinetic characteristics of the two <VEGF> antibodies <VEGF-Ang-2> TvAb6 and <VEGF> G6-31 in a Ka-Kd plot.

Figure 13 Schematic view of surface plasmon resonance (Biacore) assay to detect simultaneous binding of ANGPT2 and VEGF to bispecific antibodies

30 **Figure 14** Results from surface plasmon resonance (Biacore) experiments showing that TvAb6 binds simultaneously to ANGPT2 and VEGF.

Figure 15A + B A) Schematic representation of the bispecific and simultaneous Biacore binding assay of the <VEGF-ANG-2> bispecific antibodies. B) Biacore data demonstrating simultaneous binding of ANG-2 and VEGF to TvAb-2441-bevacicumab_LC06

5 **Figure 16A +B** Tie2 phosphorylation of the bispecific antibodies <VEGF-ANG-2>TvAb-2441-bevacizumab-LC06 and <VEGF-ANG-2>TvAb-2441, in comparison with the anti-Ang2 antibodies <ANG-2>Ang2i_LC06 and < ANG-2>Ang2k_LC08

10 **Figure 17** Schematic representation of human Angiopoietin interaction ELISA

Figure 18 VEGF-induced HUVEC proliferation of <VEGF-ANG-2>TvAb-2441-bevacizumab-LC06 and <VEGF-ANG-2>TvAb-2441-bevacizumab-LC08 and bevacizumab

15 **Figure 19** In vivo anti-angiogenic efficacy of bispecific antibody <VEGF-ANG-2> bevacizumab-LC06 antibody in comparison to <ANG-2> ANG2i-LC06, and the combination of <ANG-2> ANG2i-LC06 and Avastin (bevacizumab) in Calu3 xenograft model monitored via labeled anti-CD31 antibody and the relative change of CD31 signal during therapy.

20 **Experimental Procedure**

Examples

Materials & general methods

25 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.

5 **Gene synthesis**

Desired gene segments were 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 (MGWSCILFLVATATGVHS), which targets proteins for secretion in eukaryotic cells, and 5'-BamHI and 3'-XbaI restriction sites. 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).

25 **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 Example 1)

30 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:

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

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

- 10 - 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,
- 15 - 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.

20 The fusion genes comprising the heavy chain sequences of the selected antibody and the C-terminal scFv fusion as described below were generated by PCR and/or gene synthesis and assembled with known recombinant methods and techniques by connection of the according nucleic acid segments e.g. using unique NsiI and EcoRI sites in the genomic heavy chain vectors. The subcloned nucleic acid
25 sequences were verified by DNA sequencing. For transient and stable transfections larger quantities of the plasmids were prepared by plasmid preparation from transformed E. coli cultures (Nucleobond AX, Macherey-Nagel).

Expression vectors (for Example 10-14)

An expression vector was used which composed of the following elements:

- 30 - a hygromycin resistance gene as a selection marker,
- an origin of replication, oriP, of Epstein-Barr virus (EBV),
- an origin of replication from the vector pUC18 which allows replication

of this plasmid in *E. coli*

- a beta-lactamase gene which confers ampicillin resistance in *E. coli*,
- the immediate early enhancer and promoter from the human cytomegalovirus (HCMV),
- 5 - the human 1-immunoglobulin polyadenylation ("poly A") signal sequence, and
- unique BamHI and XbaI restriction sites.

The immunoglobulin fusion genes comprising the heavy or light chain constructs as well as "knobs-into-hole" constructs with C-terminal VH and VL domains were
10 prepared by gene synthesis and cloned into pGA18 (ampR) plasmids as described. The pG18 (ampR) plasmids carrying the synthesized DNA segments and the Roche expression vector were digested with BamHI and XbaI restriction enzymes (Roche Molecular Biochemicals) and subjected to agarose gel electrophoresis. Purified heavy and light chain coding DNA segments were then ligated to the isolated
15 Roche expression vector BamHI/XbaI fragment resulting in the final expression vectors. The final expression vectors were transformed into *E. coli* cells, expression plasmid DNA was isolated (Miniprep) and subjected to restriction enzyme analysis and DNA sequencing. Correct clones were grown in 150 ml LB-Amp medium, again plasmid DNA was isolated (Maxiprep) and sequence integrity confirmed by
20 DNA sequencing.

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..

25 Transient transfections in HEK293-F system (for Example 1)

Antibodies were generated by transient transfection of the two plasmids encoding the heavy or modified heavy chain, respectively and the corresponding light chain using the HEK293-F system (Invitrogen) according to the manufacturer's instruction. Briefly, HEK293-F cells (Invitrogen) growing in suspension either in a
30 shake flask or in a stirred fermenter in serumfree FreeStyle 293 expression medium (Invitrogen) were transfected with a mix of the two respective expression plasmids and 293fectin or fectin (Invitrogen). For e.g. 2 L shake flask (Corning) HEK293-F cells were seeded at a density of 1.0×10^6 cells/mL in 600 mL and incubated at 120

rpm, 8% CO₂. The day after the cells were transfected at a cell density of ca. 1.5E*6 cells/mL with ca. 42 mL mix of A) 20 mL Opti-MEM (Invitrogen) with 600 µg total plasmid DNA (1 µg/mL) encoding the heavy or modified heavy chain, respectively and the corresponding light chain in an equimolar ratio and B) 20 ml
5 Opti-MEM + 1.2 mL 293 fectin or fectin (2 µl/mL). According to the glucose consumption glucose solution was added during the course of the fermentation. The supernatant containing the secreted antibody was harvested after 5-10 days and antibodies were either directly purified from the supernatant or the supernatant was frozen and stored.

10 **Transient transfections in HEK293-F system (for Example 10-14)**

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
15 37°C/8 % CO₂ and the cells were seeded in fresh medium at a density of 1-2x10⁶ 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. "Knobs-into-hole" DNA-
20 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 in a 1:1:2 molar ratio for a 250 ml final transfection volume. "Knobs-into-hole" DNA-293fectin complexes with two heavy chains were
25 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 DNA in a 1:1 molar ratio for a 250 ml final transfection volume. CrossMab 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-
30 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. 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.

35 **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 et. al., Protein Science, 1995, 4, 2411-1423.

5 **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 Streptavidin A-96 well microtiter plates (Roche) were coated with 100 µL/well biotinylated anti-human IgG capture molecule F(ab')₂<h-Fcγ₁ 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 μ L/well PBST and bound antibody was detected with 100 μ L F(ab')₂-hFc γ POD (Dianova) at 0.1 μ g/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 μ L/well PBST and the bound detection antibody was detected by addition of 100 μ L ABTS/well. Determination of absorbance was performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

10 Protein purification

Proteins were purified from filtered cell culture supernatants referring to standard protocols. In brief, antibodies were applied to a Protein A Sepharose column (GE Healthcare) and washed with PBS. Elution of antibodies was achieved at acidic pH followed by immediate neutralization of the sample. Aggregated protein was separated from monomeric antibodies by size exclusion chromatography (Superdex 200, GE Healthcare) in 20 mM Histidine, 140 mM NaCl pH 6.0. Monomeric antibody fractions were pooled, concentrated if required using e.g. a MILLIPORE Amicon Ultra (30 MWCO) centrifugal concentrator and stored at -80 °C. Part of the samples were provided for subsequent protein analytics and analytical characterization e.g. by SDS-PAGE, size exclusion chromatography, mass spectrometry and Endotoxin determination (see Figures 3 and 4).

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

5 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
10 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
15 equipped with a NanoMate source.

VEGF binding ELISA

The binding properties of the tetravalent antibodies (TvAb) was evaluated in an ELISA assay with full-length VEGF165-His protein (R&D Systems) (Figure 5). For this sake Falcon polystyrene clear enhanced microtiter plates were coated with
20 100 µl 2 µg/mL recombinant human VEGF165 (R&D Systems) in PBS for 2 h at room temperature or over night at 4°C. The wells were washed three times with 300µl PBST (0,2% Tween 20) and blocked with 200 µl 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300µl PBST. 100 µL/well of a dilution series (40 pM-0.01 pM) of purified <VEGF-ANG-
25 2> TvAb and as a reference the human anti-ANG-2 antibody <ANG-2> antibody Mab536 (Oliner et al., Cancer Cell. 2004 Nov;6(5):507-16, US 2006/0122370) and the anti VEGF antibody <VEGF> antibody G6-31 (Liang et al., J Biol Chem. 2006 Jan 13;281(2):951-61; US 2007/0141065) in PBS (Sigma) was added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells
30 were washed three times with 300µl PBST (0,2% Tween 20) and bound antibody was detected with 100 µL/well 0.1 µg/ml F(ab') <hFcgamma>POD (Immuno research) in 2% BSA 0,1% Tween 20 as detection antibody for 1 h on a microtiterplate shaker at room temperature. Unbound detection antibody was washed away three times with 300 µL/well PBST and the bound detection antibody

was detected by addition of 100 μ L ABTS/well. Determination of absorbance was performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

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

In order to further corroborate the ELISA findings the binding of <VEGF> antibodies G6-31 or Avastin and <VEGF-Ang-2> TvAb6 or TvAb-2441-bevacizumab-LC06 or TvAb-2441-bevacizumab-LC08 to VEGF was quantitatively analyzed using surface plasmon resonance technology on a Biacore T100 instrument according to the following protocol and analyzed using the T100 software package: Briefly <VEGF> antibodies were captured on a CM5-Chip via binding to a Goat Anti Human IgG (JIR 109-005-098). The capture antibody was immobilized by amino coupling using standard amino coupling as follows: HBS-N buffer served as running buffer, activation was done by mixture of EDC/NHS with the aim for a ligand density of 700 RU. The Capture-Antibody was diluted in coupling buffer NaAc, pH 5.0, c = 2 μ g/mL, finally still activated carboxyl groups were blocked by injection of 1 M Ethanolamine. Capturing of Mabs <VEGF> antibodies was done at a flow of 5 μ L/min and c(Mabs<VEGF>) = 10 nM, diluted with running buffer + 1 mg/mL BSA; a capture level of approx. 30 RU should be reached. rhVEGF (rhVEGF, R&D-Systems Cat.-No, 293-VE) was used as analyte. The kinetic characterization of VEGF binding to<VEGF> antibodies was performed at 37°C in PBS + 0.005 % (v/v) Tween20 as running buffer. The sample was injected with a flow of 50 μ L/min and an association of time 80 sec. and a dissociation time of 1200 sec with a concentration series of rhVEGF from 300 - 0.29 nM. Regeneration of free capture antibody surface was performed with 10 mM Glycin pH 1.5 and a contact time of 60 sec after each analyte cycle. Kinetic constants were calculated by using the usual double referencing method (control reference: binding of rhVEGF to capture molecule Goat Anti Human IgG, blanks on the measuring flow cell, rhVEGF concentration "0", Model: Langmuir binding 1:1, (Rmax set to local because of capture molecule binding). Figure 11 shows a schematic view of the Biacore assay.

ANG-2 binding ELISA

The binding properties of the tetravalent antibodies (TvAb) was evaluated in an ELISA assay with full-length Angiopoietin-2-His protein (R&D Systems) (Figure

6a). For this sake Falcon polystyrene clear enhanced microtiter plates were coated with 100 μ l 1 μ g/mL recombinant human Angiopoietin-2 (R&D Systems, carrier-free) in PBS for 2 h at room temperature or over night at 4°C. The wells were washed three times with 300 μ l PBST (0,2% Tween 20) and blocked with 200 μ l 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300 μ l PBST. 100 μ L/well of a dilution series (40pM-0.01 pM) of purified <VEGF-ANG-2> TvAb and as a reference <ANG-2> antibody Mab536 and VEGF> antibody G6-31 in PBS (Sigma) was added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells were washed three times with 300 μ l PBST (0,2% Tween 20) and bound antibody was detected with 100 μ L/well 0.1 μ g/ml F(ab') <hk>POD (Biozol Cat.No. 206005) in 2% BSA 0,1% Tween 20 as detection antibody for 1 h on a microtiterplate shaker at room temperature. Unbound detection antibody was washed away three times with 300 μ L/well PBST and the bound detection antibody was detected by addition of 100 μ L ABTS/well. Determination of absorbance was performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

Comparative binding to ANG-1 and ANG-2 (ANG-1 and ANG-2 binding ELISA)

The binding properties of antibodies were evaluated in an ELISA assay with full-length Angiopoietin-2-His protein (R&D Systems #623-AN/CF or in house produced material) or Angiopoietin-1-His (R&D systems #923-AN). Therefore 96 well plates (Falcon polystyrene clear enhanced microtiter plates or Nunc Maxisorb) were coated with 100 μ l 1 μ g/mL recombinant human Angiopoietin-1 or Angiopoietin-2 (carrier-free) in PBS (Sigma) for 2 h at room temperature or over night at 4°C. The wells were washed three times with 300 μ l PBST (0,2% Tween 20) and blocked with 200 μ l 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300 μ l PBST. 100 μ L/well of a dilution series (40pM-0.01 pM) of purified test antibody in PBS was added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells were washed three times with 300 μ l PBST (0,2% Tween 20) and bound antibody was detected with 100 μ L/well 0.1 μ g/ml F(ab') <hk>POD (Biozol Cat.No. 206005) in 2% BSA 0,1% Tween 20 as detection antibody for 1 h on a microtiterplate shaker at room temperature. Unbound detection antibody was washed away three times with 300 μ L/well PBST and the bound detection antibody

was detected by addition of 100 μ L ABTS/well. Determination of absorbance was performed on a Tecan Fluor Spectrometer at a measurement wavelength of 405 nm (reference wavelength 492 nm).

ANG-2 binding BIACORE

5 Binding of the antibodies to the antigen e.g. human ANG-2 were investigated by surface plasmon resonance using a BIACORE T100 instrument (GE Healthcare Biosciences AB, Uppsala, Sweden). Briefly, for affinity measurements goat α hIgG-Fc γ polyclonal antibodies were immobilized on a CM5 chip via amine coupling for presentation of the antibodies against human ANG-2 (Figure 6B).
10 Binding was measured in HBS buffer (HBS-P (10 mM HEPES, 150 mM NaCl, 0.005% Tween 20, pH 7.4), 25°C. Purified ANG-2-His (R&D systems or in house purified) was added in various concentrations between 6,25 nM and 200 nM in solution. Association was measured by an ANG-2-injection of 3 minutes; dissociation was measured by washing the chip surface with HBS buffer for 3
15 minutes and a KD value was estimated using a 1:1 Langmuir binding model. Due to heterogeneity of the ANG-2 preparation no 1:1 binding could be observed; KD values are thus only relative estimations. Negative control data (e.g. buffer curves) were subtracted from sample curves for correction of system intrinsic baseline drift and for noise signal reduction. Biacore T100 Evaluation Software version 1.1.1
20 was used for analysis of sensorgrams and for calculation of affinity data. Alternatively, Ang-2 could be captured with a capture level of 2000-1700 RU via a PentaHisAntibody (PentaHis-Ab BSA-free, Qiagen No. 34660) that was immobilized on a CM5 chip via amine coupling (BSA-free) (see below).

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

25 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 0.5 μ g/ml Tie-2 protein (R&D Systems, UK, Cat.No.313-TI) for at least 2 hours (h). Thereafter the wells were blocked with PBS supplemented with 0.2% Tween-20 and 2% BSA (Roche
30 Diagnostics GmbH, DE) for 1 h. Dilutions of purified antibodies in PBS were incubated together with 0.2 μ g/ml huAngiopoietin-2 (R&D Systems, UK, Cat.No. 623-AN) for 1 h at RT. After washing a mixture of 0.5 μ g/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 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.

5 **ANG-2-VEGF bridging ELISA**

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

For this sake Falcon polystyrene clear enhanced microtiter plates were coated with 100 µl 2 µg/mL recombinant human VEGF165 (R&D Systems) in PBS for 2 h at
15 room temperature or over night at 4°C. The wells were washed three times with 300µl PBST (0,2% Tween 20) and blocked with 200 µl 2% BSA 0,1% Tween 20 for 30 min at room temperature and subsequently washed three times with 300µl PBST. 100 µL/well of a dilution series (40pM-0.01 pM) of purified <VEGF-ANG-2> TvAb and as a reference <ANG-2> antibody Mab536 and VEGF> antibody
20 G6-31 in PBS (Sigma) was added to the wells and incubated for 1 h on a microtiterplate shaker at room temperature. The wells were washed three times with 300µl PBST (0,2% Tween 20) and bound antibody was detected by addition of 100 µl 0.5 µg/ml human ANG-2-His (R&D Systems) in PBS. The wells were washed three times with 300µl PBST (0,2% Tween 20) and bound ANG-2 was
25 detected with 100 µl 0.5 µg/mL <ANG-2>mIgG1-Biotin antibody (BAM0981, R&D Systems) for 1 h at room temperature. Unbound detection antibody was washed away with three times 300µl PBST (0,2% Tween 20) and bound antibody was detected by addition of 100 µl 1:2000 Streptavidin-POD conjugate (Roche Diagnostics GmbH, Cat. No.11089153) 1:4 diluted in blocking buffer for 1h at
30 room temperature. Unbound Streptavidin-POD conjugate was washed away with three-six times 300µl PBST (0,2% Tween 20) and bound Strepatavidin-POD conjugate 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).

**Demonstration of simultaneous binding of bispecific tetravalent antibody
<VEGF-Ang-2> TvAb6 to VEGF-A and Ang-2 by Biacore**

In order to further corroborate the data from the bridging ELISA an additional assay was established to confirm simultaneous binding to VEGF and Ang-2 using surface plasmon resonance technology on a Biacore T100 instrument according to the following protocol and analyzed using the T100 software package (T100 Control, Version 2.01, T100 Evaluation, Version 2.01, T100 Kinetics Summary, Version 1.01): Ang-2 was captured with a capture level of 2000-1700 RU in PBS, 0.005 % (v/v) Tween20 running buffer via a PentaHisAntibody (PentaHis-Ab BSA-free, Qiagen No. 34660) that was immobilized on a CM5 chip via amine coupling (BSA-free). HBS-N buffer served as running buffer during coupling, activation was done by mixture of EDC/NHS. The PentaHis-Ab BSA-free Capture-Antibody was diluted in coupling buffer NaAc, pH 4.5, c = 30 µg/mL, finally still activated carboxyl groups were blocked by injection of 1 M Ethanolamine; ligand densities of 5000 and 17000 RU were tested. Ang-2 with a concentration of 500 nM was captured by the PentaHis-Ab at a flow of 5 µL/min diluted with running buffer + 1 mg/mL BSA. Subsequently, <Ang-2, VEGF> bispecific antibody binding to Ang-2 and to VEGF was demonstrated by incubation with rhVEGF and formation of a sandwich complex. For this sake, bispecific <VEGF-Ang-2> TvAb6 was bound to Ang-2 at a flow of 50 µL/min and a concentration of 100 nM, diluted with running buffer + 1 mg/mL BSA and simultaneous binding was detected by incubation with VEGF (rhVEGF, R&D-Systems Cat.-No, 293-VE) in PBS + 0.005 % (v/v) Tween20 running buffer at a flow of 50 µL/min and a VEGF concentration of 150 nM. Association time 120 sec, dissociation time 1200 sec. Regeneration was done after each cycle at a flow of 50 µL/min with 2 x 10 mM Glycin pH 2.0 and a contact time of 60 sec. Sensorgrams were corrected using the usual double referencing (control reference: binding of bispecific antibody and rhVEGF to capture molecule PentaHisAb). Blanks for each Ab were measured with rhVEGF concentration "0". A scheme of the Biacore assay is shown in Figure 13. An alternative Biacore assay format is shown in Figure 15.

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.

10 **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, $\leq$ passages) per 96 well were incubated in 100 μ l 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 ng/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-Glo™ Luminescent Cell Viability Assay kit according to the manual (Promega, # G7571/2/3). Luminescence was determined in a spectrophotometer.

15 **Design of tetravalent bispecific and tetravalent monospecific antibodies**

The bispecific antibodies binding to VEGF (VEGF-A) and ANG-2 (Angiopoietin-2) according to the invention comprise a first antigen-binding site that binds to VEGF and a second antigen-binding site that binds to ANG-2. As first antigen-binding site binding to VEGF, e.g. the heavy chain variable domain of SEQ ID NO: 23, and the light chain variable domains of SEQ ID NO: 24 which are both derived from the human phage display derived anti-VEGF antibody G6-31 which is described in detail in Liang, W.C., et al., J Biol Chem. 281(2) (2006) 951-61 and in US 2007/0141065, can be used. Alternatively e.g. the second antigen-binding site specifically binding to VEGF comprises the heavy chain variable domains of SEQ ID NO: 7, or SEQ ID NO: 100, and the light chain variable domains SEQ ID NO:8 or SEQ ID NO: 101 from the anti-VEGF antibodies <VEGF>bevacizumab and <VEGF>B20-4.1., preferably from <VEGF>bevacizumab.

As second antigen-binding site comprises the heavy chain variable domains SEQ ID NO: 31, and the light chain variable domains SEQ ID NO: 32 or SEQ ID NO: 32 with the mutations T92L, H93Q and W94T (Kabat numbering), which are both derived from the human anti-ANG-2 antibody <ANG-2> Mab536 which is described in detail in Oliner, J., et al., Cancer Cell. 6(5) (2004) 507-16, and in US 2006/0122370, can be used. Alternatively e.g. the second antigen-binding site specifically binding to ANG-2 comprises the heavy chain variable domains of SEQ ID NO: 44, SEQ ID NO: 52, SEQ ID NO: 60, SEQ ID NO: 68, SEQ ID NO:

76, SEQ ID NO: 84 or SEQ ID NO: 92, and the light chain variable domains
SEQ ID NO: 45, SEQ ID NO: 53, SEQ ID NO: 61, SEQ ID NO: 69, SEQ ID
NO: 77, SEQ ID NO: 85, SEQ ID NO: 93 from the anti-ANG-2 antibodies
<ANG-2> Ang2s_R3_LC03, <ANG-2>Ang2i_LC06, <ANG-2>Ang2i_LC07,
5 <ANG-2> Ang2k_LC08, <ANG-2> Ang2s_LC09, <ANG-2> Ang2i_LC10, or
<ANG-2> Ang2k_LC11, preferably from <ANG-2>Ang2i_LC06, or <ANG-2>
Ang2k_LC08.

To generate agents that combine features of both antibodies, novel tetravalent
bispecific antibody-derived protein entities were constructed. In these molecules,
10 recombinant single-chain binding molecules of one antibody are connected via
recombinant protein fusion technologies to the other antibody which was retained
in the format of a full-length IgG1. This second antibody carries the desired second
binding specificity.

By gene synthesis and recombinant molecular biology techniques, the heavy chain
variable domain (VH) and the light chain variable domain (VL) of the respective
15 antibody were linked by a glycine serine (G4S)3 or (G4S)4 single-chain-linker to
give a single chain Fv (scFv), which was attached to the C- terminus of the other
antibody heavy chain using a (G)6- or (G4S)3-linker.

In addition, cysteine residues were introduced in the VH (including Kabat position
20 44,) and VL (including Kabat position 100) domain of the scFv binding to ANG-2
or VEGF as described earlier (e.g. WO 94/029350; Reiter, Y., et al., Nature
biotechnology (1996) 1239-1245; Young, N.M., et al, FEBS Letters (1995) 135-
139; or Rajagopal, V., et al., Protein Engineering (1997) 1453-59).

All these molecules were recombinantly produced, purified and characterized and
25 protein expression, stability and biological activity was evaluated.

A summary of the bispecific antibody designs that were applied to generate
tetravalent bispecific <VEGF-ANG-2>, <ANG-2-VEGF> antibodies and
tetravalent monospecific <ANG-2> antibodies is given in Table 3. For this study,
we use the term 'TvAb' to describe the various tetravalent protein entities.

30 In order to obtain the bispecific tetravalent antibodies <VEGF-ANG-2> TvAb5 and
TvAb6 the single chain Fv (scFv) binding to Angiopoietin-2 derived from the
heavy chain variable domain (VH) of SEQ ID NO: 31, and the light chain variable
domain (VL) of SEQ ID NO: 32 with the mutations T92L, H93Q and W94T

derived from the human anti-ANG-2 antibody <ANG-2> Mab536 was fused to the sequence corresponding to the C-terminus of the heavy chain vector of the human anti-VEGF antibody <VEGF> G6-31 of SEQ ID NO: 23 and co-expressed with the respective light chain expression vector based on SEQ ID NO: 24. A representation of the designed formats is shown in Figure 1B and listed in Table 3.

In order to obtain the bispecific tetravalent antibodies TvAb9 and TvAb15 the single chain Fv (scFv) binding to VEGF derived from the heavy chain variable domain (VH) of SEQ ID NO: 23, and the light chain variable domain (VL) of SEQ ID NO: 24 derived from the human anti-VEGF antibody <VEGF> G6-31 was fused to the sequence corresponding to the C-terminus of the heavy chain vector of the human anti-ANG-2 antibody <ANG-2> Mab536 of SEQ ID NO: 31 and co-expressed with the respective light chain expression vector based on SEQ ID NO: 32. A representation of the designed formats is shown in Figure 1B and listed in Table 3.

Table 3 – The different bispecific tetravalent antibody formats with C- terminal scFv attachments and the corresponding TvAb-nomenclature. An “-“ in the table means “not present”

Molecule Name (TvAb-nomenclature for bispecific antibodies)	Antibody backbone derived from	scFv derived from	Variable Domains VH and VL: SEQ ID NO :	Position of scFv attached to antibody	Single-chain-linker	Peptide linker	scFv disulfide VH44/VL100 stabilized
G6-31 (1000)	<VEGF> G6-31	-	23 + 24	-	-	-	-
Mab536 (1000)	<ANG-2> Mab536	-	31 + 32	-	-	-	-

Molecule Name (TvAb-nomenclature for bispecific antibodies)	Antibody backbone derived from	scFv derived from	Variable Domains VH and VL: SEQ ID NO :	Position of scFv attached to antibody	Single-chain-linker	Peptide-linker	scFv disulfide VH44/VL100 stabilized
bevacizumab	<VEGF> bevacizumab	-	23 + 24	-	-	-	-
Ang2i_LC06 (LC06)	<ANG-2>Ang2i_LC06	-	52 + 53	-	-	-	-
Ang2k_LC06 (LC08)	<ANG-2>Ang2k_LC08	-	68 + 69	-	-	-	-
TvAb5 (2310)	<VEGF>G6-31	<ANG-2> Mab536	23 + 24, 31 + 32 with the mutations T92L, H93Q and W94T	C-term. HC	(G4S)3	(G)6	-

Molecule Name (TvAb-nomenclature for bispecific antibodies)	Antibody backbone derived from	scFv derived from	Variable Domains VH and VL: SEQ ID NO :	Position of scFv attached to antibody	Single-chain-linker	Peptide-linker	scFv disulfide VH44/VL100 stabilized
TvAb6 (2331)	<VEGF> G6-31	<ANG-2> Mab536	23 + 24, 31 + 32 with the mutations T92L, H93Q and W94T	C-term. HC	(G4S)3	(G4S)3	scFv disulfide VH44/VL100 stabilized
TvAb9 (2330)	<ANG-2> Mab536	<VEGF> > G6-31	31 + 32, and 23 + 24	C-term. HC	(G4S)3	(G4S)3	-
TvAb15 (2431)	<ANG-2> Mab536	<VEGF> > G6-31	31 + 32, and 23 + 24	C-term. HC	(G4S)4	(G4S)3	scFv disulfide VH44/VL100 stabilized
TvAb-2441-bevacizumab-LC06	bevacizumab	LC06	7 + 8 and 52 + 53	C-term. HC	(G4S)4	(G4S)4	scFv disulfide VH44/VL100 stabilized

Molecule Name (TvAb-nomenclature for bispecific antibodies)	Antibody backbone e derived from	scFv derived from	Variable Domains VH and VL: SEQ ID NO :	Position of scFv attached to antibody	Single-chain-linker	Peptide-linker	scFv disulfide VH44/ VL100 stabilized
TvAb-2441-bevacizumab-LC08	bevacizumab	LC08	7 + 8 and 68 + 69	C-term. HC	(G4S)4	(G4S)4	scFv disulfide VH44/VL 100 stabilized
TvAb-3421-bevacizumab-LC06	bevacizumab	LC06	7 + 8 and 52 + 53	N-term. HC	(G4S)4	(G4S)2	scFv disulfide VH44/VL 100 stabilized
TvAb-4421-bevacizumab-LC06	bevacizumab	LC06	7 + 8 and 52 + 53	C-term LC	(G4S)4	(G4S)2	scFv disulfide VH44/VL 100 stabilized
TvAb-4461-bevacizumab-LC06	bevacizumab	LC06	7 + 8 and 52 + 53	C-term LC	(G4S)4	(G4S)6	scFv disulfide VH44/VL 100 stabilized

The TvAb formats are based e.g. on

- 5 a) aa) the human anti-VEGF antibody <VEGF> G6-31 and ab) two single chain Fv (scFv) binding to Angiopoietin-2 derived from the heavy chain variable domain (VH) of SEQ ID NO: 31, and the light chain variable domain (VL) of SEQ ID NO: 32 with the mutations T92L, H93Q and W94T, which are linked to the C-terminus of the heavy chain of the anti-VEGF antibody <VEGF> G6-31 (SEQ ID NO: 23); or
- 10 b) ba) the human anti-ANG-2 antibody <ANG-2> Mab536 and bb) two single chain Fv (scFv) binding to VEGF derived from the heavy chain variable domain (VH) of SEQ ID NO: 23, and the light chain variable domain (VL) of SEQ ID NO: 24, which are linked to the C-terminus of the heavy chain of the anti-ANG-2 antibody <ANG-2> Mab536 (SEQ ID NO: 31); or
- 15 c) ca) the human anti-VEGF antibody <VEGF> bevacizumab (Avastin) and cb) two single chain Fv (scFv) binding to Angiopoietin-2 derived from the heavy chain variable domain (VH) of SEQ ID NO: 52 or of SEQ ID NO: 68, and the light chain variable domain (VL) of SEQ ID NO: 53 or of SEQ ID NO: 69, which are linked to the C-terminus of the heavy chain of the anti-VEGF antibody <VEGF> bevacizumab (Avastin) (the Sequences of the resulting fusion peptide are SEQ ID NO: 102 or SEQ ID NO: 103, which are co-expressed with the light chain of bevacizumab SEQ ID NO: 104. (Alternatively two single chain Fv (scFv) binding to Angiopoietin-2 can also be linked to the C-terminus of the light chain or the N-terminus of the heavy chain).
- 20

25 Alternatively to the single two single chain Fv (scFv) also single chain Fab fragments can be used as described above (using peptide connectors for the fusion to C or N-termini), in EP Appl. No 09004909.9 and in Example 10.

Example 1

Expression & purification of bispecific tetravalent antibodies

30 <VEGF-ANG-2> TvAb5, TvAb6, TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab -LC08

Light and heavy chains of the corresponding tetravalent bispecific antibodies TvAb5 and TvAb6 were constructed in genomic expression vectors as described

above). The plasmids were amplified in *E. coli*, purified, and subsequently transfected for transient expression of recombinant proteins in HEK293-F cells (utilizing Invitrogen's FreeStyle 293 system). After 7 days, HEK 293-F cell supernatants were harvested, filtered and the bispecific antibodies were purified by protein A and size exclusion chromatography. Homogeneity of all bispecific antibody constructs was confirmed by SDS-PAGE under non reducing and reducing conditions and analytical size exclusion chromatography. Under reducing conditions (Figure 3), polypeptide heavy chains of <VEGF-ANG-2> TvAb6 carrying the C-terminal scFv fusion showed upon SDS-PAGE apparent molecular sizes of ca. 75 kDa analogous to the calculated molecular weights. Mass spectrometry confirmed the identity of the purified antibody constructs. Expression levels of all constructs were analysed by Protein A HPLC and were similar to expression yields of 'standard' IgGs. Protein yields achieved up to 150 mg of TvAb6 <VEGF-ANG-2> per liter of cell-culture supernatant as determined by Protein A HPLC.

Size exclusion chromatography analysis of the purified non-disulfide stabilized construct TvAb5 with C-terminal fused scFv at the heavy chain showed compared to 'standard' IgGs an increased tendency to aggregate again after purification of monomeric antibody via size exclusion chromatography (so-called "daisy chain" phenomenon). This finding has been supported by other examples (Rajagopal, V., et al., *Prot. Engin.* (1997) 1453-1459; Kobayashi, H., et al, *Nucl Med Biol.* (1998) 387-393 or Schmidt, M., et al, *Oncogene* (1999) 18, 1711 – 1721) showing that molecules that contained scFvs that were not stabilized by interchain disulfides between VH and VL exhibited an increased tendency to aggregate and reduced yields. To address the problems with aggregation of such bispecific antibodies, disulfide-stabilization of the scFv moieties was applied. For that we introduced single cysteine replacements within VH and VL of the scFv at defined positions (positions VH44/VL100 according to the Kabat numbering scheme). These mutations enable the formation of stable interchain disulfides between VH and VL, which in turn stabilize the resulting disulfide-stabilized scFv module. Introduction of the VH44/VL100 disulfides in the scFv at the C-terminus of the Fv in TvAb6 <VEGF-ANG-2> lead to a stable tetravalent antibody that showed no aggregation tendency any longer after purification and remained in a monomeric state (Figure 4). In addition, TvAb6 <VEGF-ANG-2> showed no increase in aggregation tendency upon repeated freeze-thaw cycles e.g. at the concentration applied for in vitro and in vivo of 3 mg/kg.

All other TvAb molecules described in Table 3 (e.g. TvAb-2441-bevacizumab - LC06 and TvAb-2441-bevacizumab -LC08) were prepared and analytically characterized analogously to the procedure described.

Example 2

5 **Simultaneous binding of bispecific tetravalent antibody <VEGF-ANG-2> TvAb6, TvAb-2441-bevacizumab -LC06 and TvAb-2441-bevacizumab -LC08 to VEGF-A and ANG-2**

10 The binding of the scFv modules and of the Fvs retained in the IgG-module of the different bispecific antibody formats were compared to the binding of the 'wildtype' IgGs from which the binding modules and bispecific antibodies were derived. These analyses were carried out at equimolar concentrations by performing biochemical binding ELISAs and by applying Surface Plasmon Resonance (Biacore).

15 For <VEGF-ANG-2> TvAb6 is was shown by VEGF binding ELISA as described above that it binds to VEGF comparable to its parent antibody G6-31 at an equimolar concentration of 0.625 pM (Figure 5). This finding could be expected as the Fv region of the TvAb is identical to that of G6-31. The slight difference between <VEGF-ANG-2> TvAb6 and <VEGF> G6-31 is due to small differences in protein concentration and a slight steric interference of the C-terminal scFv with binding of the <hFc>-POD detection antibody and can be overcome by application of a <hk> POD (Biozol Cat.No. 206005) detection antibody like used for the ANG-2 binding ELISA.

25 Using Biacore these findings were confirmed using a classical concentration series at 37 °C (Figure 11). These data showed fast Kon-rates $k(a)$ of $4.7\text{--}4.8 \times 10^6 \text{ 1/(Ms)}$, saturation was reached with the highest concentrations of VEGF. Koff-rates reached limits of technical specification.(i.e. $5 \times 10^{-6} \text{ (s/s)}$) probably due to still bivalent binding (avidity effect) under this conditions as a consequence of the dimeric analyte rhVEGF, although a very low ligand density was used resulting in final VEGF-response of 10-15 RU. Nevertheless, the kinetic constants of the different <VEGF> antibodies could be compared by this method and within the error of the method there was no significant difference in the kinetic constants of the tetravalent bispecific antibody <VEGF-Ang-2> TvAb6 and the original antibody <VEGF> G6-31 detectable. The kinetic constants for <VEGF-Ang-2>

30

TvAb6 and <VEGF> G6-31 under these conditions were virtually identical by this method. Thus, it can be concluded that TvAb6 completely retained its VEGF binding properties. Tab. 4 shows the respective kinetic constants and Figure 12 shows the kinetic characteristics of the two <VEGF> antibodies <VEGF-Ang-2> TvAb6 and <VEGF> G6-31 in a Ka-Kd plot.

Tab. 14: Kinetic properties of <VEGF-Ang-2> TvAb6 and <VEGF> G6-31

Measured at 37°C	Ka	kd	t1/2	KD
Antibodies	[1/(Ms)]	[1/s]	[min]	[M]
<VEGF> G6-31	4.83E+06	9.33E-06	1237.8	1.93E-12
<VEGF-Ang-2> TvAb6	4.72E+06	7.24E-06	1596.7	1.53E-12

In a further experiment it was shown by ANG-2 binding ELISA using a <hk>-POD detection antibody (Biozol Catalogue No. 206005) as described above that <VEGF-ANG-2> TvAb6 binds to ANG-2 in a manner comparable to that of Mab536 at an equimolar concentration of 0.039 pM (Figure 6A). This showed that the scFv module of TvAb6 retained its binding properties in the TvAb construct.

In order to further corroborate this finding <ANG-2> Mab536 and <VEGF-ANG-2> TvAb6 were immobilized by a secondary antibody on a Biacore CM5 chip and binding kinetics to human ANG-2 were determined. Due to heterogeneity of the ANG-2 preparation no 1:1 binding can be observed; KD values are thus only relative estimations. The Biacore analysis showed that <VEGF-ANG-2> TvAb6 has an estimated KD value of 4.4 nM for ANG-2. In comparison, Mab536 has an estimated KD value of 1.6 nM. Within the error of the method no difference in binding mode and affinities between <ANG-2> Mab536 and <VEGF-ANG-2> TvAb6 could be observed (Figure 6B). Thus, it can be concluded that the scFv module of TvAb6 completely retained its binding properties in the TvAb construct.

In order to prove that <VEGF-ANG-2> TvAb6 was able to bind simultaneously to VEGF and ANG-2 bridging ELISA assays and Biacore assays as described above were applied.

By applying the VEGF-ANG-2-bridging ELISA described above it was shown that only <VEGF-ANG-2> TvAb6 was able to bind simultaneously to VEGF and ANG-2 at an equimolar concentration of 0.625 pM whereas the monospecific “standard” IgG1 antibodies <ANG-2> Mab536 and <VEGF> G6-31 were not
5 capable of simultaneously binding to VEGF and ANG-2 (Figure 7).

Figure 14 shows the respective data from the Biacore assay. Simultaneous binding of both antigens Ang-2 and VEGF could be shown for the tetravalent bispecific antibody <VEGF-Ang-2> TvAb6. Negative controls were as expected: The monospecific antibody <Ang-2> Mab536 showed only binding to Ang-2, but no
10 VEGF-binding. The monospecific antibody <VEGF> G6-31 showed binding to VEGF but no binding to Ang-2 at all (data not shown). From the relative response units of the tetravalent bispecific antibody <VEGF-Ang-2> TvAb6 binding to the Ang-2 coated surface, and subsequent binding to dimeric VEGF binding the stoichiometry could be calculated to be in the range from 1:1 to 1:1.4. Taken
15 together, by applying the described ELISA and Biacore assays it was shown that only <VEGF-Ang-2> TvAb6 was able to bind simultaneously to VEGF and Ang-2 whereas the monospecific “standard” IgG1 antibodies <Ang-2> Mab536 and <VEGF> G6-31 were not capable of simultaneously binding to VEGF and Ang-2 (Figure 15).

Similar results were obtained with the constructs TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 in an analogous Biacore assay shown in Fig. 15A. Binding of the antibodies to the antigen e.g. human ANG-2 and VEGF were investigated by surface plasmon resonance using a BIACORE T100 instrument (GE Healthcare Biosciences AB, Uppsala, Sweden). Briefly, for affinity
20 measurements goat<hIgG-Fc> polyclonal antibodies were immobilized on a CM4 chip via amine coupling for presentation of the bispecific antibodies against human ANG-2 and VEGF. Binding was measured in HBS buffer (HBS-P (10 mM HEPES, 150 mM NaCl, 0.005% Tween 20, pH 7.4), 25°C. Purified ANG-2-His (R&D systems or in house purified) was added in various concentrations between
25 6,25 nM and 200 nM in solution. Association was measured by an ANG-2-injection of 3 minutes; dissociation was measured by washing the chip surface with HBS buffer for 3 minutes and a KD value was estimated using a 1:1 Langmuir binding model. Due to heterogeneity of the ANG-2 preparation no 1:1 binding could be observed; KD values are thus only relative estimations.
30

VEGF (R&D systems) was added in various concentrations between 6,25 nM and 200 nM in solution. Association was measured by an VEGF-injection of 3 minutes; dissociation was measured by washing the chip surface with HBS buffer for 3 minutes and a KD value was estimated using a 1:1 Langmuir binding model.

- 5 The order of injection of the binding partners can switched, first VEGF and then Ang2 or vice versa.

Negative control data (e.g. buffer curves) were subtracted from sample curves for correction of system intrinsic baseline drift and for noise signal reduction. Biacore T100 Evaluation Software version 1.1.1 was used for analysis of sensorgrams and
10 for calculation of affinity data.

Antibody	Affinity hAng-2	Affinity hVEGF
TvAb-2441-bevacizumab-LC06	2,3 nM	0,35 nM
TvAb-2441-bevacizumab-LC08	0,7 nM	0,34 nM
G6-31	--	< 0,1 nM
MAb536	3 nM	--
bevacizumab	--	0,59 nM

Finally, simultaneous binding of TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 could be shown by incubating with ANGPT2 and VEGF in a consecutive manner. As shown in Figure 15B ANGPT2 and VEGF can bind
15 simultaneously to the bispecific antibodies.

Example 3**In vivo efficacy of disulfide-stabilized bispecific tetravalent antibody <VEGF-ANG-2> TvAb6 in comparison to <ANG-2> Mab536, <VEGF> G6-31 and the combination of Mab536 and G6-31 in the staged subcutaneous Colo205 xenograft model in Scid beige mice**

5 The purified disulfide-stabilized <VEGF-ANG-2> TvAb6 (n00.2331 see Table 3) was compared to the antibodies <ANG-2> Mab536, <VEGF> G6-31 and the combination of <ANG-2> Mab536 and <VEGF> G6-31 in two staged subcutaneous Colo205 xenograft model studies (Ang2_PZ_Colo205_003 and
10 Ang2_PZ_Colo205_005) in female Scid beige mice at different doses.

Antibodies: <ANG-2> Mab536 was provided as frozen stock solution (c = 4.5 mg/mL), <VEGF> G6-31 was provided as frozen solution (c = 0.6 mg/mL) and <VEGF-ANG-2> TvAb6 was provided as frozen stock solution (c = 0.5 mg/mL) in 20 mM Histidine, 140 mM NaCl, pH 6.0. Antibody solution was diluted
15 appropriately in PBS from stock prior injections where required and PBS was applied as vehicle.

Cell lines and culture conditions: Colo205 human colorectal cancer cells were originally obtained from ATCC and after expansion deposited in the Roche Penzberg internal cell bank. Tumor cell line was routinely cultured in RPMI 1640
20 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 % CO₂. Passage 2-5 was 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
25 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 was carried out on regular basis. Diet food (Provimi Kliba 3337) and water (acidified pH 2.5-3) were
30 provided ad libitum. Age of mice at start of the study was about 10 weeks.

Monitoring: Animals were controlled daily for clinical symptoms and detection of adverse effects. For monitoring throughout the experiment body weight of animals was documented and tumor volume was measured by caliper after staging.

5 Tumor cell injection: At day of injection Colo205 cells were centrifuged, washed once and resuspended in PBS. After an additional washing with PBS cell concentration and cell size were determined using a cell counter and analyzer system (Vi-CELL, Beckman Coulter). For injection of Colo205 cells, the final titer was adjusted to 5.0×10^7 cells/ml, viability ca. 90%. Subsequently 100 μ l of this suspension corresponding to 2.5×10^6 cells per animal was injected s.c. into the right flank of the mice.

Treatment of animals started at day of randomisation, 16 days after cell transplantation (study Ang2_PZ_Colo205_003) and 14 days after cell transplantation (study Ang2_PZ_Colo205_005) at a mean tumor volume of 100 mm³ or 150 mm³, respectively.

15 Dose schedule until Day 74 (see Fig 8A) of Study Ang2_PZ_Colo205_003:

Group	No of animals	Compound	Dose (mg/kg)	Route/Mode of administration	No of treatments	Cumulative Dosis mg/kg
1	10	Vehicle		i.p. once weekly	4	
2	10	<VEGF> G6-31	6 mg/kg	i.p. once weekly	8	48
3	10	<ANG-2> Mab536	6 mg/kg	i.p. once weekly	8	48
4	10	<VEGF> G6-31 + <ANG-2> Mab536	5mg/kg + 6 mg/kg	i.p. once weekly i.p. once weekly	8 8	40 48
5	10	<VEGF-ANG-2> TvAb6	7mg/kg	i.p. once weekly	8	56

In the study Ang2_PZ_Colo205_003 <VEGF-ANG-2> TvAb6 was by mistake underdosed with respect to an equimolar ratio. The dose of <VEGF-ANG-2> TvAb6 was adjusted in study Ang2_PZ_Colo205_005 so that the animals received an equimolar ratio of ANG-2 and VEGF binding sites by <VEGF-ANG-2> TvAb6 as well as the combination of <VEGF> G6-31 and <ANG-2> Mab536.

Tumor growth inhibition until Day 74 (see Fig 8a) Ang2_PZ_Colo205_003 study:

<VEGF-ANG-2> TvAb6 at a dose of 7 mg/kg exhibited efficacy comparable to that of the combination of <VEGF> G6-31 at 5 mg/kg and <ANG-2> Mab536 at 6 mg/kg and <VEGF> G6-31 as single agent at a dose of 6 mg/kg (Figure 8A) and was superior to single agent <ANG-2> Mab536 at a dose of 6 mg/kg. As the subcutaneous Colo205 model is very responsive to the <VEGF> G6-31 antibody that blocks human as well as murine VEGF resulting in almost complete tumor growth inhibition <VEGF-ANG-2> TvAb6 could thus not be differentiated from G6-31 as single agent (6 mg/kg) under the chosen experimental conditions, while <VEGF-ANG-2> TvAb6 showed a comparable inhibition like the combination of <ANG-2> Mab536 and <VEGF> G6-31 at a clearly lower cumulative dose (<VEGF-ANG-2> TvAb6 = 56 mg/kg antibody compared to the combination of <ANG-2> Mab536 and <VEGF> G6-31 = 40 + 48 = 88 mg/kg antibody).

Dose schedule of Study until Day 63 Ang2_PZ_Colo205_005:

Group	No of animals	Compound	Dose (mg/kg)	Route/ Mode of administration	No of treatment	Cumulative Dosis
6	10	Vehicle		i.p. once weekly	6	
7	10	<VEGF> G6-31	3	i.p. once weekly	7	21mg/kg
8	10	<VEGF> G6-31 +	3	i.p. once weekly	7	21 mg/kg
		<ANG-2> Mab536	3	i.p. once weekly	7	21 mg/kg
9	10	<ANG-2> Mab536	3	i.p. once weekly	7	21 mg/kg
10	10	<VEGF-ANG-2> TvAb6	4	i.p. once weekly	7	28 mg/kg

Tumor growth inhibition until day 63 Ang2_PZ_Colo205_005 study:

5 <VEGF-ANG-2> TvAb6 at a dose of 4 mg/kg exhibited efficacy comparable to that of the combination of <VEGF> G6-31 and <ANG-2> Mab536 at 3 mg/kg each and was superior to either single agent <VEGF> G6-31 as well as <ANG-2> Mab536 at a dose of 3 mg/kg (Figure 8B). This is the first example showing that at a lower dose (with respect to the summarized concentration of antibody – the cumulative dose of the combination is 21+21 = 42 m/kg versus 28 mg/kg of the bispecific antibody TvAb6) a bispecific antibody targeting VEGF and ANG-2 can result in strong anti-tumor efficacy comparable to the combination of the respective single agents blocking VEGF and ANG-2 and superior to either single agent.

10

Example 4**Blocking of VEGF-induced tube formation**

In order to confirm that the anti-VEGF related activities were retained in the bispecific tetravalent <VEGF-ANG-2> TvAb6 is was shown in a VEGF induced tube formation assay AngioKit TCS CellWorks (CellSystems) that <VEGF-ANG-2> TvAb6 mediated dose dependent inhibition of tube formation comparable to the monospecific antibody <VEGF> G6-31. The AngioKit TCS CellWorks assay was performed according to the following procedure: Cells were stimulated each time with 2 ng/ml VEGF before treatment with antibodies on day 1, 4, 7 and 9. Vascular tubes were visualized by staining of endothelial cells using a CD31-PE antibody (BD Pharmingen #555446) on day 11. Pictures were taken at a magnification of 4x and values for tube length and number of branch points were quantitatively analysed using the Angiogenesis Tube Formation Application Module in MetaMorph (Molecular Devices). Values and standard deviation were calculated by duplicates and analysis of 4 pictures per specimen. Figure 9 shows the respective results and Figure 10 A and B the quantitative analysis. Angiotensin-2 has no influence on tube formation and thus inhibition of ANG-2 was not studied in this assay. The data show that the bispecific <VEGF-ANG-2> TvAb6 and the monospecific <VEGF> G6-31 antibodies are equally efficacious in inhibiting VEGF stimulated tube formation.

Example 5**Tie2 phosphorylation**

In order to confirm that the anti-ANGPT2 related activities were retained in the bispecific tetravalent <VEGF-ANGPT2> antibodies TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 it was shown that TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 interfere with ANGPT2 stimulated Tie2 phosphorylation in a comparable manner as their mother clones LC06 and LC08 in the ANGPT2 stimulated Tie2 phosphorylation assay as described above.

In a first experiment both bispecific antibodies TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 showed a dose-dependent interference with ANGPT2 stimulated Tie2 phosphorylation with IC50 values comparable to those of the mother clones LC06 and LC08 as shown in Figure 16A. TvAb-2441-

bevacizumab-LC06 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 721 ng/ml, whereas LC06 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 508 ng/ml. TvAb-2441-bevacizumab-LC08 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 364 ng/ml, whereas LC08 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 499 ng/ml.

In a second experiment both bispecific antibodies TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 showed a dose-dependent interference with ANGPT2 stimulated Tie2 phosphorylation with IC50 values comparable to those of the mother clones LC06 and LC08 as shown in Figure 16B. TvAb-2441-bevacizumab-LC06 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 488 ng/ml, whereas LC06 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 424 ng/ml. TvAb-2441-bevacizumab-LC08 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 490 ng/ml, whereas LC08 interfered with ANGPT2 stimulated Tie2 phosphorylation with a IC50 value of approx. 399 ng/ml.

Taken together these data show that the bispecific tetravalent <VEGF-ANGPT2> antibodies TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 interfere with ANGPT2 stimulated Tie2 phosphorylation in a manner comparable to their mother clones LC06 and LC08 within the error of this cellular assay.

Example 6

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 0.5 µg/ml Tie-2 protein (R&D Systems, UK, Cat.No.313-TI) for at least 2 hours (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 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 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.

5

Summary data for Ang2 interaction ELISA:

<VEGF-ANG-2> bispecific antibody (or monospecific parent antibodies)	AVG IC50 (ng/ml)	STDEV
	hANG2	
<VEGF-ANG-2> G6_31	>20000	
TvAb-2441_G6_31_Ang2i_LC06	75	39
TvAb-2441_G6_31_Ang2k_LC08	66	31
TvAb-2441_bevacizumab_LC06	44	8
TvAb-2441_bevacizumab_LC08	42	11
<ANG-2>Mab 536	15	8
<VEGF >Bevacizumab	>20000	
TvAb-3421_bevacizumab_LC06	31	1
TvAb-4421_bevacizumab_LC06	35	17
TvAb-4461_bevacizumab_LC06	46	10

Example 7

Inhibition of hVEGF binding to hVEGF Receptor (ELISA)

10

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 0.5 µg/ml hVEGF-R protein (R&D Systems, UK, Cat.No.321-FL) for at least 2 hours (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 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.

Summary data for VEGF interaction ELISA:

<VEGF-ANG-2> bispecific antibody	AVG IC50 (ng/ml)	STDEV
	VEGF	
<VEGF-ANG-2> G6_31	1431	130
TvAb-2441_G6_31_Ang2i_LC06	1654	213
TvAb-2441_G6_31_Ang2k_LC08	1392	184
TvAb-2441_bevacizumab_LC06	2831	503
TvAb-2441_bevacizumab_LC08	2305	972
TvAb-<ANG-2>Mab 536	>20000	
TvAb-<VEGF >Bevacizumab	1584	357
TvAb-3421_bevacizumab_LC06	2660	284
TvAb-4421_bevacizumab_LC06	1980	1319
TvAb-4461_bevacizumab_LC06	1677	394

Example 8**HUVEC proliferation**

In order to confirm that the anti-VEGF related activities were retained in the bispecific tetravalent <VEGF-ANG2> antibodies TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 it was shown that TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 interfere with VEGF-induced HUVEC proliferation in a comparable manner as their mother clones LC06 and LC08 in the VEGF-induced HUVEC proliferation assay as described above.

Figure 18 shows that indeed TvAb-2441-bevacizumab-LC06 and TvAb-2441-bevacizumab-LC08 interfere in a concentration dependent manner with VEGF-induced HUVEC proliferation comparable to the parental antibody bevacizumab.

Example 9**ELISA Binding assay to human ANG-1 and to human ANG-2**

The binding of parent <ANG-2> antibodies Ang2i-LC06, Ang2i-LC07 and Ang2k-LC08 to human ANG-1 and human ANG-2 was determined in an ANG-1 or ANG-2 binding ELISA as described above (see Comparative binding to ANG-1 and ANG-2 (ANG-1 and ANG-2 binding ELISA)). Briefly, the ELISA-type assay is based on the immobilization of human wild-type Angiopoietin-1 or -2 in a microtiter plate. Binding of an antibody directed against the immobilized ANG-1 or ANG-2 is measured via an <human Fc> (anti-IgG) antibody with a POD conjugate. A dilution series of the <ANG-2>antibody allows to determine an EC₅₀ concentration. As a reference the human anti-ANG-2 antibody <ANG-2> antibody Mab536 (Oliner et al., Cancer Cell. 2004 Nov;6(5):507-16, US 2006/0122370) was used. The determined EC₅₀ concentrations are summarized in the table below.

Antibody	hANG-1 binding EC ₅₀	hANG-2 binding EC ₅₀
<ANG-2>Mab536	2538 ng/mL	133 ng/mL
<ANG-2>Ang2i-LC06	> 8000 ng/mL	84 ng/mL
<ANG-2>Ang2i-LC07	> 8000 ng/mL	3006 ng/mL

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<ANG-2>Ang2i-LC08	4044 ng/mL	105 ng/mL
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5 All antibodies are specifically binding to ANG-2. MAb536 and Ang2k-LC08 show also specific binding towards ANG-1, whereas Ang2i-LC06 and Ang2i-LC07 are not specifically binding to ANG-1 as they have an EC50-value of above 8000 ng/ml (detection limit).

Example 10

Expression & Purification of bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecules scFab-Avastin-LC06-2620, scFab-Avastin-Ang2i-LC06-2640 and scFab-Avastin-Ang2i-LC06-2641

10 Analogous to the procedures described in Example 1 and in the materials and methods above, the bispecific, tetravalent single chain Fab <VEGF-ANG-2> antibody molecules scFab-Avastin- LC06-2620, scFab-Avastin- LC06-2640 and scFab-Avastin- LC06-2641, all three based on <VEGF> bevacizumab and <ANG-2> Ang2i-LC06 were expressed and purified. Binding affinities and other
15 properties were determined as described in the the Examples above. The relevant (eventually modified) light and heavy chains amino acid sequences of these bispecific antibodies are given in SEQ ID NO: 109 -110 (scFab-Avastin-LC06-2620), in SEQ ID NO: 111 -112 (scFab-Avastin-LC06-2640) and in SEQ ID NO: 113-114 (scFab-Avastin-LC06-2641).

Key data	scFab-Avastin-LC06-2620	scFab-Avastin-Ang2i-LC06-2640	scFab-Avastin-LC06-Ang2i-2641
Expression (Yield)	29µg/mL	27 µg/mL	18 µg/mL
Purification (Yield, Prot. A. homog.)	21 mg, 57%	19 mg, 86%	12 mg, 90%
Homogeneity after preparative SEC	98%	98%	99%

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Function			
hANG-2 affinity (Biacore)	1.9 E-9 M	1.8 E-9 M	1.9 E-9 M
hVEGF affinity (Biacore)	1 E-10 M	1E-10 M	1E-10 M

Example 11**Expression & Purification of bispecific, trivalent single chain Fab <VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab**

- 5 Analogous to the procedures described in Example 1 and in the materials and methods above, the bispecific, trivalent single chain Fab <VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab based on <VEGF> bevacizumab and <ANG-2> Ang2i-LC06 were expressed and purified. Binding affinities and other properties were determined as described in the the Examples above. The
- 10 relevant (eventually modified) light and heavy chains amino acid sequences of this bispecific antibody are given in SEQ ID NO: 115-117 (Avastin-LC06-KiH-C-scFab).

Key data	Avastin-LC06-KiH-C-scFab
Expression (Yield)	15 µg/mL
Purification (Yield, Prot. A. homog.)	4,8 mg, 91 %
Homogeneity after preparative SEC	97%
Function	
hANG-2 affinity (Biacore)	4.4 E-9 M
hVEGF affinity (Biacore)	1 E-10 M

Example 12**Expression & Purification of bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS**

Analogous to the procedures described in Example 1 and in the materials and methods above (see also , the bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS based on <VEGF> bevacizumab and <ANG-2> Ang2i-LC06 were expressed and purified. Binding affinities and other properties were determined as described in the the Examples above. Bispecific, trivalent antibody molecules of this format in general are described in EP Appl. No 09005108.7. The relevant (eventually modified) light and heavy chains amino acid sequences of this bispecific <VEGF-ANG-2> antibody are given in SEQ ID NO: 118-120 (Avastin-LC06-C-Fab-6CSS).

Key data	scFAb-Avastin-LC06-2620	scFAb-Avastin-LC06-2640	scFAb-Avastin-LC06-2641
Expression (Yield)	29 µg/mL	27 µg/mL	18 µg/mL
Purification (Yield, Prot. A. homog.)	21 mg, 57%	19 mg, 86%	12 mg, 90%
Homogeneity after preparative SEC	98%	98%	99%
Function			
hANG-2 affinity (Biacore)	1.9 E-9 M	1.8 E-9 M	1.9 E-9 M
hVEGF affinity (Biacore)	1 E-10 M	1E-10 M	1E-10 M

Example 13**Expression & Purification of bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules Avastin-LC06-CH1-CL, Avastin-LC06-VH-VL and Avastin-LC06-VH-VL-SS**

- 5 Analogous to the procedures described in Example 1 and in the materials and methods above, the bispecific, bivalent domain exchanged <VEGF-ANG-2> antibody molecules Avastin-LC06-CH1-CL (CH-CL exchange as described in WO 2009/080253), Avastin-LC06-VH-VL (VH-VL exchange as described in WO 2009/080252) and Avastin-LC06-VH-VL-SS (VH-VL exchange as described in WO 2009/080252 and an additional introduced VH44 VL100 disulfide bridge) based on <VEGF> bevacizumab and <ANG-2> Ang2i-LC06 were expressed and purified. Binding affinities and other properties were determined as described in the Examples above. The relevant (eventually modified) light and heavy chains amino acid sequences of these bispecific antibodies are given in SEQ ID NO: 121
10 -124 (Avastin-LC06-CH1-CL), in SEQ ID NO: 125 -128 (Avastin-LC06-VH-VL) and in SEQ ID NO: 129 -132 (Avastin-LC06-VH-VL-SS).

Key data	Avastin-LC06-CM-CH1-CL	Avastin-LC06-CM-VH-VL	Avastin-LC06-VH-VL-SS
Expression (Yield)	87 µg/mL	44 µg/mL	65 µg/mL
Purification (Yield, Prot. A. homog.)	50 mg, 62%	22 mg, 95%	91 mg, 74%
Homogeneity after preparative SEC	84%	> 99 %	95 %
Function			
hANG-2 affinity (Biacore)	1.3 E-9 M	2.1 E-9 M	1.46 E-9 M
hVEGF affinity (Biacore)	1 E-10 M	1 E-10 M	1 E-10 M

Example 14**Expression & Purification of bispecific, bivalent ScFab-Fc fusion <VEGF-ANG-2> antibody molecules Avastin-LC06-N-scFab and Avastin-LC06-N-scFabSS**

Analogous to the procedures described in Example 1 and in the materials and methods above, the bispecific, bivalent ScFab-Fc fusion <VEGF-ANG-2> antibody molecules Avastin-LC06-N-scFab and Avastin-LC06-N-scFabSS based on <VEGF> bevacizumab and <ANG-2> Ang2i-LC06 were expressed and purified.. Binding affinities and other properties were determined as described in the the Examples above. The relevant modified heavy chains amino acid sequences of these bispecific antibodies are given in SEQ ID NO: 133-134 (Avastin-LC06-N-scFab), and in SEQ ID NO: 135 -136 (Avastin-LC06-N-scFabSS).

Key data	Avastin-LC06-N-scFab	Avastin-LC06-N-scFabSS
Expression (Yield)		62 µg/mL
Purification (Yield, Prot. A. homog.)		43 %
Function		
hANG-2 affinity (Biacore)		1 nM
hVEGF affinity (Biacore)		1 nM

Example 15

Inhibition of hVEGF binding to hVEGF Receptor (ELISA), Blocking of VEGF-induced tube formation, Inhibition of huANG-2 binding to Tie-2 (ELISA), Tie2 phosphorylation, and HUVEC proliferation of the bispecific, <VEGF-ANG-2> antibody molecules of Examples 10 to 14

Inhibition of hVEGF binding to hVEGF Receptor (ELISA), blocking of VEGF-induced tube formation, Inhibition of huANG-2 binding to Tie-2 (ELISA), Tie2 phosphorylation, and HUVEC proliferation of the bispecific, <VEGF-ANG-2>

antibody molecules of Examples 10 to 14 can be determined analogously to the procedures described in Materials and Methods and Examples 4 to 9 above.

Example 16

5 In vivo efficacy of bispecific antibody <VEGF-ANG-2> antibody in comparison to <ANG-2> ANG2i-LC06, and the combination of <ANG-2> ANG2i-LC06 and Avastin in the refractory Colo205 xenograft model in Scid beige mice (after resistance to bevacizumab (Avastin) treatment)

Cell lines and culture conditions:

10 Colo205 human colorectal cancer cells were originally obtained from ATCC and after expansion deposited in the Roche Penzberg internal cell bank. Tumor cell line was 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% CO₂. Passage 2-5 was used for transplantation.

15 Animals:

Female SCID beige mice; age 4–5 weeks at arrival (purchased from Charles River Germanyd) 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
20 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 was 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 was about 10 weeks.

25 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 Ø 100µm) the final cell titer was adjusted to 2.5×10^7 / ml. Tumor
30 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 was

5 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 were shaved and for cell injection skin of anaesthetized animals was carefully lifted up with an anatomic forceps and 100 μ l cell suspension ($= 2.5 \times 10^6$ cells) was injected subcutaneously in the right flank of the animals.

Treatment of animals

10 Pretreatment:

Animal treatment started 14 days after cell transplantation (study Ang2_PZ_Colo205_008) at a mean tumor volume of 100 mm³ to 150 mm³, respectively. Mice were treated once weekly with Avastin (10 mg/kg) for a time period of 5 weeks.

15 Secondary treatment:

Thereafter mice were randomized for 2nd treatment and divided to four groups with 10 mice in each group. Tumor volume at start of secondary treatment at day 51 was in the range from 336 to 341 mm³. Mice were treated once weekly i.p. with the different compounds as indicated in following table .

Group	No of animals	Compound	Dose (mg/kg) (nMol/kg)	Route/Mode of administration	No of treatments	Cumulative dose (mg/kg)
11	10	Avastin	10 mg/kg (68 nMol/kg)	i.p. once weekly	11	110
12	10	ANG2i-LC06	10 mg/kg (68 nMol/kg)	i.p. once weekly	6	60
13	10	ANG2i-LC06 + Avastin	10 mg/kg (68 nMol/kg) + 10 mg/kg (68 nMol/kg)	i.p. once weekly i.p. once weekly	6 11	60 110
14	10	TvAb-2441-bevacizumab-LC06	13 mg/kg (64 nMol/kg)	i.p. once weekly	6	78

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 $\varnothing > 1.5$ cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

Results: Tumor growth inhibition based on medians (in percent) at day 91

	TGI
ANG2i-LC06 10 mg/kg (68 nMol/kg) i.p.; Avastin 10 mg/kg (68 nMol/kg) i.p.	45.3
ANG2i-LC06 10 mg/kg i.p. (68 nMol/kg)	44.4

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TvAb-2441-bevacizumab-LC06_13 mg/kg i.p. (64 nMol/kg)	60.4
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5 The results show that the bispecific <VEGF-ANG-2> antibody TvAb-2441-bevacizumab-LC06 showed a higher tumor growth inhibition (at lower doses) in the bevacizumab(Avastin)- resistant xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibody ANG2i-LC06 alone or the combination of ANG2i-LC06 and Avastin.

Examples 17

In vivo inhibition of tumor angiogenesis in s.c. Calu-3 NSCLC xenograft

10 - Detection via non-invasive in vivo imaging of angiogenesis using anti-CD31 labeled with

Cell lines and culture conditions:

15 This human lung adenocarcinoma cancer cell line has been established from a human caucasian male with lung cancer. Cells were obtained from Roche, Kamakura and passaged in house for working cell bank. Tumor cells are routinely cultured in RPMI1640 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% CO₂. Culture passage is performed with trypsin / EDTA 1x (PAN) splitting one time / week.

Animals:

20 Female BALB/c nude 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
25 the animal facility for one week to get accustomed to new environment and for observation. Continuous health monitoring was 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 was 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 $\varnothing$ 100 μ m) the final cell titer was adjusted to 5.0×10^7 / 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 was 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 were shaved and for cell injection skin of anaesthetized animals was carefully lifted up with an anatomic forceps and 100 μ l cell suspension ($= 5.0 \times 10^6$ cells) was injected subcutaneously in the right flank of the animals.

Treatment of animals

At study day 35, mice were randomized to statistically well distributed groups, depending on their body weight and tumor size. For the treatment with therapeutic antibodies, each group consisted of 10 mice and treatment with therapeutic antibodies was applied once weekly i.p. for a 6 week time period. (see Fig 19)

Group 1: vehicle (Xolair) 10 mg/kg

Group 2: Avastin 10 mg/kg

Group 3: Combination of monospecific <VEGF> Avastin 10 mg/kg plus monospecific <ANG-2> Ang2i-LC06 10 mg/kg (= Avastin / Ang2i-LC06)

Group 4: Bispecific <VEGF-ANG-2> antibody 2441-Avastin-scFv-LC06 13.3 mg/kg

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 $\varnothing > 1.5$ cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

Blood vessel and angiogenesis monitoring with labeled anti-CD 31 antibody

Preliminary studies revealed that anti-CD31 antibody as best agent for imaging tumor vasculature. This agent targets mouse endothelial CD31 receptors and visualizes single blood vessels with a low signal-to-background ratio. Therefore, imaging for anti-CD31 antibody represents a feasible way to image tumor vasculature. Three mice of each therapy group have been chosen and injected i.v. with 50 μ g/mouse anti-CD3 antibody labeled covalently with the organic fluorophore Alexa610 at day 35, 49 and 79. Near-infrared imaging was carried out 24 hrs after each application of the labeled antibody under inhalation anesthesia. An increase or decrease of tumor vasculature was visualized by using the compare image tool of the MAESTRO system. Under treatment with the control mab Xolair and the therapeutic antibody Avastin an increase of tumor blood vessels from day 35 to day 79 was observed. In contrast, the combined treatment with Avastin plus Ang2i-LC06 and 2441-Avastin-scFv-LC06 exhibited a decrease of tumor vasculature (Fig 19).

Tumor regions were quantified by manually drawing measurement areas and signal intensities were evaluated in intensity values (total signal / exposure time). The average changes of CD31 signals from day 35 to 49 and from day 49 to 79 were plotted in Fig 19. All treatment groups revealed an increase in tumor vasculature from day 35 to 49. While CD31 tumor signals steadily accelerated in group 1 (Xolair) and group 2 (Avastin), tumor vasculature significantly decreased in group 3 (Combination of Avastin plus <ANG-2> Ang2i-LC06) and group 4 (Bispecific <VEGF-ANG-2> antibody 2441-Avastin-scFv-LC06), with group 4 showing clearly the most pronounced antiangiogenic effect (Fig 19).

Immediately after the last *in vivo* imaging studies, tumors were explanted (day 79), fixed in formalin and embedded in paraffin for *ex vivo* studies. Fluorescence microscopy showed numerous well defined capillaries in tumors treated with control mab Xolair. Several tumor blood vessels were observed in mice treated

with Avastin. In contrast, treatment groups 3 and 4 had significantly fewer and less defined blood vessels in the tumors compared to treatment groups 1 and 2 whereas group 4 showed the most pronounced effect. Group 4 revealed lower microvessel density, capillaries were generally smaller and unstructured and they exhibited weaker anti-CD31 fluorescence signals as Group 1, 2 and 3. Histochemical HE-staining showed intratumoral necrotic regions for up to 90% of all regions in the treatment group with the bispecific antibody of group 4 which is clearly higher than for the other treatment groups (data not shown) .

Example 18

In vivo efficacy of bispecific antibodies <VEGF-ANG-2> and compared to the parent monospecific antibodies (alone or in combination) in the staged subcutaneous Colo205 xenograft model in Scid beige mice

Cell lines and culture conditions:

Colo205 human colorectal cancer cells were originally obtained from ATCC and after expansion deposited in the Roche Penzberg internal cell bank. Tumor cell line was 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% CO₂. Passage 2-5 was 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 was 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 was about 10 weeks.

Tumor cell injection:

At day of injection Colo205 cells were centrifuged, washed once and resuspended in PBS. After an additional washing with PBS cell concentration and cell size were determined using a cell counter and analyzer system (Vi-CELL, Beckman Coulter).

For injection of Colo205 cells, the final titer was adjusted to 5.0×10^7 cells/ml, viability ca. 90%. Subsequently 100 μ l of this suspension corresponding to 2.5×10^6 cells per animal was injected s.c. into the right flank of the mice.

- 5 Treatment of animals started at day of randomisation, 16 days after cell transplantation (study Ang2_PZ_Colo205_009)) at a mean tumor volume of 100 mm³, respectively.

Dose schedule of Study Ang2_PZ_Colo205_009:

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	10	i.p. once weekly
	+ Avastin	10	i.p. once weekly
10	<VEGF-ANG-2> TvAb-2441-bevacizumab-LC06	13.3	i.p. once weekly
10	<VEGF-ANG-2> Avastin-LC06- CH1-CL	20	i.p. once weekly
10	<VEGF-ANG-2> scFAB-Avastin-LC06-2620	16.6	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 $\varnothing > 1.5$ cm), body weight loss more than 20% from baseline, tumor ulceration or poor general condition of the animals.

Results:**Tumor growth inhibition (TGI) based on medians (in percent) at day 61**

	TGI
<VEGF> Avastin	66
< ANG-2> Ang2i-LC06	47
Ang2i-LC06 + Avastin	78
<VEGF-ANG-2> TvAb-2441-bevacizumab-LC06	87
<VEGF-ANG-2> Avastin-LC06- CH1-CL	92
<VEGF-ANG-2> scFAb-Avastin-LC06-2620	86

The results show that all three bispecific <VEGF-ANG-2> Avastin (bevacizumab)-ANG2i-LC06 antibodies (all based on the bevacizumab sequences SEQ ID No: 7 and 8 and on ANG2i-LC06 sequences SEQ ID No: 52 and 53) showed a higher tumor growth inhibition in xenograft tumor model Colo205 in Scid beige mice compared to the treatment with monospecific antibodies ANG2i-LC06 and Avastin alone or the combination of ANG2i-LC06 and Avastin.

Example 19

Expression & Purification and properties of bispecific <VEGF-ANG-2> antibody molecules scFab-Avastin-LC10-2620, scFab-Avastin-LC10-2640 and scFab-Avastin-LC10-2641, Avastin-LC10-KiH-C-scFab, Avastin-LC10-C-Fab-6CSS, Avastin-LC10-CH1-CL, Avastin-LC10-VH-VL and Avastin-LC10-VH-VL-SS, Avastin-LC10-N-scFab and Avastin-LC10-N-scFabSS

By replacing the VH and VL domains of Ang2i-LC06 (SEQ ID No: 52 and 53) with the corresponding VH and VL domains of Ang2i-LC10 (SEQ ID No: 84 and 85) and using the (apart from such replacement) analogous procedures and sequences described in Example 10 to 14, the bispecific, <VEGF-ANG-2> antibody molecules scFab-Avastin-LC10-2620, scFab-Avastin-LC10-2640 and scFab-Avastin-LC10-2641, Avastin-LC10-KiH-C-scFab, Avastin-LC10-C-Fab-6CSS, Avastin-LC10-CH1-CL, Avastin-LC10-VH-VL and Avastin-LC10-VH-VL-SS, Avastin-LC10-N-scFab and Avastin-LC10-N-scFabSS, all based on <VEGF> bevacizumab and <ANG-2> Ang2i-LC10 are expressed and purified.

Binding affinities and other in vitro properties are determined as described in the the Examples above.

Example 20

In vivo efficacy of bispecific antibody <VEGF-ANG-2> molecules scFab-Avastin-LC10-2620, scFab-Avastin-LC10-2640 and scFab-Avastin-LC10-2641, Avastin-LC10-KiH-C-scFab, Avastin-LC10-C-Fab-6CSS, Avastin-LC10-CH1-CL, Avastin-LC10-VH-VL and Avastin-LC10-VH-VL-SS, Avastin-LC10-N-scFab and Avastin-LC10-N-scFabSS.

In vivo efficacy of bispecific antibody <VEGF-ANG-2> molecules scFab-Avastin-LC10-2620, scFab-Avastin-LC10-2640 and scFab-Avastin-LC10-2641, Avastin-LC10-KiH-C-scFab, Avastin-LC10-C-Fab-6CSS, Avastin-LC10-CH1-CL, Avastin-LC10-VH-VL and Avastin-LC10-VH-VL-SS, Avastin-LC10-N-scFab and Avastin-LC10-N-scFabSS is determined analogously to the corresponding Examples above.

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Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

The claims defining the invention are as follows:

1. A bispecific antibody specifically binding to human vascular endothelial growth factor (VEGF) and human angiopoietin-2 (ANG-2) 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.
2. The bispecific antibody according to claim 1, wherein
 - i) said antigen-binding sites are each a pair of an antibody heavy chain variable domain and an antibody light chain variable domain;
 - ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, SEQ ID NO: 9, SEQ ID NO: 17, or SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 2, SEQ ID NO: 10, SEQ ID NO: 18, or SEQ ID NO: 95, and a CDR1 region of SEQ ID NO: 3, SEQ ID NO: 11, SEQ ID NO: 19, or SEQ ID NO: 96, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, SEQ ID NO: 12, SEQ ID NO: 20, or SEQ ID NO: 97, a CDR2 region of SEQ ID NO: 5, SEQ ID NO: 13, SEQ ID NO: 21, or SEQ ID NO: 98, and a CDR1 region of SEQ ID NO: 6, SEQ ID NO: 14, SEQ ID NO: 22, or SEQ ID NO: 99;
 - iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 25, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 54, SEQ ID NO: 62, SEQ ID NO: 70, SEQ ID NO: 78, or SEQ ID NO: 86, a CDR2 region of SEQ ID NO: 26, SEQ ID NO: 39, SEQ ID NO: 47, SEQ ID NO: 55, SEQ ID NO: 63, SEQ ID NO: 71, SEQ ID NO: 79, or SEQ ID NO: 87, and a CDR1 region of SEQ ID NO: 27, SEQ ID NO: 40, SEQ ID NO: 48, SEQ ID NO: 56, SEQ ID NO: 64, SEQ ID NO: 72, SEQ ID NO: 80, or SEQ ID NO: 88, and in the light chain variable domain a CDR3 region of SEQ ID NO: 28, SEQ ID NO: 28 with the mutations T92L, H93Q and W94T, SEQ ID NO: 41, SEQ ID NO: 49, SEQ ID NO: 57, SEQ ID NO: 65, SEQ ID NO: 73, SEQ ID NO: 81, or SEQ ID NO: 89, a CDR2

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region of SEQ ID NO:29, SEQ ID NO: 42, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 66, SEQ ID NO: 74, SEQ ID NO: 82 or SEQ ID NO: 90, and a CDR1 region of SEQ ID NO:30, SEQ ID NO: 43, SEQ ID NO: 51, SEQ ID NO: 59, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 83, or SEQ ID NO: 91.

3. The bispecific antibody according to claim 2, wherein

ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6; and

iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 46, a CDR2 region of, SEQ ID NO: 47, and a CDR1 region of SEQ ID NO: 48, and in the light chain variable domain a CDR3 region of SEQ ID NO: 49, a CDR2 region of SEQ ID NO: 50, and a CDR1 region of SEQ ID NO: 51.

4. The bispecific antibody according to claim 3, wherein

ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8, and

iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 52, and as light chain variable domain a SEQ ID NO: 53.

5. The bispecific antibody according to claim 2, wherein

ii) said first antigen-binding site specifically binding to VEGF comprises in

the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6;

iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 62, a CDR2 region of SEQ ID NO: 63, and a CDR1 region of SEQ ID NO: 64, and in the light chain variable domain a CDR3 region of SEQ ID NO: 65, a CDR2 region of SEQ ID NO: 66, and a CDR1 region of SEQ ID NO: 67.

6. The bispecific antibody according to claim 5, wherein

ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8; and

iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 68, and as light chain variable domain a SEQ ID NO: 69.

7. The bispecific antibody according to claim 2, wherein

ii) said first antigen-binding site specifically binding to VEGF comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR1 region of SEQ ID NO:3, and in the light chain variable domain a CDR3 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO:5, and a CDR1 region of SEQ ID NO:6;

iii) said second antigen-binding site specifically binding to ANG-2 comprises in the heavy chain variable domain a CDR3 region of SEQ ID NO: 78, a CDR2 region of SEQ ID NO: 79, and a CDR1 region of SEQ ID NO: 80, and in the light chain variable domain a CDR3 region of SEQ ID NO: 81, a CDR2 region of SEQ ID NO: 82, and a CDR1 region of

SEQ ID NO: 83.

8. The bispecific antibody according to claim 7, wherein

ii) said first antigen-binding site specifically binding to VEGF comprises as heavy chain variable domain SEQ ID NO: 7, and as light chain variable domain SEQ ID NO: 8; and

iii) said second antigen-binding site specifically binding to ANG-2 comprises as heavy chain variable domain SEQ ID NO: 84, and as light chain variable domain a SEQ ID NO: 85.

9. The bispecific antibody according to any one of claims 1 to 8, wherein

the ratio of the binding affinities $KD(\text{antigen-binding site specific for VEGF})/KD(\text{antigen-binding site specific for ANG-2})$ is 1.0- 10.0.

10. The bispecific antibody according to any one of claims 1 to 9, wherein the second antigen-binding site that specifically binds to human ANG- 2 does not specifically bind to human Angiopoetin 1 (ANG-1).

11. The bispecific antibody according to any one of claims 1 to 10, wherein said antibody is bivalent, trivalent or tetravalent.

12. A pharmaceutical composition comprising an antibody according to any one of claims 1 to 11.

13. The pharmaceutical composition according to claim 12 for the treatment of cancer or vascular diseases.

14. The bispecific antibody according to any one of claims 1 to 11 for the treatment of cancer or vascular diseases.

15. The use of an antibody according to any one of claims 1 to 11 for the manufacture of a medicament for the treatment of cancer or vascular diseases.

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- 5
- 10
- 15
- 20
16. A method for treating cancer or a vascular disease by administering an antibody according to any one of claims 1 to 11 or a pharmaceutical composition of claim 12 to a patient in need of such treatment.
 17. A nucleic acid encoding a bispecific antibody according to any one of claims 1 to 11.
 18. An expression vector containing the nucleic acid according claim 17 capable of expressing said nucleic acid in a prokaryotic or eukaryotic host cell.
 19. A prokaryotic or eukaryotic host cell comprising a vector according to claim 18.
 20. A method for the production of a bispecific antibody according to any one of claims 1 to 11, wherein a nucleic acid according to claim 17 is expressed in a prokaryotic or eukaryotic host cell and said bispecific antibody is recovered from said cell or the cell culture supernatant.
 21. An antibody obtained by the method of claim 20.
 22. A bispecific antibody as claimed in claim 1 and uses thereof, substantially as herein described with reference to the examples.

Figure 1A

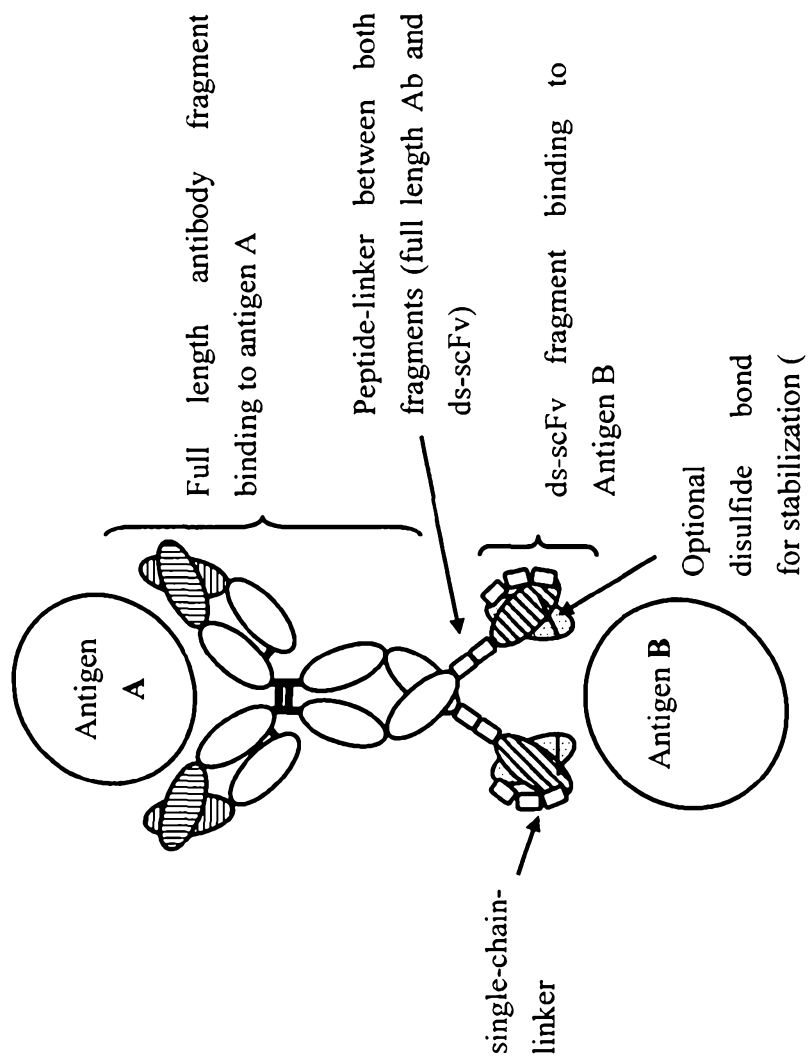


Figure 1B

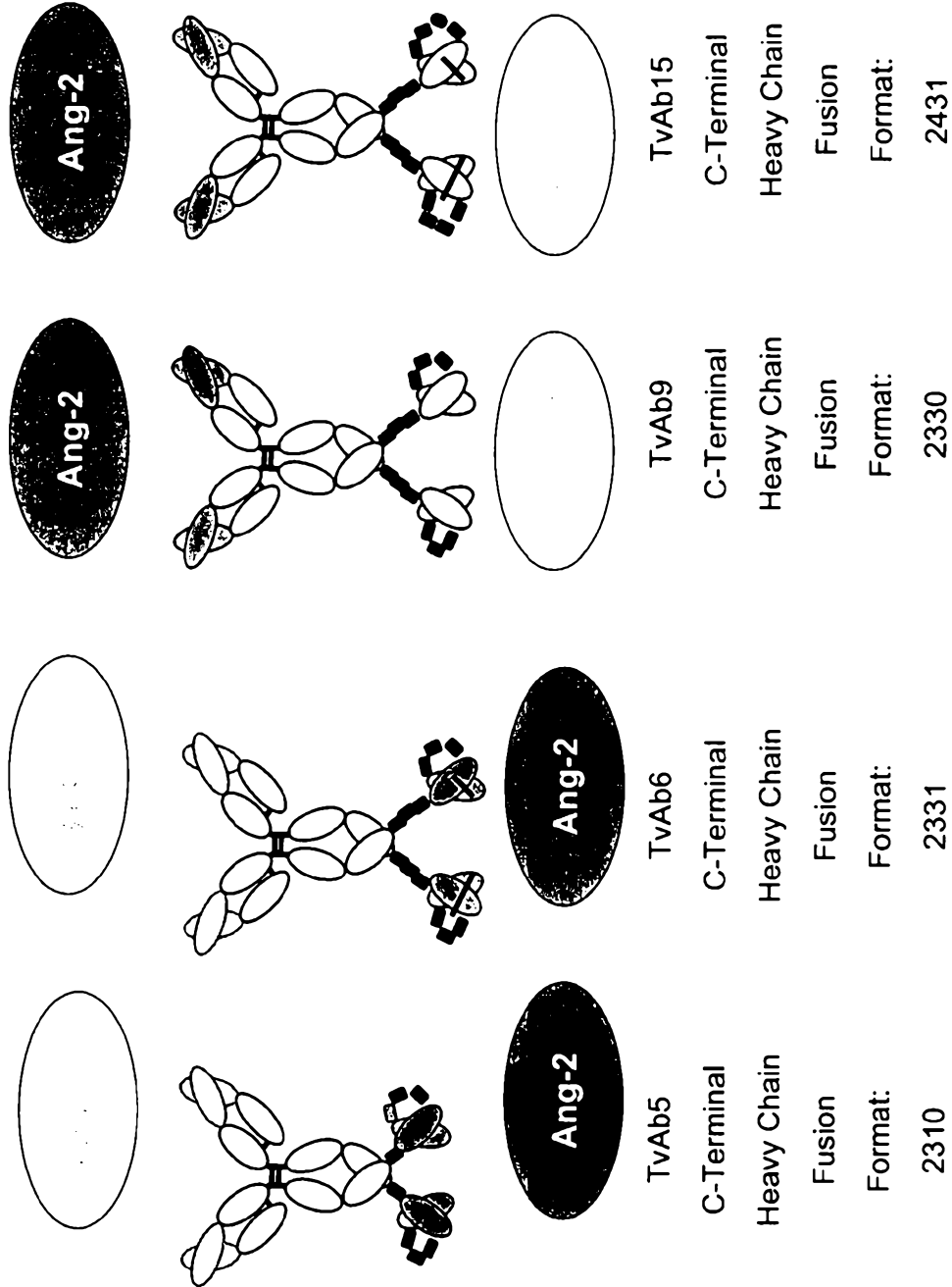


Figure 2A

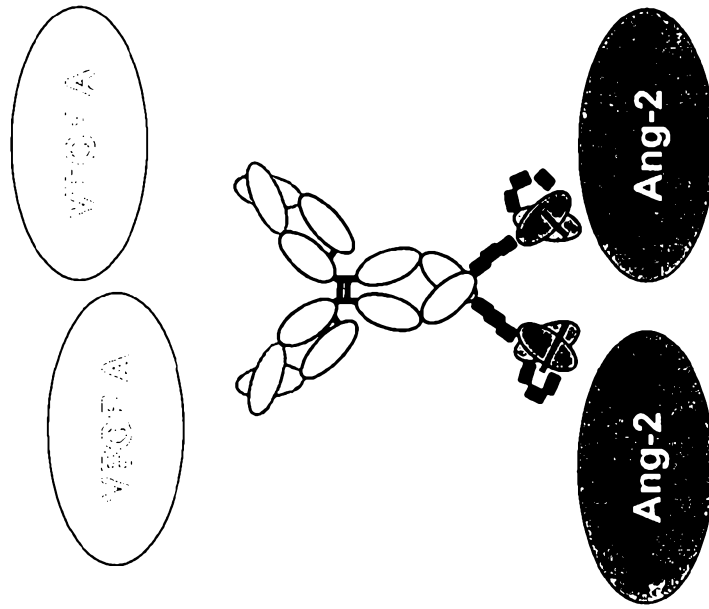


Figure 2B - part one

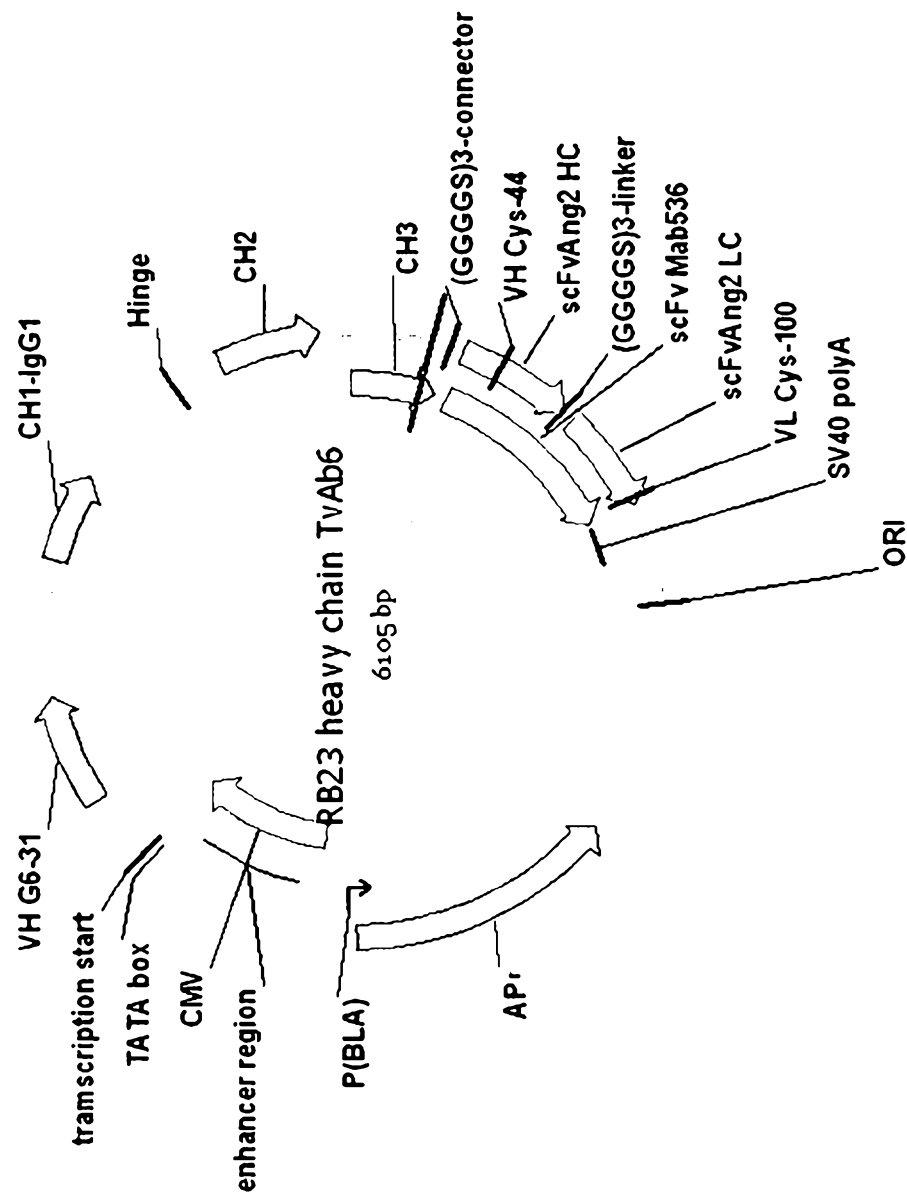


Figure 3

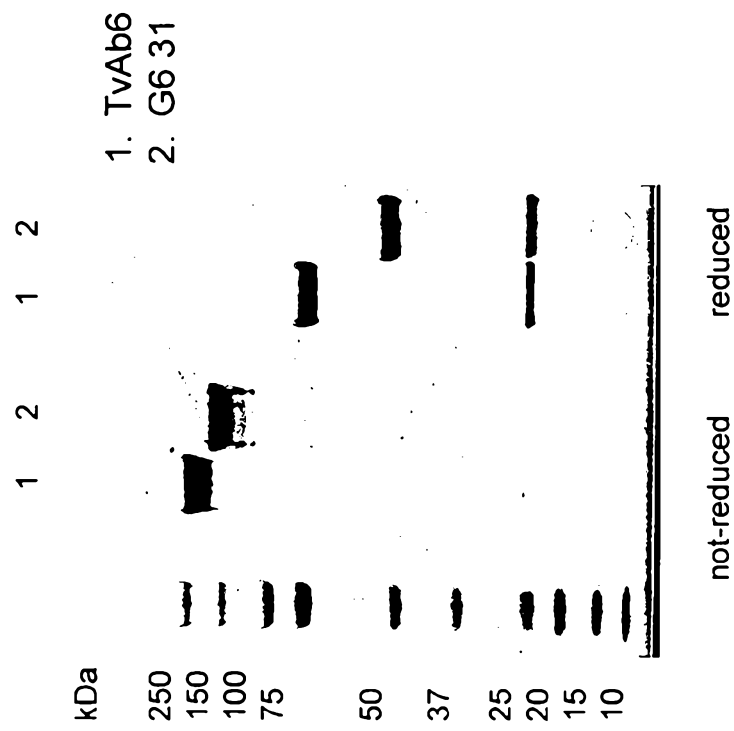
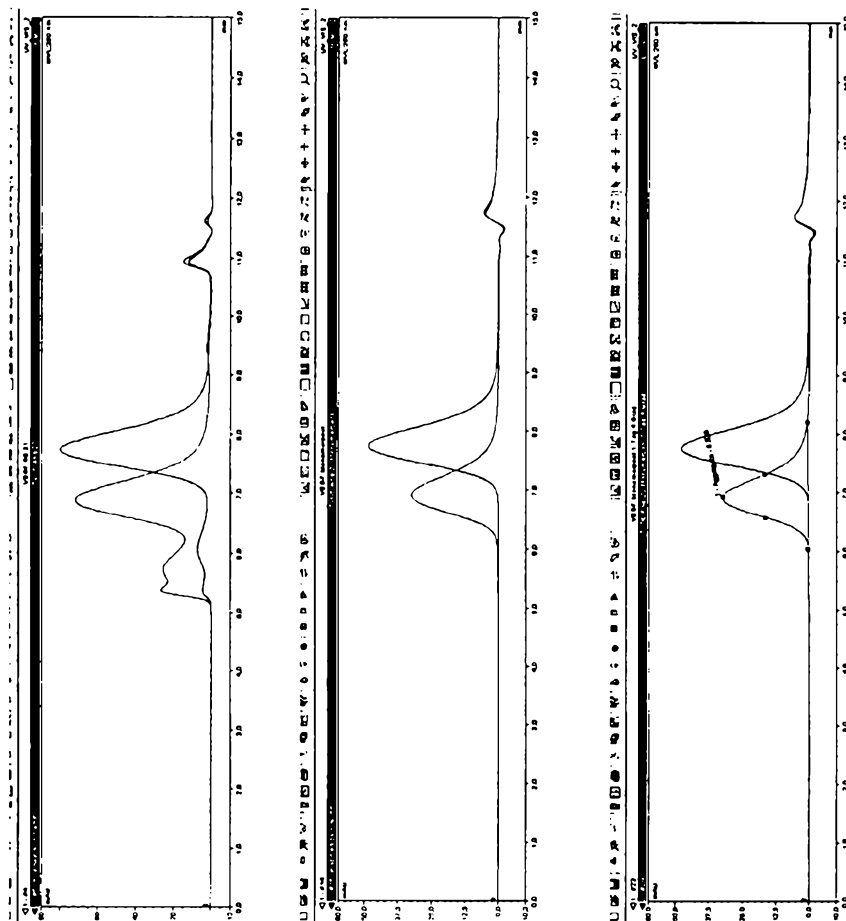


Figure 4

1. Protein A Pool
G6-31: 10 % aggregates
TvAb6: 25 % aggregates

2. SEC Pool, after purification
G6-31: > 99 % monomer
TvAb6: > 99 % monomer

3. SEC Pool after 24 h at 4 °C
G6-31: > 99 % monomer
TvAb6: > 99 % monomer

Figure 5 –part one

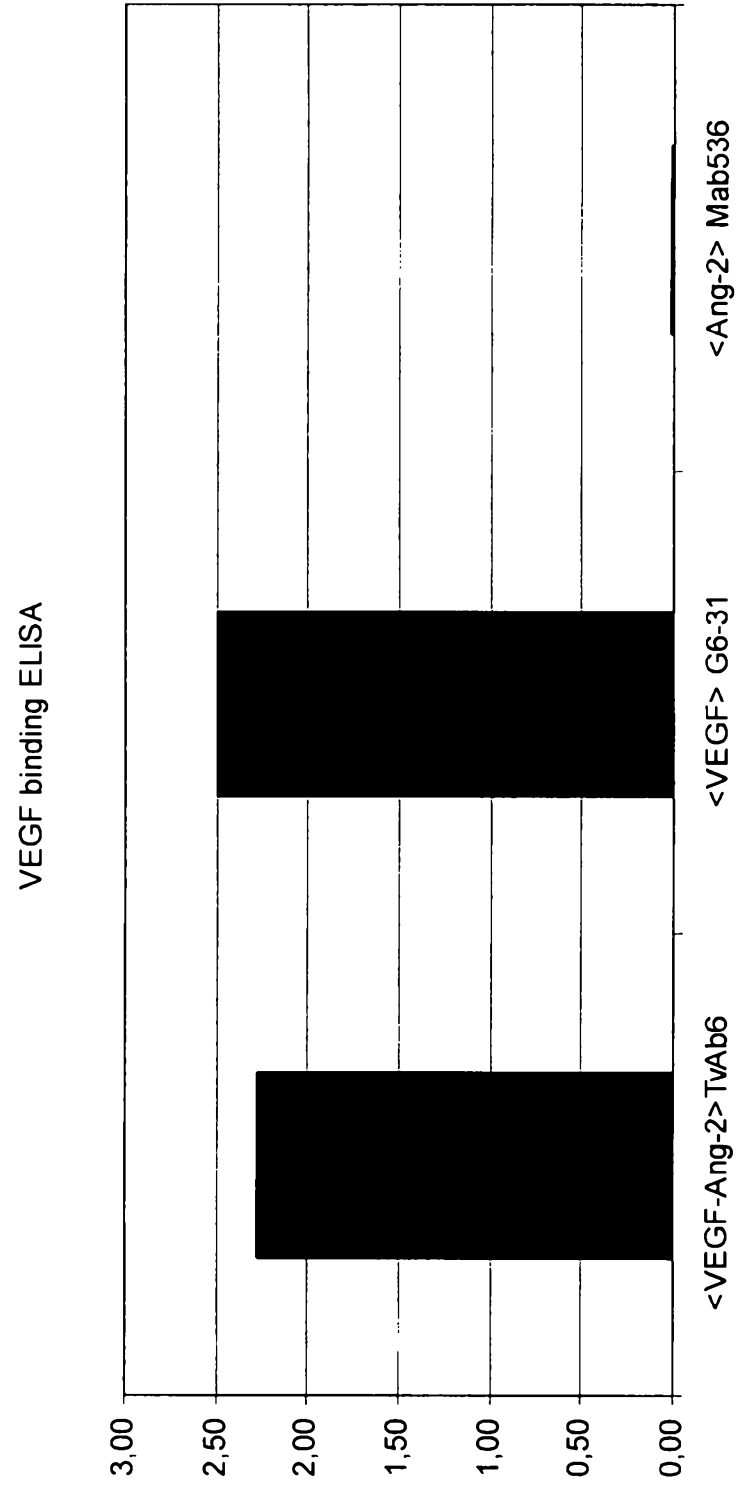


Figure 5—part two

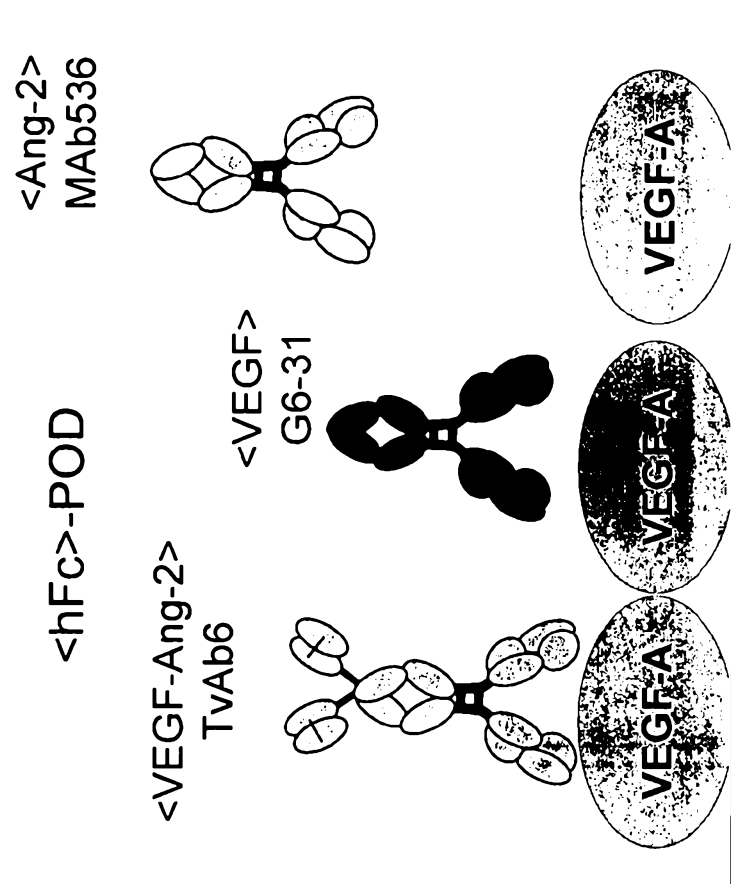


Figure 6A

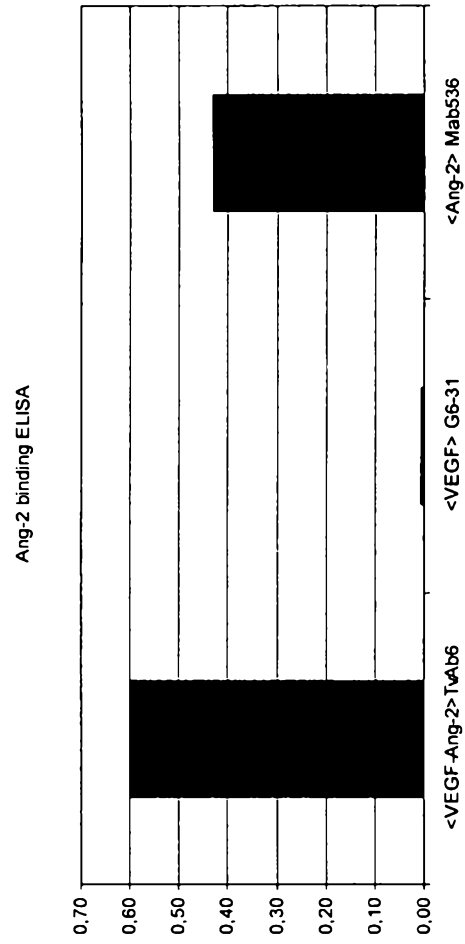
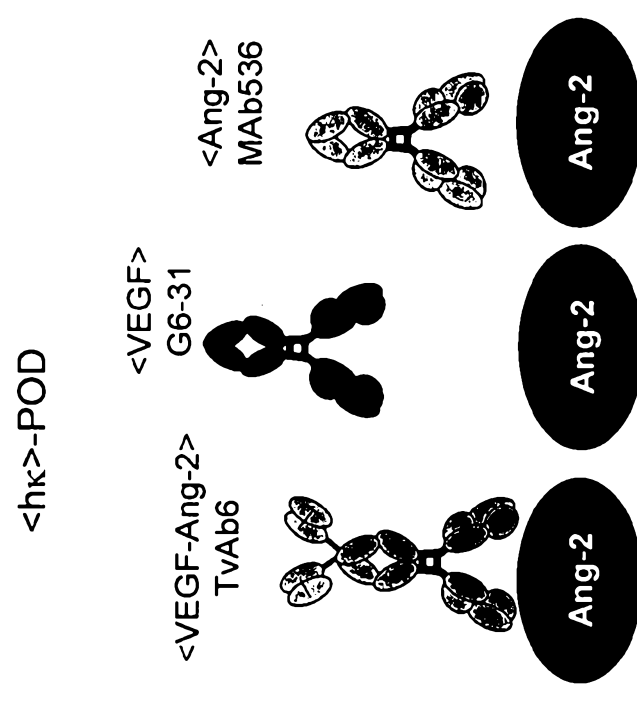
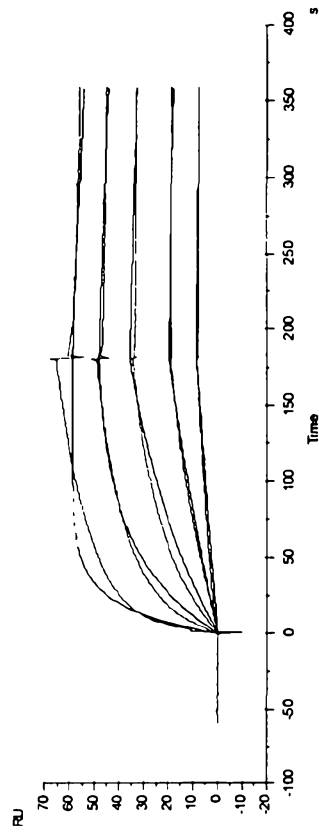


Figure 6B

Binding of hAng-2 to <Ang-2> Mab536 (1:1 Langmuir Binding Model)



Binding of hAng-2 to <VEGF-Ang-2> TvAb6

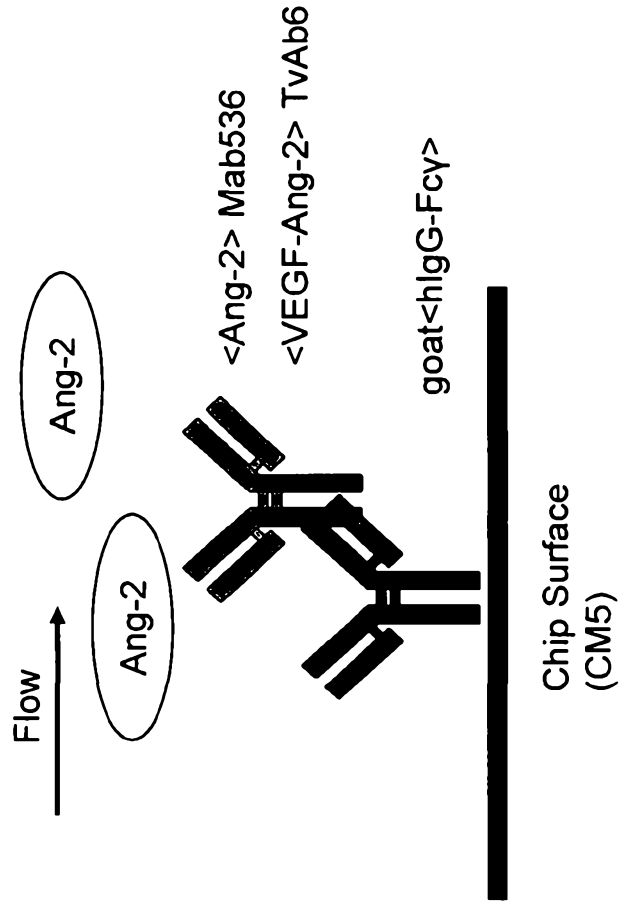
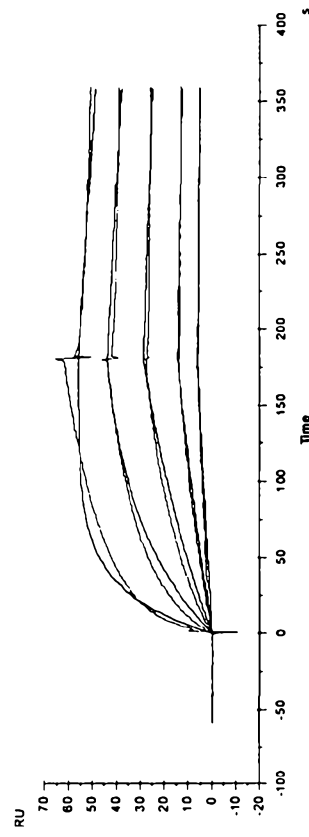


Figure 7—part one

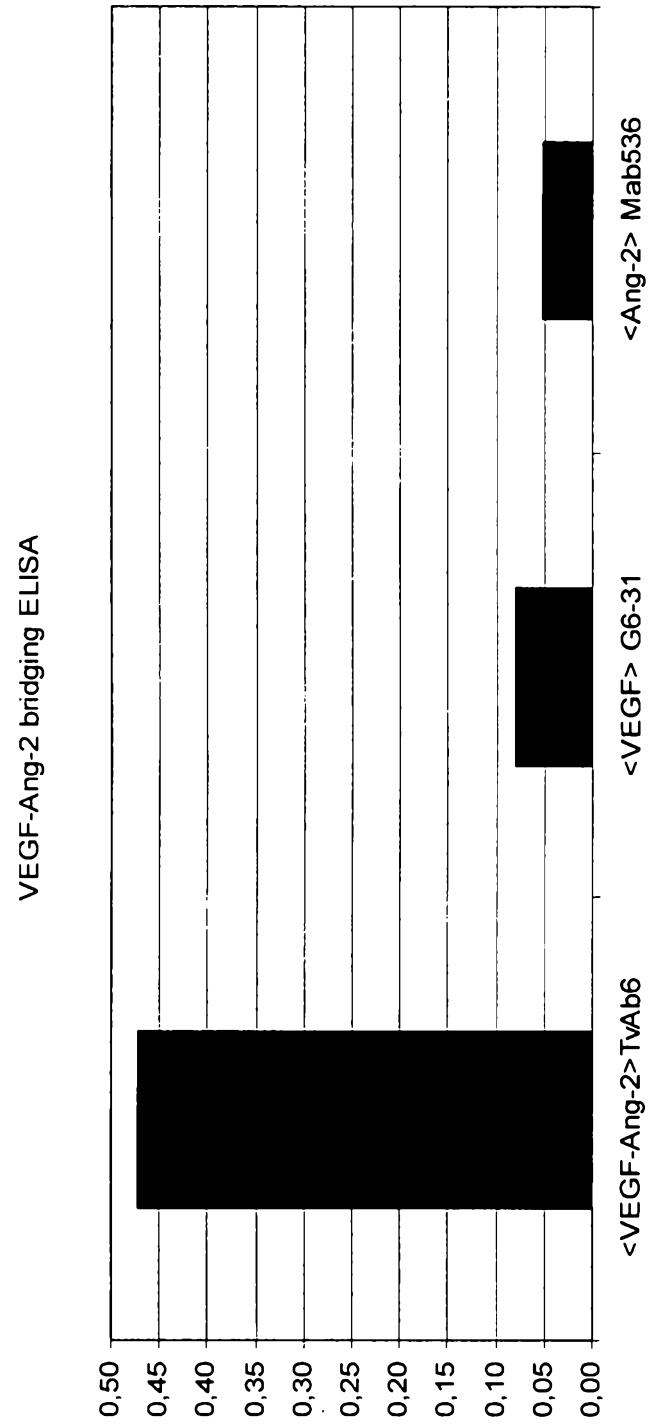
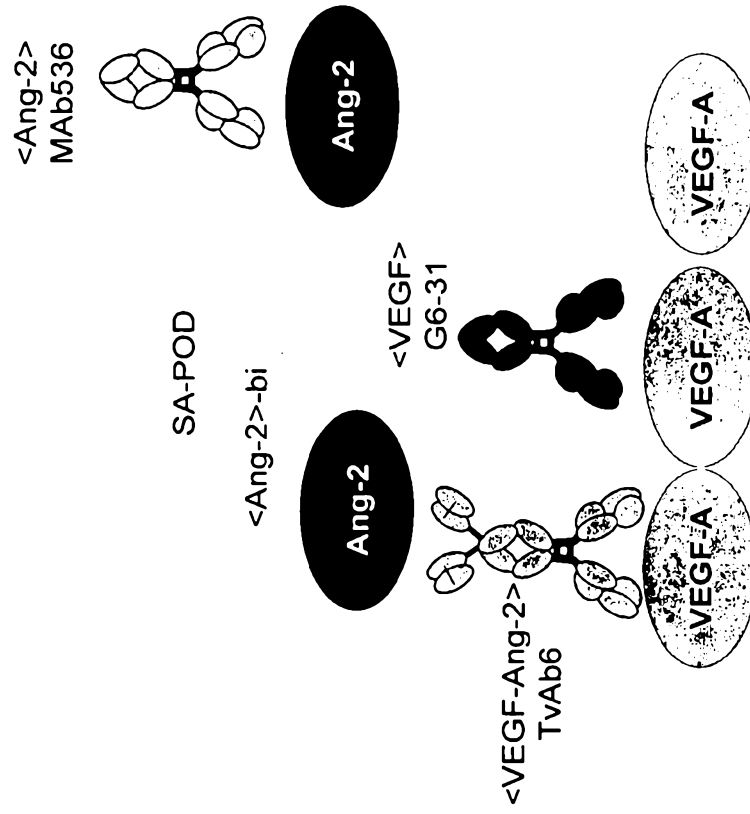


Figure 7-part two



ANG2_PZ_COLO205_003

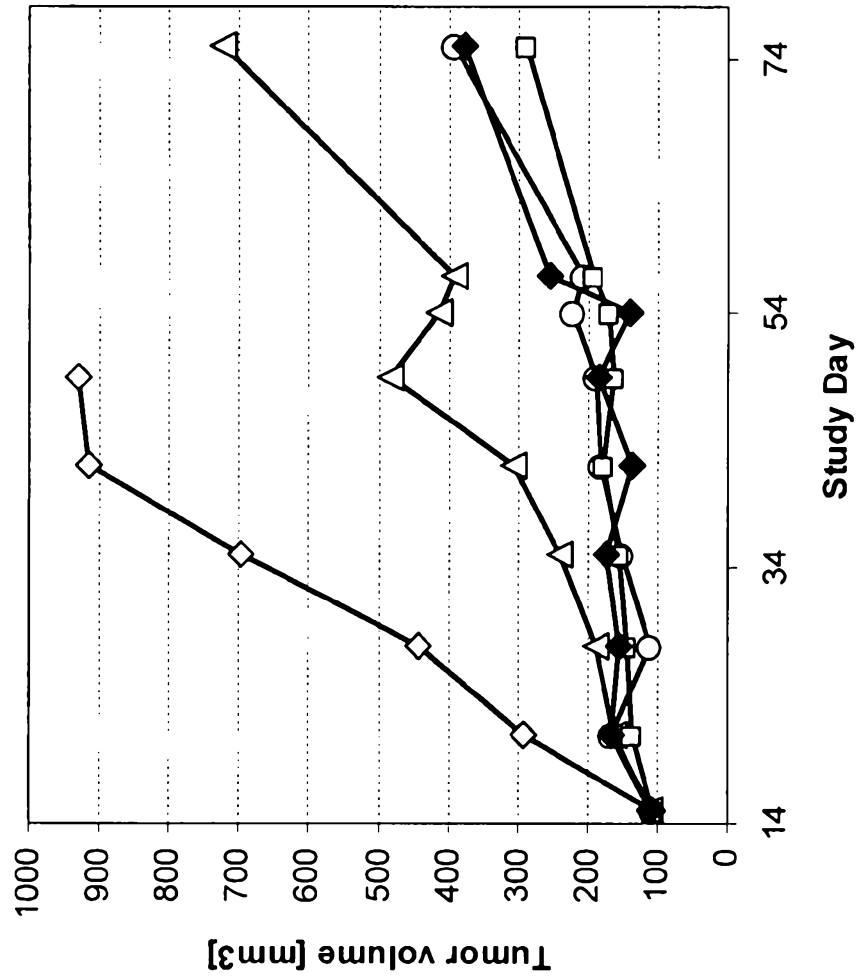
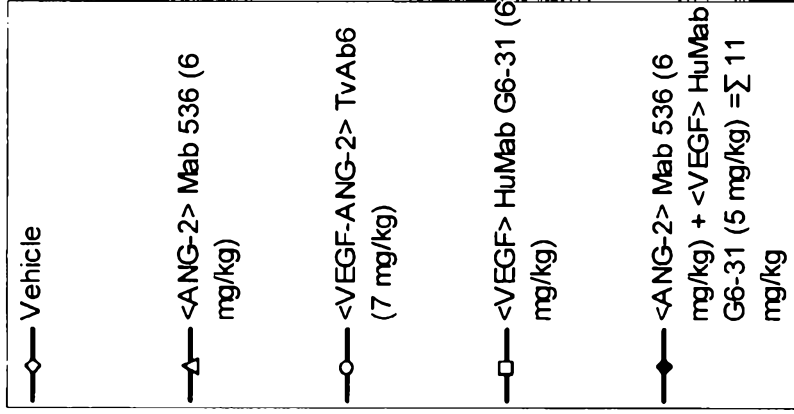


Figure 8a



ANG2_PZ_COLO205_005

Figure 8b

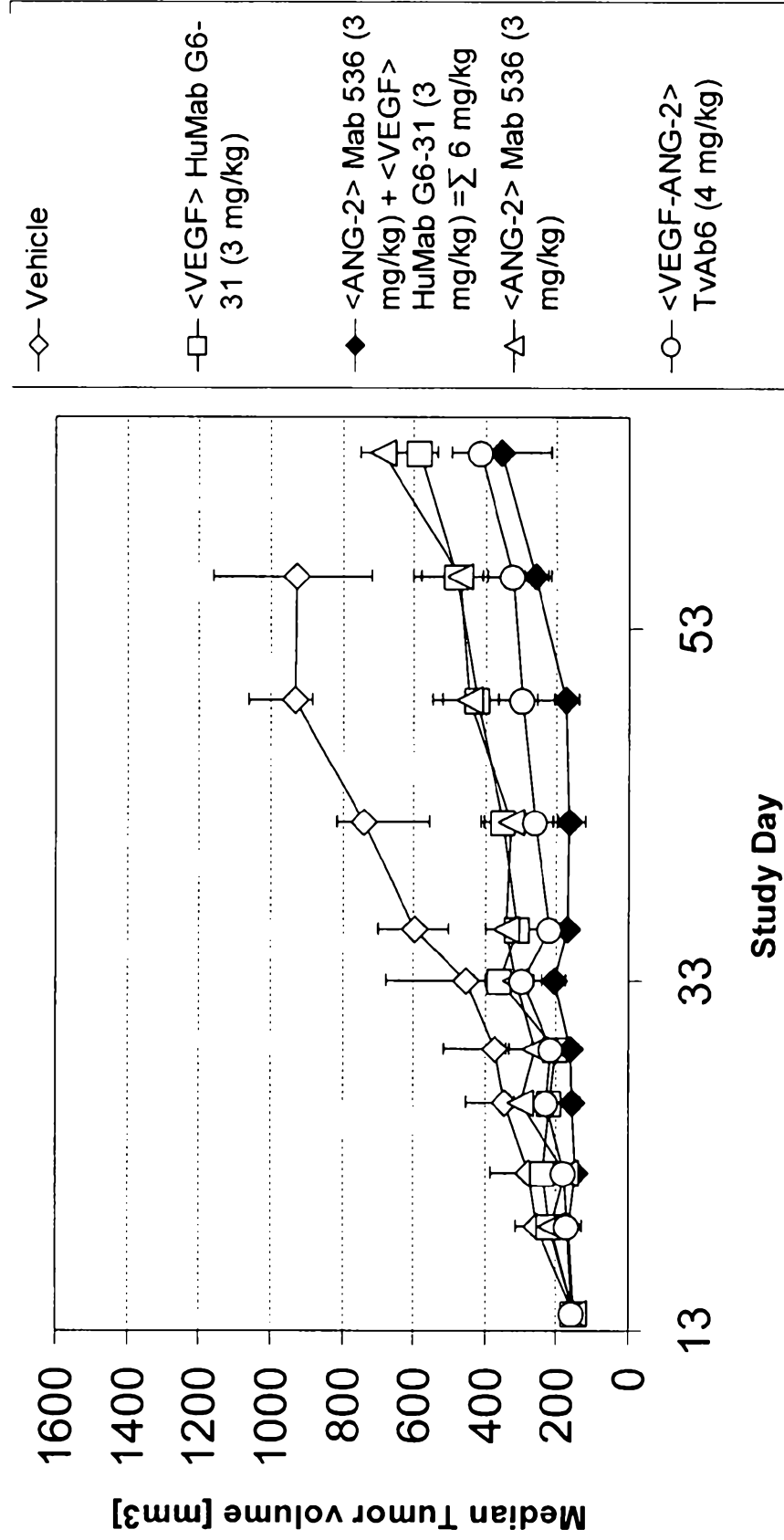


Figure 9

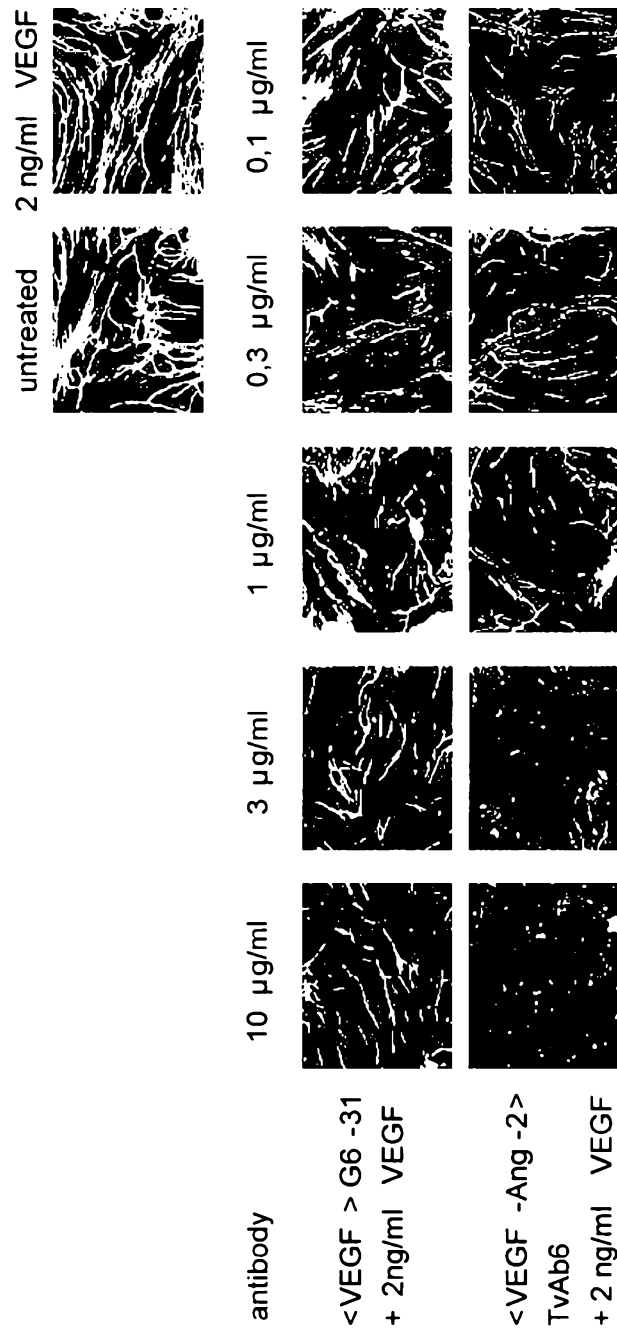


Figure 10A

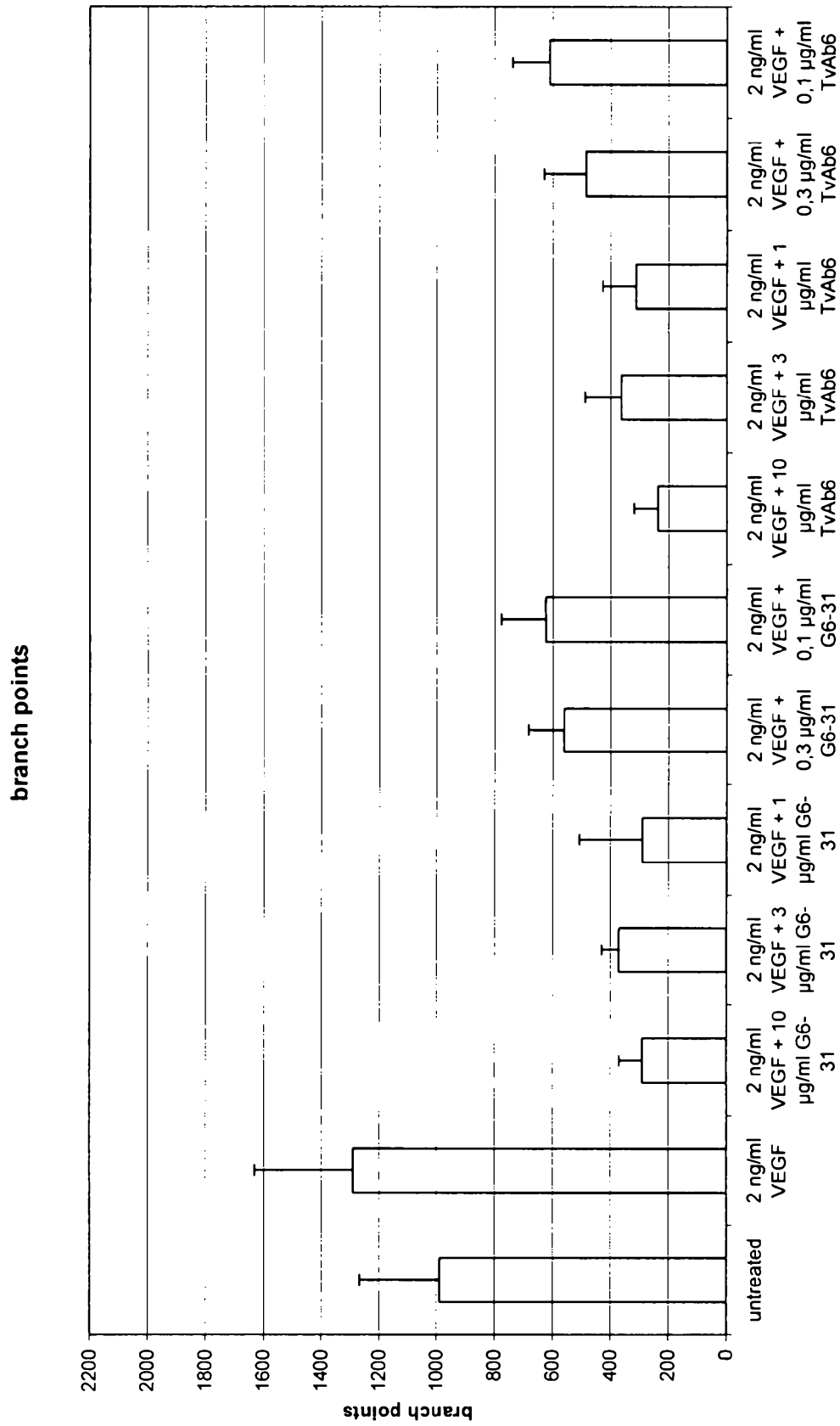


Figure 10B

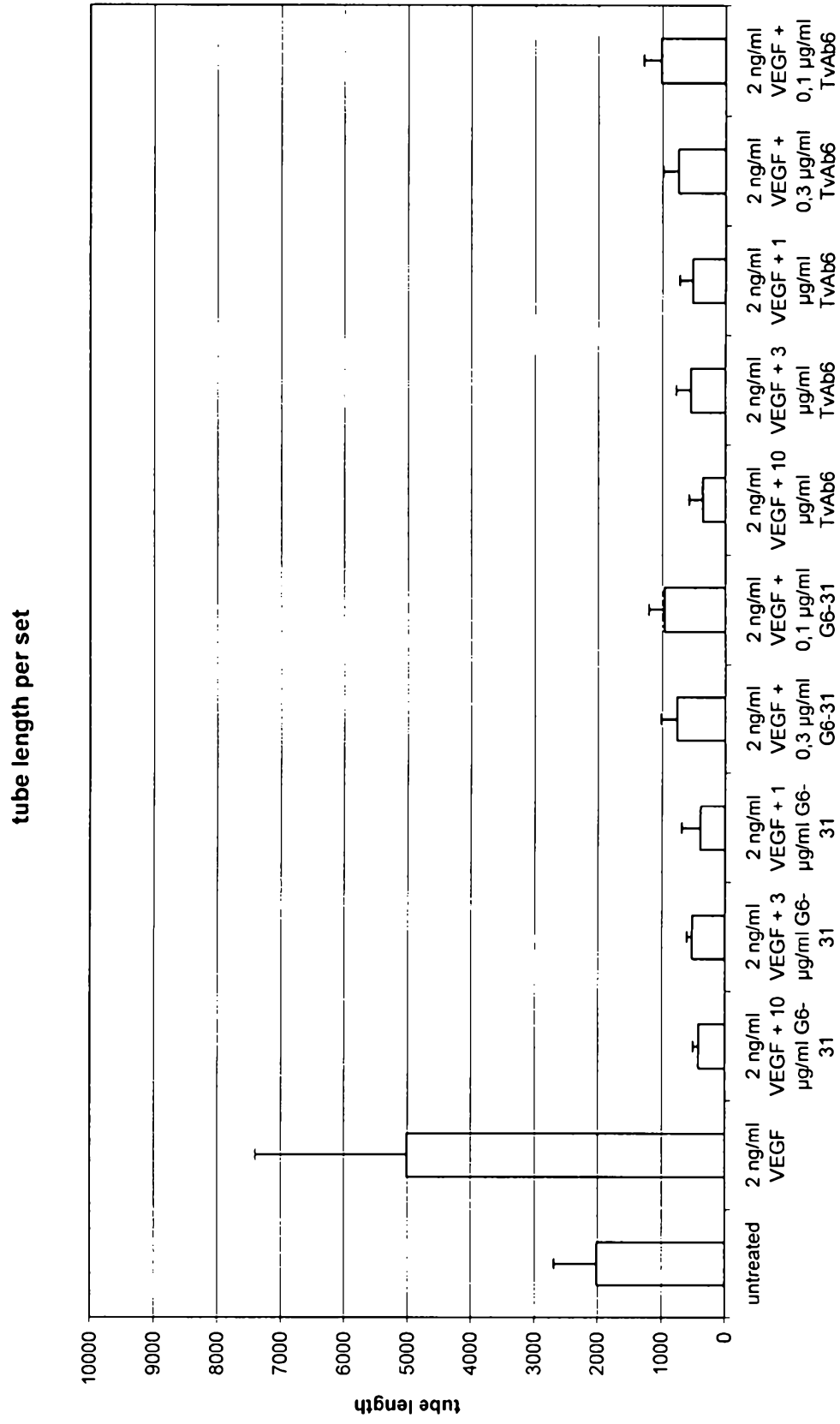


Figure 11

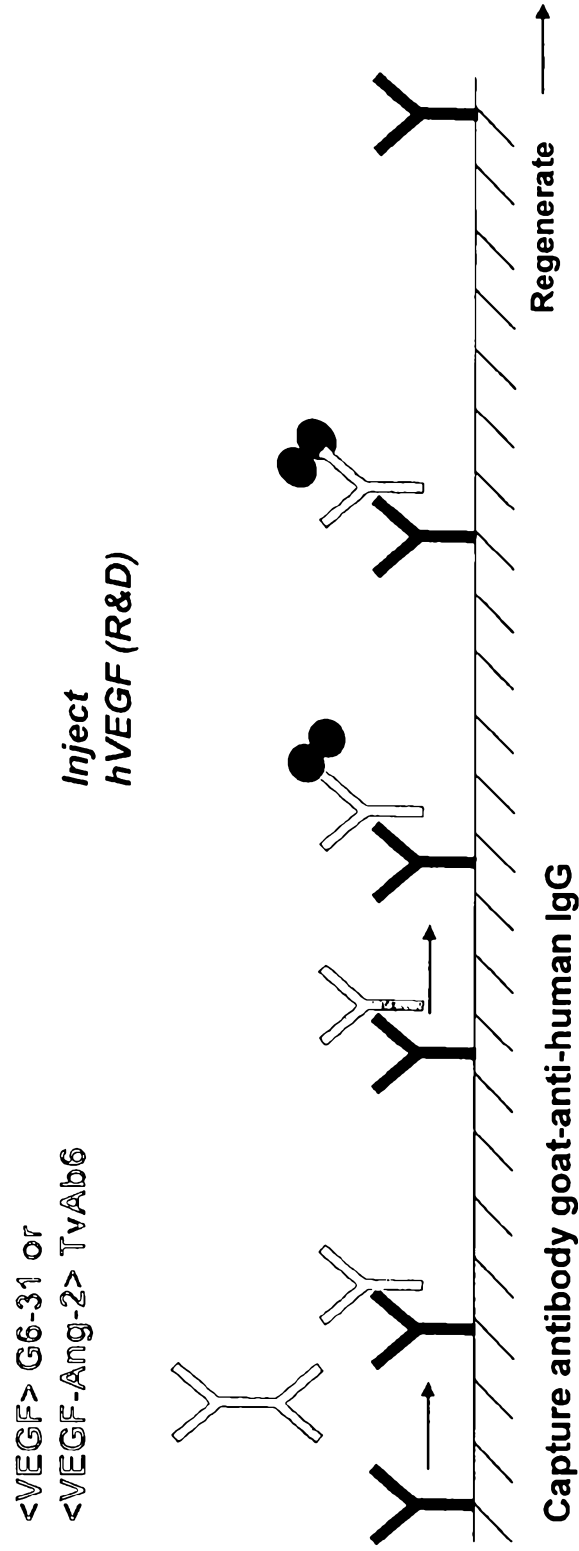


Figure 13

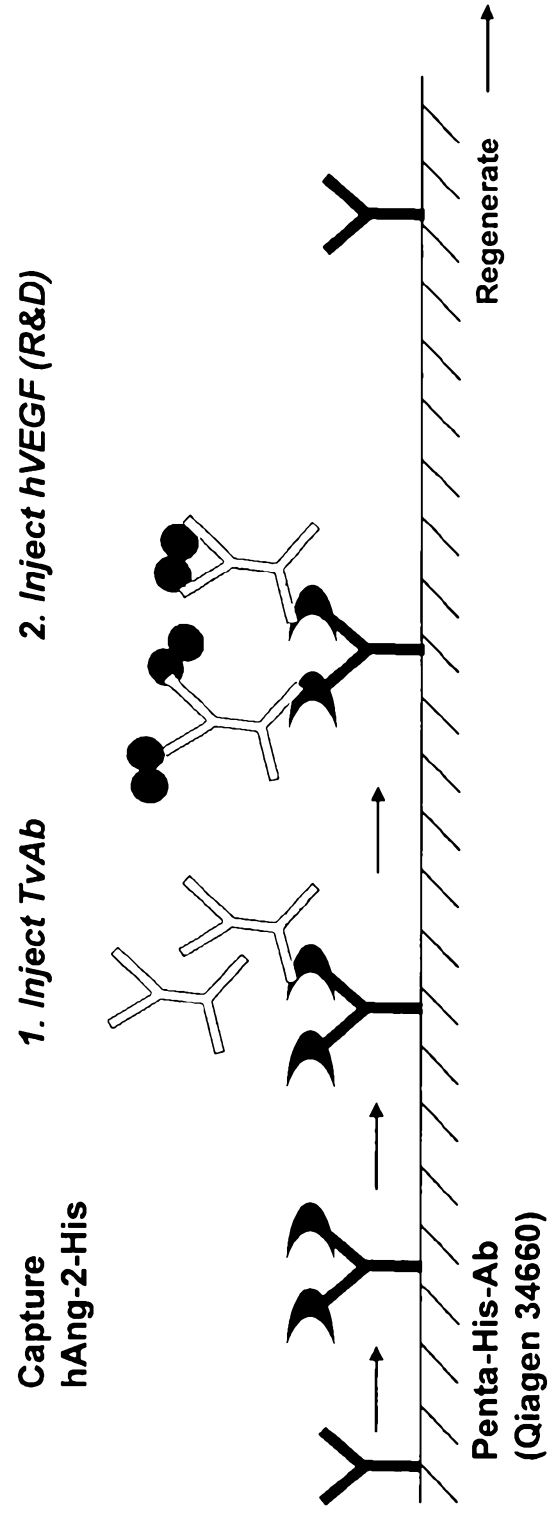


Figure 14

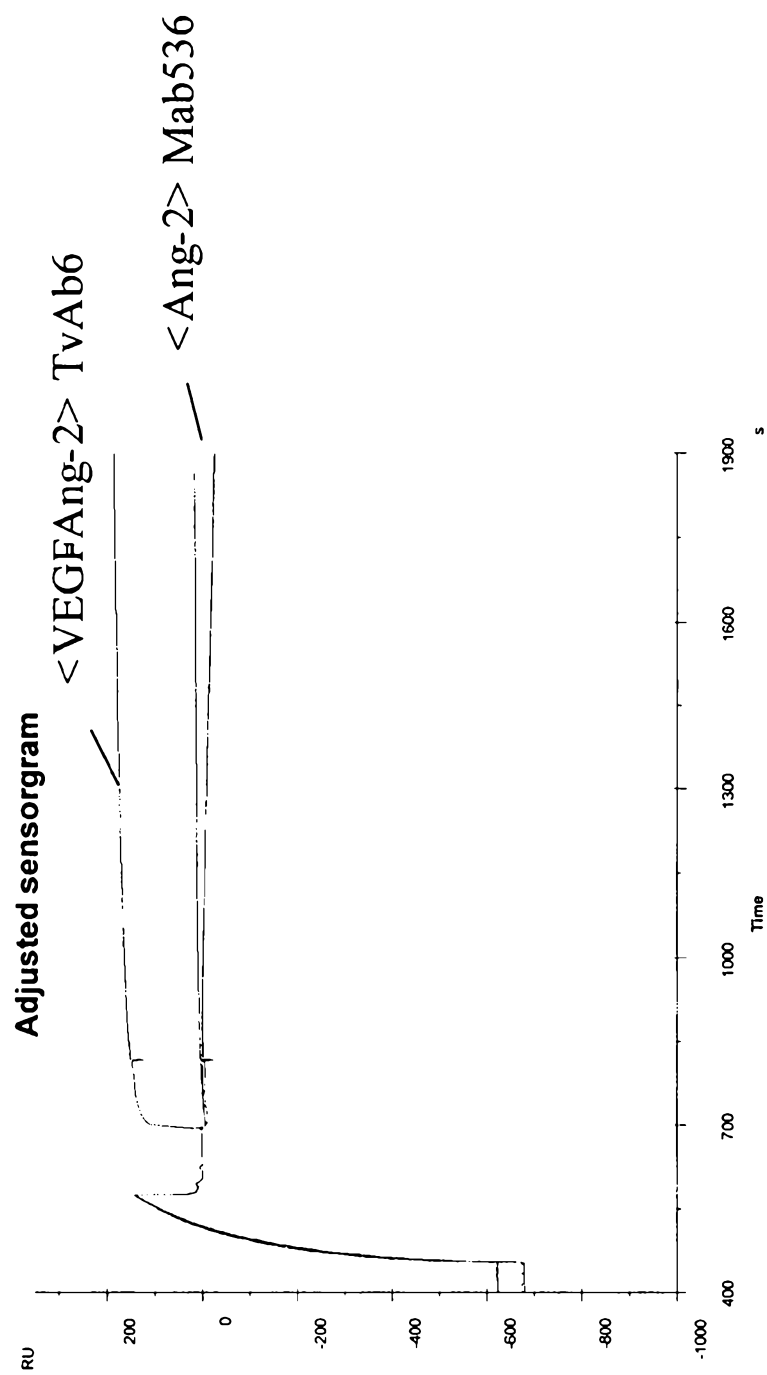


Fig 15A

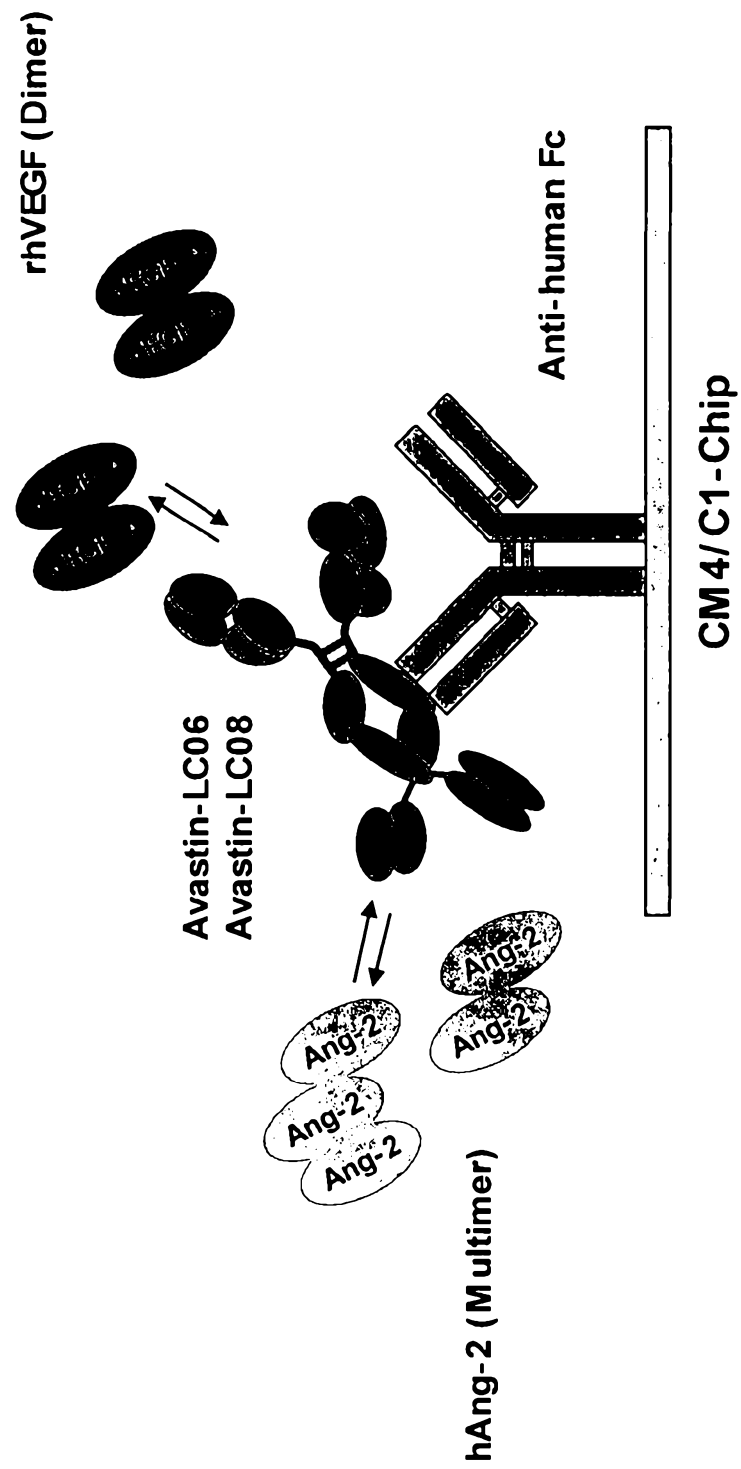


Fig 15B

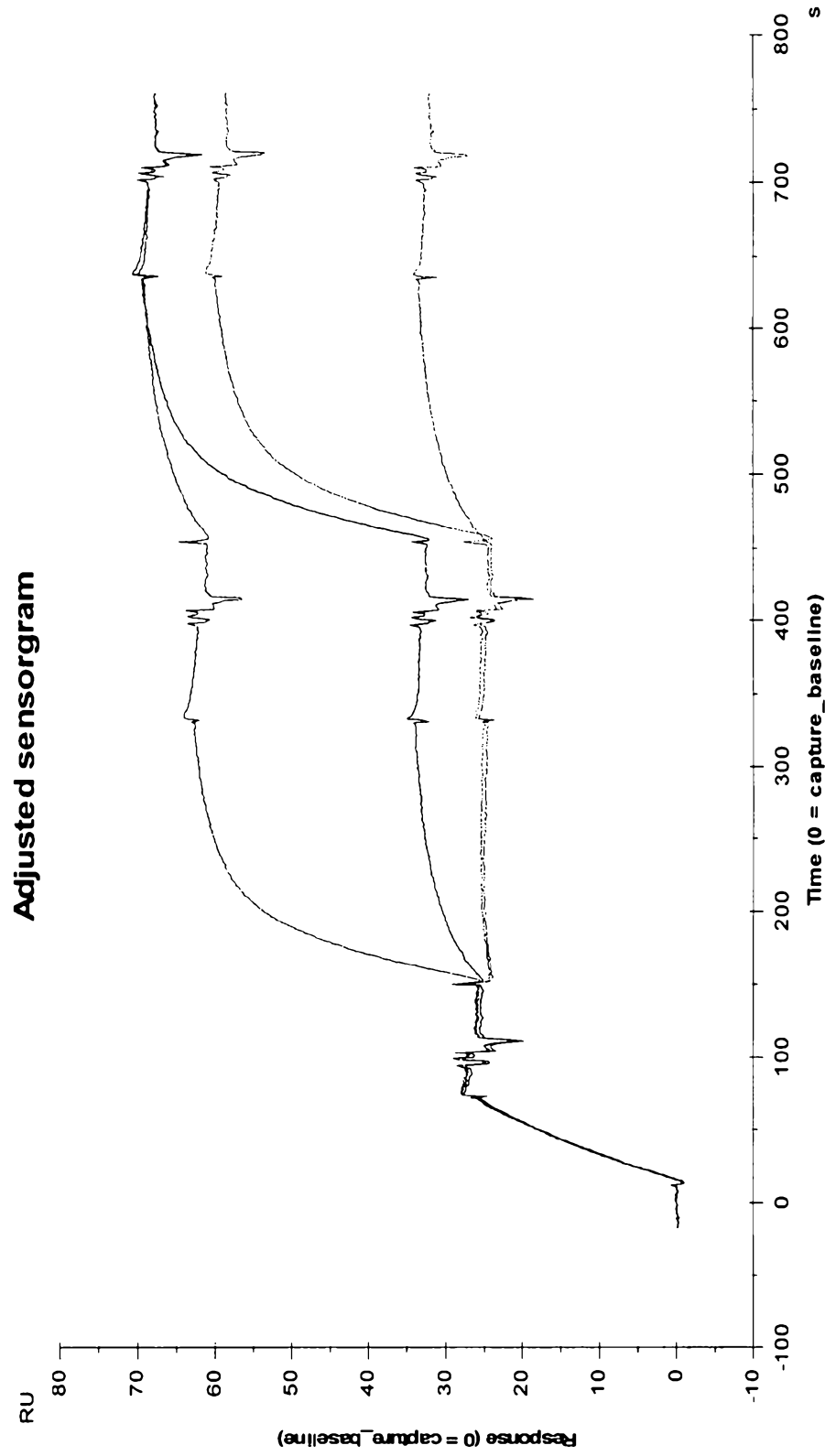


Fig 16A

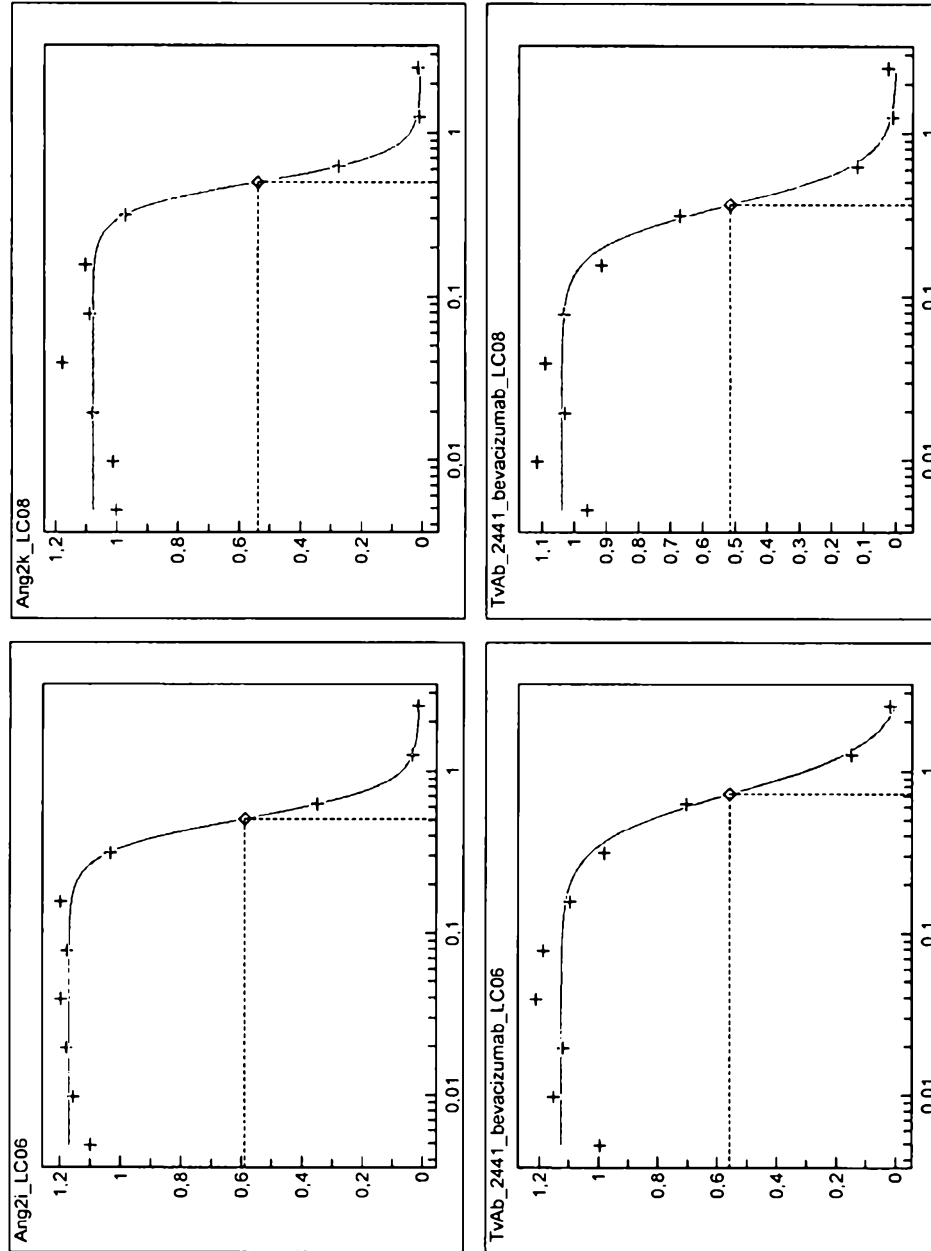


Fig 16B

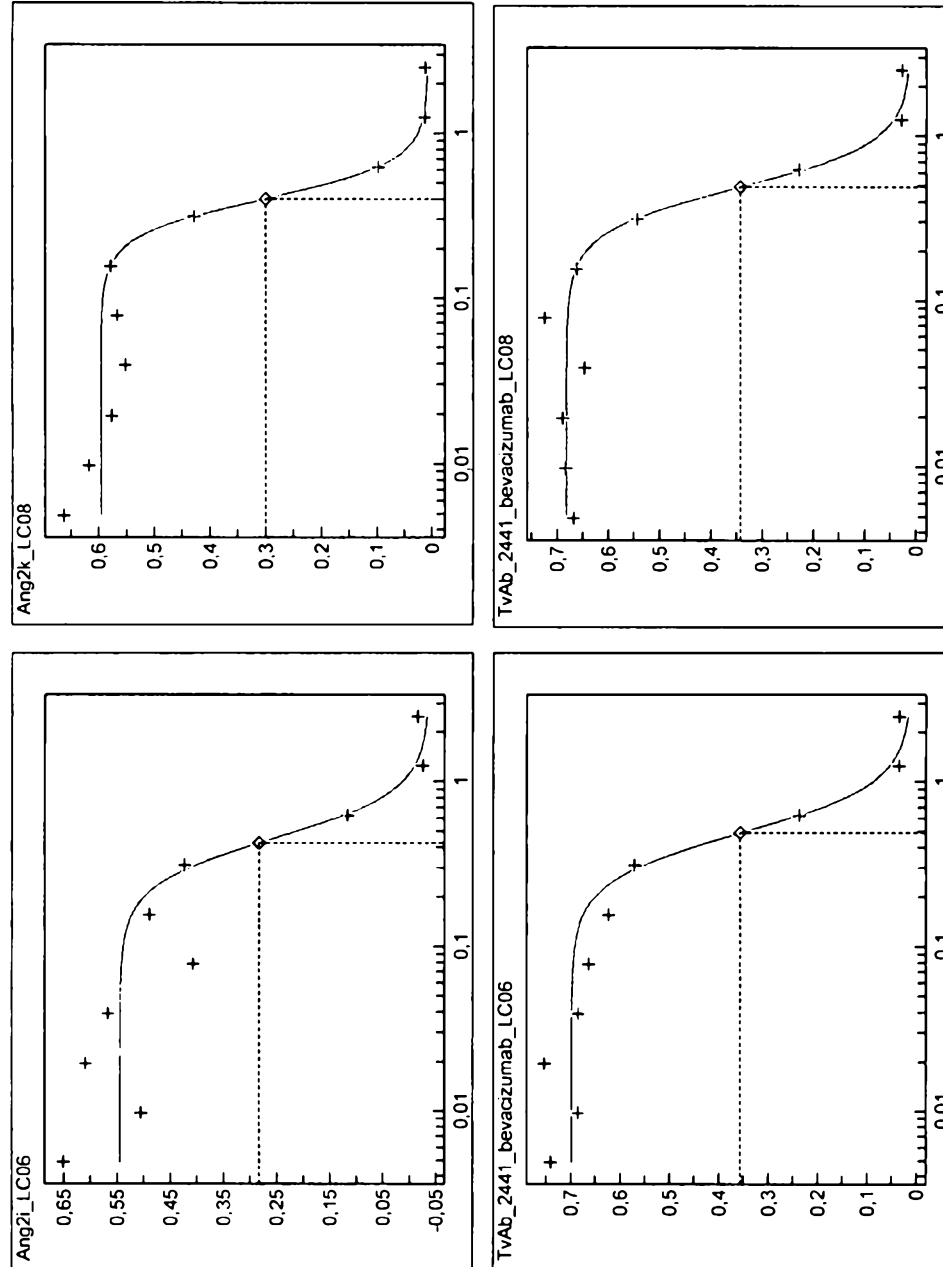


Fig 17

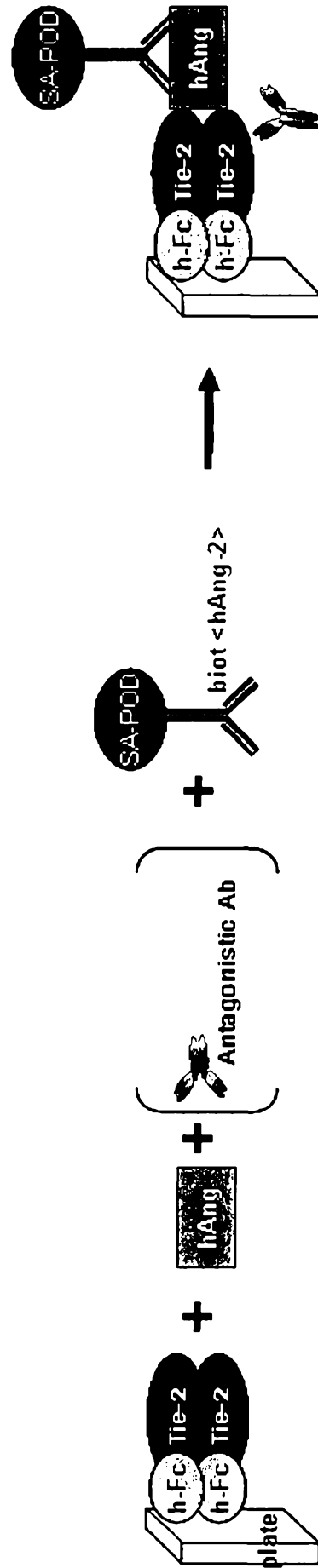


Fig 18

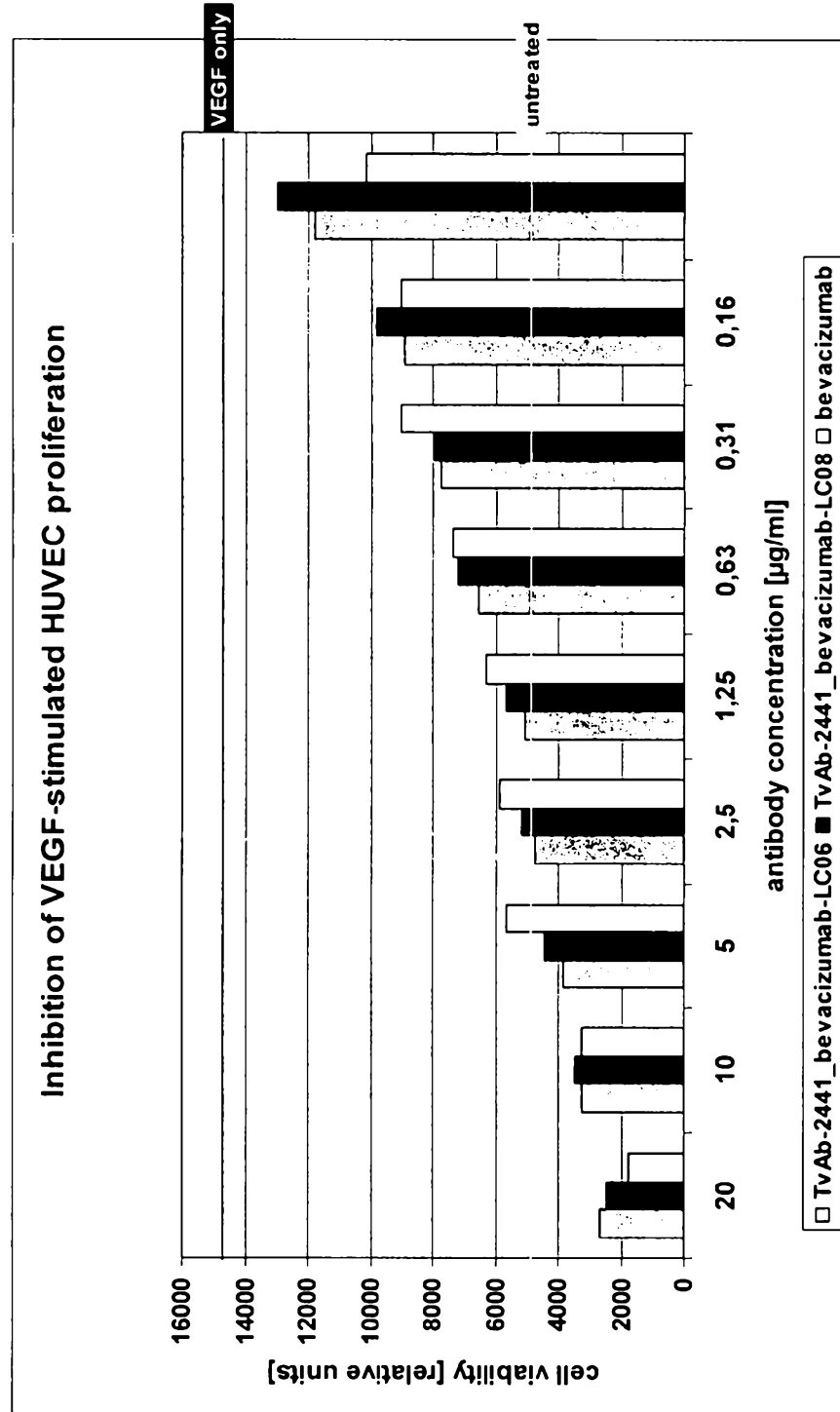
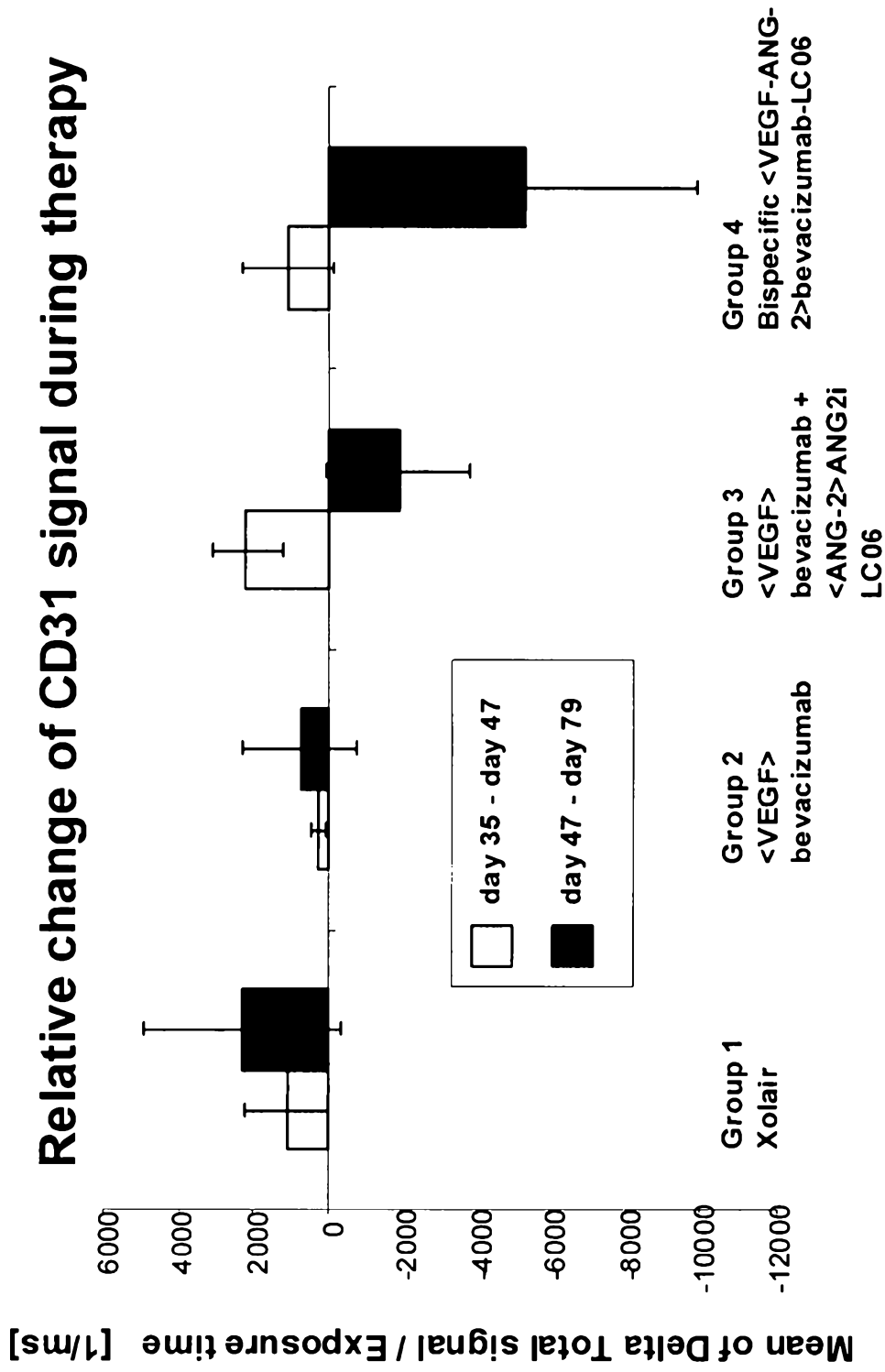


Fig 19



SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Bispecific anti-VEGF/anti-ANG-2 antibodies

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<150> EP 08017607.6

<151> 2008-10-08

<150> EP 08021834.0

<151> 2008-12-16

<160> 136

<170> PatentIn version 3.2

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Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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50 55 60

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Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 16

<211> 107

<212> PRT

<213> Artificial

<220>

<223> light chain variable domain, <VEGF>ranibizumab

<400> 16

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 17
<211> 11
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <VEGF>HuMab G6-31

<400> 17

Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 18
<211> 17
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <VEGF>HuMab G6-31

<400> 18

Gly Ile Thr Pro Ala Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 19
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <VEGF>HuMab G6-31

<400> 19

Asp Tyr Trp Ile His
1 5

<210> 20
<211> 9
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, <VEGF>HuMab G6-31

<400> 20

Gln Gln Gly Tyr Gly Asn Pro Phe Thr
1 5

<210> 21
<211> 7
<212> PRT
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<220>
<223> light chain CDR2, <VEGF>HuMab G6-31

<400> 21

Ser Ala Ser Phe Leu Tyr Ser
1 5

<210> 22
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <VEGF>HuMab G6-31

<400> 22

Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala
1 5 10

<210> 23
<211> 120
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <VEGF> HuMab G6-31

<400> 23

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Asp Tyr
20 25 30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Gly Ile Thr Pro Ala Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Val Phe Phe Leu Pro Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 24
<211> 107
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, <VEGF> HuMab G6-31

<400> 24

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Asn Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 25
<211> 13
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <ANG-2> Mab 536

<400> 25

Asp Leu Leu Asp Tyr Asp Ile Leu Thr Gly Tyr Gly Tyr
1 5 10

<210> 26
<211> 17
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <ANG-2> Mab 536

<400> 26

Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 27
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <ANG-2> Mab 536

<400> 27

Ser Tyr Gly Met His
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, <ANG-2> Mab 536

<400> 28

Met Gln Gly Thr His Trp Pro Pro Thr
1 5

<210> 29
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, <ANG-2> Mab 536

<400> 29

Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 30
<211> 16
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <ANG-2> Mab 536

<400> 30

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 31
<211> 122
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <ANG-2> Mab 536

<400> 31

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Leu Asp Tyr Asp Ile Leu Thr Gly Tyr Gly Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 32

<211> 112

<212> PRT

<213> Artificial

<220>

<223> light chain variable domain, <ANG-2> Mab 536

<400> 32

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 33
<211> 20
<212> PRT
<213> Artificial

<220>
<223> (G4S)4 linker

<400> 33

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 34
<211> 104
<212> PRT
<213> Homo sapiens

<400> 34

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
1 5 10 15

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
20 25 30

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
35 40 45

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
50 55 60

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
65 70 75 80

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
85 90 95

Thr Val Ala Pro Thr Glu Cys Ser
100

<210> 35
<211> 330
<212> PRT
<213> Homo sapiens

<400> 35

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

180	185	190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn		
195	200	205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly		
210	215	220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu		
225	230	235
240		
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr		
245	250	255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn		
260	265	270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe		
275	280	285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn		
290	295	300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr		
305	310	315
320		
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
325	330	
<210> 36		
<211> 327		
<212> PRT		
<213> Homo sapiens		
<400> 36		
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg		
1	5	10
15		
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr		
20	25	30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser		
35	40	45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 37
<211> 107
<212> PRT
<213> Homo sapiens

<400> 37

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 38
<211> 7
<212> PRT
<213> Artificial

<220>

<223> heavy chain CDR3, <ANG-2> Ang2s_R3_LC03

<400> 38

Asp Leu Gly Tyr Asp Tyr Val
1 5

<210> 39

<211> 19

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR2, <ANG-2> Ang2s_R3_LC03

<400> 39

Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala Pro
1 5 10 15

Val Lys Gly

<210> 40

<211> 5

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR1, <ANG-2> Ang2s_R3_LC03

<400> 40

Asn Ala Trp Met Ser
1 5

<210> 41

<211> 10

<212> PRT

<213> Artificial

<220>

<223> light chain CDR3, <ANG-2> Ang2s_R3_LC03

<400> 41

Gln Gln Tyr Asp Asn Leu Pro Met Tyr Thr
1 5 10

<210> 42

<211> 7

<212> PRT

<213> Artificial

<220>

<223> light chain CDR2, <ANG-2> Ang2s_R3_LC03

<400> 42

His Ala Ser Asn Leu Glu Thr

1 5

<210> 43

<211> 11

<212> PRT

<213> Artificial

<220>

<223> light chain CDR1, <ANG-2> Ang2s_R3_LC03

<400> 43

Gln Ala Ser Gln Asp Ile Ser Asn Arg Leu Asn

1 5 10

<210> 44

<211> 118

<212> PRT

<213> Artificial

<220>

<223> heavy chain variable domain, <ANG-2> Ang2s_R3_LC03

<400> 44

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala

20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala

50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Thr Thr Asp Leu Gly Tyr Asp Tyr Val Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 45
<211> 110
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, <ANG-2> Ang2s_R3_LC03

<400> 45

Asp Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr His Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Met
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
100 105 110

<210> 46
<211> 20
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <ANG-2>Ang2i_LC06

<400> 46

Ser Pro Asn Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Pro Gly
1 5 10 15

Ala Phe Asp Ile
20

<210> 47
<211> 17
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <ANG-2>Ang2i_LC06

<400> 47

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 48
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <ANG-2>Ang2i_LC06

<400> 48

Gly Tyr Tyr Met His
1 5

<210> 49
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, <ANG-2>Ang2i_LC06

<400> 49

Gln Val Trp Asp Ser Ser Ser Asp His Tyr Val
1 5 10

<210> 50
<211> 7

<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, <ANG-2>Ang2i_LC06
<400> 50

Asp Asp Ser Asp Arg Pro Ser
1 5

<210> 51
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <ANG-2>Ang2i_LC06
<400> 51

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 52
<211> 129
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <ANG-2>Ang2i_LC06
<400> 52

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

			85						90					95			
Ala	Arg	Ser	Pro	Asn	Pro	Tyr	Tyr	Tyr	Asp	Ser	Ser	Gly	Tyr	Tyr	Tyr		
			100					105					110				

Pro	Gly	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser		
		115					120					125					

Ser

<210> 53
 <211> 110
 <212> PRT
 <213> Artificial

<220>
 <223> light chain variable domain, <ANG-2>Ang2i_LC06

<400> 53

Gln	Pro	Gly	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln		
1				5				10						15			

Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile	Gly	Ser	Lys	Ser	Val		
			20					25					30				

His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Val	Tyr		
		35					40					45					

Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser		
	50					55					60						

Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Gly		
65					70					75					80		

Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Ser	Ser	Asp	His		
			85						90					95			

Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Gln				
			100					105					110				

<210> 54
 <211> 20
 <212> PRT
 <213> Artificial

<220>

<223> heavy chain CDR3, <ANG-2>Ang2i_LC07

<400> 54

Ser	Pro	Asn	Pro	Tyr	Tyr	Tyr	Asp	Ser	Ser	Gly	Tyr	Tyr	Tyr	Pro	Gly
1				5					10					15	

Ala	Phe	Asp	Ile
			20

<210> 55

<211> 17

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR2, <ANG-2>Ang2i_LC07

<400> 55

Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 56

<211> 5

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR1, <ANG-2>Ang2i_LC07

<400> 56

Gly	Tyr	Tyr	Met	His
1				5

<210> 57

<211> 11

<212> PRT

<213> Artificial

<220>

<223> light chain CDR3, <ANG-2>Ang2i_LC07

<400> 57

Gln Val Trp Asp Ser Asp Ser Asp Gln Gly Val

1 5 10

<210> 58
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, <ANG-2>Ang2i_LC07

<400> 58

Asp Asp Ser Glu Arg Pro Ser
1 5

<210> 59
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <ANG-2>Ang2i_LC07

<400> 59

Gly Gly Asn Phe Ile Gly Gly Lys Ser Val His
1 5 10

<210> 60
<211> 129
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <ANG-2>Ang2i_LC07

<400> 60

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr
100 105 110

Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

Ser

<210> 61
<211> 110
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, <ANG-2>Ang2i_LC07
<400> 61

Gln Pro Val Leu Thr Gln Ser Pro Ser Val Ser Val Ala Pro Gly Glu
1 5 10 15

Thr Ala Arg Val Ala Cys Gly Gly Asn Phe Ile Gly Gly Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Ile Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Ile Ile Thr Arg Ala Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr His Cys Gln Val Trp Asp Ser Asp Ser Asp Gln
85 90 95

Gly Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 62
<211> 15
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <ANG-2>Ang2k_LC08

<400> 62

Pro	Thr	Leu	Asp	Ile	Tyr	Met	Gly	Tyr	Tyr	Gly	Met	Asp	Val
1				5				10				15	

<210> 63
<211> 17
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <ANG-2>Ang2k_LC08

<400> 63

Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 64
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <ANG-2>Ang2k_LC08

<400> 64

Ser	Tyr	Gly	Met	His
1				5

<210> 65
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, <ANG-2>Ang2k_LC08

<400> 65

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1 5 10

<210> 66
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, <ANG-2>Ang2k_LC08

<400> 66

Asn Asn Asp Gln Arg Pro Ser
1 5

<210> 67
<211> 13
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <ANG-2>Ang2k_LC08

<400> 67

Ser Gly Phe Ala Ser Asn Ile Gly Ser Asn Ser Val Asn
1 5 10

<210> 68
<211> 124
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <ANG-2> Ang2k_LC08

<400> 68

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Pro Thr Leu Asp Ile Tyr Met Gly Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 69
<211> 112
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, <ANG-2> Ang2k_LC08

<400> 69

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Phe Ala Ser Asn Ile Gly Ser Asn
20 25 30

Ser Val Asn Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asn Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 70
<211> 7

<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <ANG-2> Ang2s_LC09

<400> 70

Asp Leu Gly Tyr Asp Tyr Val
1 5

<210> 71
<211> 19
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <ANG-2> Ang2s_LC09

<400> 71

Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala Pro
1 5 10 15

Val Lys Gly

<210> 72
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <ANG-2> Ang2s_LC09

<400> 72

Asn Ala Trp Met Ser
1 5

<210> 73
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, <ANG-2> Ang2s_LC09

<400> 73

Met Gln Ala Leu Gln Ile Pro
1 5

<210> 74
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> light chain CDR2, <ANG-2> Ang2s_LC09

<400> 74

Leu Gly Ser Asn Arg Ala Ser
 1 5

<210> 75
 <211> 16
 <212> PRT
 <213> Artificial

<220>
 <223> light chain CDR1, <ANG-2> Ang2s_LC09

<400> 75

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
 1 5 10 15

<210> 76
 <211> 119
 <212> PRT
 <213> Artificial

<220>
 <223> heavy chain variable domain, <ANG-2> Ang2s_LC09

<400> 76

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
 50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Thr Asp Leu Gly Tyr Asp Tyr Val Trp Gly Ser Pro Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 77

<211> 109

<212> PRT

<213> Artificial

<220>

<223> light chain variable domain, <ANG-2> Ang2s_LC09

<400> 77

Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile
1 5 10 15

Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
20 25 30

Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
50 55 60

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

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Ile Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Thr Val Leu Arg Thr
100 105

<210> 78

<211> 20

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR3, <ANG-2> Ang2i_LC10

<400> 78

Ser	Pro	Asn	Pro	Tyr	Tyr	Tyr	Asp	Ser	Ser	Gly	Tyr	Tyr	Tyr	Pro	Gly
1				5					10					15	

Ala	Phe	Asp	Ile
			20

<210> 79

<211> 17

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR2, <ANG-2> Ang2i_LC10

<400> 79

Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 80

<211> 5

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR1, <ANG-2> Ang2i_LC10

<400> 80

Gly	Tyr	Tyr	Met	His
1				5

<210> 81

<211> 11

<212> PRT

<213> Artificial

<220>

<223> light chain CDR3, <ANG-2> Ang2i_LC10

<400> 81

Gln	Val	Trp	Asp	Ser	Ser	Ser	Asp	His	Trp	Val
1				5					10	

<210> 82
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, <ANG-2> Ang2i_LC10

<400> 82

Asp Asp Ser Asp Arg Pro Ser
1 5

<210> 83
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <ANG-2> Ang2i_LC10

<400> 83

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 84
<211> 129
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <ANG-2> Ang2i_LC10

<400> 84

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr

65					70					75					80	
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Arg	Ser	Pro	Asn	Pro	Tyr	Tyr	Tyr	Asp	Ser	Ser	Gly	Tyr	Tyr	Tyr	
			100					105					110			
Pro	Gly	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	
		115					120					125				
Ser																
<210>	85															
<211>	105															
<212>	PRT															
<213>	Artificial															
<220>																
<223>	light chain variable domain, <ANG-2> Ang2i_LC10															
<400>	85															
Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	
1			5						10					15		
Cys	Gly	Gly	Asn	Asn	Ile	Gly	Ser	Lys	Ser	Val	His	Trp	Tyr	Gln	Gln	
			20					25					30			
Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Val	Tyr	Asp	Asp	Ser	Asp	Arg	
		35					40					45				
Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	
	50					55					60					
Ala	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	
65					70					75					80	
Tyr	Cys	Gln	Val	Trp	Asp	Ser	Ser	Ser	Asp	His	Trp	Val	Phe	Gly	Gly	
				85					90					95		
Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln								
			100					105								

<210> 86
<211> 15
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <ANG-2> Ang2k_LC11

<400> 86

Pro	Thr	Leu	Asp	Ile	Tyr	Met	Gly	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
1				5				10						15

<210> 87
<211> 17
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <ANG-2> Ang2k_LC11

<400> 87

Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 88
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <ANG-2> Ang2k_LC11

<400> 88

Ser	Tyr	Gly	Met	His
1				5

<210> 89
<211> 12
<212> PRT
<213> Artificial

<220>
<223> light chain CDR3, <ANG-2> Ang2k_LC11

<400> 89

Gln Val Trp Asp Ser Ser Ser Asp His Pro Gly Val

1 5 10

<210> 90
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR2, <ANG-2> Ang2k_LC11

<400> 90

Asp Asp Ser Asp Arg Pro Ser
1 5

<210> 91
<211> 11
<212> PRT
<213> Artificial

<220>
<223> light chain CDR1, <ANG-2> Ang2k_LC11

<400> 91

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 92
<211> 124
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain, <ANG-2> Ang2k_LC11

<400> 92

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Pro Thr Leu Asp Ile Tyr Met Gly Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 93
<211> 106
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain, <ANG-2> Ang2k_LC11

<220>
<221> misc_feature
<222> (98)..(98)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (102)..(102)
<223> Xaa can be any naturally occurring amino acid

<400> 93

Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Arg Ile Thr
1 5 10 15

Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln
20 25 30

Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp Ser Asp Arg
35 40 45

Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr
50 55 60

Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr
65 70 75 80

Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His Pro Gly Val Phe Gly
85 90 95

Gly Xaa Thr Lys Leu Xaa Val Leu Gly Gln
100 105

<210> 94
<211> 12
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR3, <VEGF>B20-4.1

<400> 94

Trp Gly His Ser Thr Ser Pro Trp Ala Met Asp Tyr
1 5 10

<210> 95
<211> 17
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR2, <VEGF>B20-4.1

<400> 95

Ala Ile Trp Pro Phe Gly Gly Tyr Thr His Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 96
<211> 8
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR1, <VEGF>B20-4.1

<400> 96

Phe Ser Ile Asn Gly Ser Trp Ile
1 5

<210> 97
<211> 9
<212> PRT

<213> Artificial

<220>

<223> light chain CDR3, <VEGF>B20-4.1

<400> 97

Gln Gln Ser Asn Thr Ser Pro Leu Thr
1 5

<210> 98

<211> 8

<212> PRT

<213> Artificial

<220>

<223> light chain CDR2, <VEGF>B20-4.1

<400> 98

Tyr Ala Ala Ser Asn Leu Ala Ser
1 5

<210> 99

<211> 11

<212> PRT

<213> Artificial

<220>

<223> light chain CDR1, <VEGF>B20-4.1

<400> 99

Arg Ala Ser Gln Val Ile Arg Arg Ser Leu Ala
1 5 10

<210> 100

<211> 117

<212> PRT

<213> Artificial

<220>

<223> heavy chain variable domain, <VEGF>B20-4.1

<400> 100

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ile Asn Gly Ser
20 25 30

Trp Ile Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Ala Ile Trp Pro Phe Gly Gly Tyr Thr His Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly His Ser Thr Ser Pro Trp Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val
115

<210> 101

<211> 108

<212> PRT

<213> Artificial

<220>

<223> light chain variable domain, <VEGF>B20-4.1

<400> 101

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val Ile Arg Arg Ser
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Ser Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 102
<211> 730
<212> PRT
<213> Artificial

<220>
<223> bevacizumab heavy chain Ang2i_LC06 scFv fusion peptide of
<VEGF-ANG-2> TvAb-2441-bevacizumab-LC06

<400> 102

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165							170						175			
Pro	Ala	Val	Leu 180	Gln	Ser	Ser	Gly	Leu 185	Tyr	Ser	Leu	Ser	Ser	Val	Val	
Thr	Val	Pro 195	Ser	Ser	Ser	Leu	Gly 200	Thr	Gln	Thr	Tyr	Ile 205	Cys	Asn	Val	
Asn	His 210	Lys	Pro	Ser	Asn	Thr 215	Lys	Val	Asp	Lys	Lys 220	Val	Glu	Pro	Lys	
Ser 225	Cys	Asp	Lys	Thr	His 230	Thr	Cys	Pro	Pro	Cys 235	Pro	Ala	Pro	Glu	Leu 240	
Leu	Gly	Gly	Pro	Ser 245	Val	Phe	Leu	Phe	Pro 250	Pro	Lys	Pro	Lys	Asp 255	Thr	
Leu	Met	Ile	Ser 260	Arg	Thr	Pro	Glu	Val 265	Thr	Cys	Val	Val	Val 270	Asp	Val	
Ser	His 275	Glu	Asp	Pro	Glu	Val	Lys 280	Phe	Asn	Trp	Tyr	Val 285	Asp	Gly	Val	
Glu	Val 290	His	Asn	Ala	Lys	Thr 295	Lys	Pro	Arg	Glu	Glu 300	Gln	Tyr	Asn	Ser	
Thr 305	Tyr	Arg	Val	Val	Ser 310	Val	Leu	Thr	Val	Leu 315	His	Gln	Asp	Trp	Leu 320	
Asn	Gly	Lys	Glu	Tyr 325	Lys	Cys	Lys	Val	Ser 330	Asn	Lys	Ala	Leu	Pro 335	Ala	
Pro	Ile	Glu	Lys 340	Thr	Ile	Ser	Lys	Ala 345	Lys	Gly	Gln	Pro	Arg 350	Glu	Pro	
Gln	Val	Tyr 355	Thr	Leu	Pro	Pro	Ser 360	Arg	Glu	Glu	Met	Thr 365	Lys	Asn	Gln	
Val	Ser 370	Leu	Thr	Cys	Leu	Val 375	Lys	Gly	Phe	Tyr	Pro 380	Ser	Asp	Ile	Ala	
Val 385	Glu	Trp	Glu	Ser	Asn 390	Gly	Gln	Pro	Glu	Asn 395	Asn	Tyr	Lys	Thr	Thr 400	

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser
465 470 475 480

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
485 490 495

Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln
500 505 510

Ala Pro Gly Gln Cys Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser
515 520 525

Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr
530 535 540

Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg
545 550 555 560

Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Pro Asn Pro Tyr
565 570 575

Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Pro Gly Ala Phe Asp Ile Trp
580 585 590

Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Pro
610 615 620

Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala
625 630 635 640

Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His Trp
645 650 655

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp
660 665 670

Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
675 680 685

Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu
690 695 700

Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His Tyr Val
705 710 715 720

Phe Gly Cys Gly Thr Lys Val Thr Val Leu
725 730

<210> 103

<211> 727

<212> PRT

<213> Artificial

<220>

<223> bevacizumab heavy chain Ang2i_LC08 scFv fusion peptide of
<VEGF-ANG-2> TvAb-2441-bevacizumab-LC08

<400> 103

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr

65					70						75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	Ser	His	Trp	Tyr	Phe	Asp	Val
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
		115					120					125			
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
	130					135					140				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145					150					155					160
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
				165					170					175	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
			180					185					190		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195					200					205			
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys
	210					215					220				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
225					230					235					240
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
				245					250					255	
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
			260					265						270	
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
		275					280					285			
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
	290					295					300				

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser
465 470 475 480

Gly Gly Gly Val Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
485 490 495

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln
500 505 510

Ala Pro Gly Lys Cys Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly
515 520 525

Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
530 535 540

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
545 550 555 560

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Pro Thr Leu Asp Ile
565 570 575

Tyr Met Gly Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
580 585 590

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Pro Val Leu Thr Gln Pro
610 615 620

Pro Ser Ala Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser
625 630 635 640

Gly Phe Ala Ser Asn Ile Gly Ser Asn Ser Val Asn Trp Tyr Gln Gln
645 650 655

Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asn Asn Asp Gln Arg
660 665 670

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser
675 680 685

Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr
690 695 700

Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val Phe Gly Cys
705 710 715 720

Gly Thr Lys Leu Thr Val Leu
725

<210> 104

<211> 214

<212> PRT

<213> Artificial

<220>

<223> light chain of bevacizumab

<400> 104

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 105
<211> 191
<212> PRT
<213> Homo sapiens

<400> 105

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg

	180		185		190
<210>	106				
<211>	504				
<212>	PRT				
<213>	Artificial				
<220>					
<223>	Human angiopoietin-2 (ANG-2) with leader and His-tag				
<400>	106				
Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala					
1	5		10		15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys					
	20		25		30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro					
	35		40		45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala					
	50		55		60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu					
65		70		75	80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys					
	85		90		95
Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile					
	100		105		110
Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly					
	115		120		125
Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp					
	130		135		140
Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu					
145		150		155	160
Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp					
	165		170		175

Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
180 185 190

Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
195 200 205

Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
210 215 220

Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn
225 230 235 240

Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
245 250 255

Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
260 265 270

Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
275 280 285

Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
290 295 300

Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
305 310 315 320

Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
325 330 335

Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
340 345 350

Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
355 360 365

Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr
370 375 380

Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg
385 390 395 400

Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile

405	410	415
Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys		
420	425	430
Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp		
435	440	445
Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln		
450	455	460
Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser		
465	470	475
Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe		
485	490	495
Ser Gly His His His His His His		
500		
<210> 107		
<211> 506		
<212> PRT		
<213> Artificial		
<220>		
<223> Human angiopoietin-1 (ANG-1) with leader and His-tag		
<400> 107		
Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His		
1	5	10
Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg		
20	25	30
Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro		
35	40	45
Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr		
50	55	60
Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser		
65	70	75
		80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
130 135 140

Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
145 150 155 160

Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
165 170 175

Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
180 185 190

Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
195 200 205

Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
225 230 235 240

Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
245 250 255

Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
260 265 270

Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
275 280 285

Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
290 295 300

Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn

305						310						315						320
Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	His	Arg	Glu	Asp	Gly	Ser	Leu	Asp			
				325					330					335				
Phe	Gln	Arg	Gly	Trp	Lys	Glu	Tyr	Lys	Met	Gly	Phe	Gly	Asn	Pro	Ser			
				340					345					350				
Gly	Glu	Tyr	Trp	Leu	Gly	Asn	Glu	Phe	Ile	Phe	Ala	Ile	Thr	Ser	Gln			
				355					360					365				
Arg	Gln	Tyr	Met	Leu	Arg	Ile	Glu	Leu	Met	Asp	Trp	Glu	Gly	Asn	Arg			
				370					375					380				
Ala	Tyr	Ser	Gln	Tyr	Asp	Arg	Phe	His	Ile	Gly	Asn	Glu	Lys	Gln	Asn			
				385					390					395				
Tyr	Arg	Leu	Tyr	Leu	Lys	Gly	His	Thr	Gly	Thr	Ala	Gly	Lys	Gln	Ser			
				405					410					415				
Ser	Leu	Ile	Leu	His	Gly	Ala	Asp	Phe	Ser	Thr	Lys	Asp	Ala	Asp	Asn			
				420					425					430				
Asp	Asn	Cys	Met	Cys	Lys	Cys	Ala	Leu	Met	Leu	Thr	Gly	Gly	Trp	Trp			
				435					440					445				
Phe	Asp	Ala	Cys	Gly	Pro	Ser	Asn	Leu	Asn	Gly	Met	Phe	Tyr	Thr	Ala			
				450					455					460				
Gly	Gln	Asn	His	Gly	Lys	Leu	Asn	Gly	Ile	Lys	Trp	His	Tyr	Phe	Lys			
				465					470					475				
Gly	Pro	Ser	Tyr	Ser	Leu	Arg	Ser	Thr	Thr	Met	Met	Ile	Arg	Pro	Leu			
				485					490					495				
Asp	Phe	Ser	Gly	His	His	His	His	His	His									
				500					505									

<210>	108
<211>	1124
<212>	PRT
<213>	Homo sapiens
<400>	108

Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu
1 5 10 15

Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
20 25 30

Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
35 40 45

Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
50 55 60

Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
65 70 75 80

Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
85 90 95

Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
100 105 110

Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
115 120 125

Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
130 135 140

Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
145 150 155 160

Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
165 170 175

His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
180 185 190

Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
195 200 205

Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
210 215 220

Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys
225 230 235 240

Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu
245 250 255

Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu
260 265 270

Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser
275 280 285

Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro
290 295 300

Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly
305 310 315 320

Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln
325 330 335

Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile
340 345 350

Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro
355 360 365

Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr
370 375 380

Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His
385 390 395 400

Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro
405 410 415

Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met
420 425 430

Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu
435 440 445

Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn

450		455		460
Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys				
465		470		475
				480
Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln				
		485		490
				495
Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu				
		500		505
				510
Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly				
		515		520
				525
His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro				
		530		535
				540
Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn				
		545		550
				555
Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val				
		565		570
				575
Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys				
		580		585
				590
Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg				
		595		600
				605
Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu				
		610		615
				620
Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro				
		625		630
				635
Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val				
		645		650
				655
Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile				
		660		665
				670
Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys				
		675		680
				685

Ile Lys Asn Ala Thr Ile Thr Gln Tyr Gln Leu Lys Gly Leu Glu Pro
690 695 700

Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser
705 710 715 720

Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln
725 730 735

Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu
740 745 750

Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile
755 760 765

Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala
770 775 780

Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr
785 790 795 800

Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr
805 810 815

Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu
820 825 830

Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu
835 840 845

Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp
850 855 860

Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly
865 870 875 880

His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly
885 890 895

Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp
900 905 910

Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile
915 920 925

Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe
930 935 940

Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe
945 950 955 960

Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr
965 970 975

Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr
980 985 990

Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu
995 1000 1005

Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser
1010 1015 1020

Tyr Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro
1025 1030 1035

Tyr Cys Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln
1040 1045 1050

Gly Tyr Arg Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr
1055 1060 1065

Asp Leu Met Arg Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro
1070 1075 1080

Ser Phe Ala Gln Ile Leu Val Ser Leu Asn Arg Met Leu Glu Glu
1085 1090 1095

Arg Lys Thr Tyr Val Asn Thr Thr Leu Tyr Glu Lys Phe Thr Tyr
1100 1105 1110

Ala Gly Ile Asp Cys Ser Ala Glu Glu Ala Ala
1115 1120

<210> 109
 <211> 946
 <212> PRT
 <213> Artificial

 <220>
 <223> Heavy chain 1 of bispecific, tetravalent single chain Fab
 <VEGF-ANG-2> antibody molecule scFAB-Avastin-LC06-2620

 <400> 109

 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
 50 55 60

 Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
 65 70 75 80

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
 100 105 110

 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125

 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160

 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175

 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190

Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195					200					205			
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys
	210					215					220				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
225					230					235					240
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
				245					250					255	
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
			260					265					270		
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
		275					280					285			
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
	290					295					300				
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
305					310					315					320
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
				325					330					335	
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
			340					345					350		
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln
		355					360					365			
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
	370					375					380				
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
385					390					395					400
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
				405					410					415	

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
450 455 460

Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr
465 470 475 480

Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
485 490 495

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Asp
500 505 510

Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn
515 520 525

Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly Asp
530 535 540

Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His Tyr
545 550 555 560

Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Arg Thr Val Ala Ala
565 570 575

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
580 585 590

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
595 600 605

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
610 615 620

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
625 630 635 640

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
645 650 655

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
660 665 670

Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
675 680 685

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
690 695 700

Gly Gly Gly Ser Gly Gly Gln Val Gln Leu Val Glu Ser Gly Ala Glu
705 710 715 720

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
725 730 735

Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly
740 745 750

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr
755 760 765

Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
770 775 780

Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
785 790 795 800

Thr Ala Val Tyr Tyr Cys Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp
805 810 815

Ser Ser Gly Tyr Tyr Tyr Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly
820 825 830

Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
835 840 845

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
850 855 860

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

865 870 875 880

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
885 890 895

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
900 905 910

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
915 920 925

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
930 935 940

Thr His
945

<210> 110
<211> 214
<212> PRT
<213> Artificial

<220>
<223> Light chain of bispecific, tetravalent single chain Fab
<VEGF-ANG-2> antibody molecule scFAB-Avastin-LC06-2620

<400> 110

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 111

<211> 956

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 1 of bispecific, tetravalent single chain Fab
<VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2640

<400> 111

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe

50						55						60				
Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	Lys	Ser	Thr	Ala	Tyr	
65					70					75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	Ser	His	Trp	Tyr	Phe	Asp	Val	
			100					105					110			
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	
		115					120					125				
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	
	130					135					140					
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	
145					150					155					160	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	
				165					170					175		
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
			180					185					190			
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	
		195					200					205				
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	
	210					215					220					
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	
225					230					235					240	
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	
				245					250					255		
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	
			260					265					270			
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	
		275					280					285				

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Pro Gly Leu Thr Gln Pro
465 470 475 480

Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly
485 490 495

Gly Asn Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro
500 505 510

Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser
515 520 525

Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
530 535 540

Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys
545 550 555 560

Gln Val Trp Asp Ser Ser Ser Asp His Tyr Val Phe Gly Thr Gly Thr
565 570 575

Lys Val Thr Val Leu Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
675 680 685

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
690 695 700

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
705 710 715 720

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
725 730 735

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
740 745 750

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
755 760 765

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
770 775 780

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
785 790 795 800

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
805 810 815

Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr
820 825 830

Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
835 840 845

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
850 855 860

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
865 870 875 880

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
885 890 895

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
900 905 910

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
915 920 925

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
930 935 940

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
945 950 955

<210> 112

<211> 214
 <212> PRT
 <213> Artificial

<220>
 <223> Light chain of bispecific, tetravalent single chain Fab
 <VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2640

<400> 112

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 113

<211> 956

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 1 of bispecific, tetravalent single chain Fab
<VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2641

<400> 113

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145		150		155		160
Thr Val Ser Trp	Asn Ser Gly Ala Leu	Thr Ser Gly Val	His Thr Phe			
	165	170	175			
Pro Ala Val Leu	Gln Ser Ser Gly Leu	Tyr Ser Leu Ser	Ser Val Val			
	180	185	190			
Thr Val Pro Ser	Ser Ser Leu Gly	Thr Gln Thr Tyr	Ile Cys Asn Val			
	195	200	205			
Asn His Lys Pro	Ser Asn Thr Lys	Val Asp Lys Lys	Val Glu Pro Lys			
	210	215	220			
Ser Cys Asp Lys	Thr His Thr Cys	Pro Pro Cys Pro	Ala Pro Glu Leu			
	225	230	235	240		
Leu Gly Gly Pro	Ser Val Phe Leu	Phe Pro Pro Lys	Pro Lys Asp Thr			
	245	250	255			
Leu Met Ile Ser	Arg Thr Pro Glu	Val Thr Cys Val	Val Val Asp Val			
	260	265	270			
Ser His Glu Asp	Pro Glu Val Lys	Phe Asn Trp Tyr	Val Asp Gly Val			
	275	280	285			
Glu Val His Asn	Ala Lys Thr Lys	Pro Arg Glu Glu	Gln Tyr Asn Ser			
	290	295	300			
Thr Tyr Arg Val	Val Ser Val Leu	Thr Val Leu His	Gln Asp Trp Leu			
	305	310	315	320		
Asn Gly Lys Glu	Tyr Lys Cys Lys	Val Ser Asn Lys	Ala Leu Pro Ala			
	325	330	335			
Pro Ile Glu Lys	Thr Ile Ser Lys	Ala Lys Gly Gln	Pro Arg Glu Pro			
	340	345	350			
Gln Val Tyr Thr	Leu Pro Pro Ser	Arg Asp Glu Leu	Thr Lys Asn Gln			
	355	360	365			
Val Ser Leu Thr	Cys Leu Val Lys	Gly Phe Tyr Pro	Ser Asp Ile Ala			
	370	375	380			

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Pro Gly Leu Thr Gln Pro
465 470 475 480

Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly
485 490 495

Gly Asn Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro
500 505 510

Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser
515 520 525

Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
530 535 540

Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys
545 550 555 560

Gln Val Trp Asp Ser Ser Ser Asp His Tyr Val Phe Gly Cys Gly Thr
565 570 575

Lys Val Thr Val Leu Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
595 600 605

Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val
610						615					620				
Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln
625					630					635					640
Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser
				645					650					655	
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His
			660					665					670		
Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys
		675					680					685			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
	690					695					700				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
705					710					715				720	
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
				725					730					735	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Gly	Tyr
			740					745					750		
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Cys	Leu	Glu	Trp	Met
		755					760					765			
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
	770					775					780				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
785					790					795					800
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				805					810					815	
Ala	Arg	Ser	Pro	Asn	Pro	Tyr	Tyr	Tyr	Asp	Ser	Ser	Gly	Tyr	Tyr	Tyr
			820					825					830		

Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
835 840 845

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
850 855 860

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
865 870 875 880

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
885 890 895

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
900 905 910

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
915 920 925

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
930 935 940

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
945 950 955

<210> 114

<211> 214

<212> PRT

<213> Artificial

<220>

<223> Light chain of bispecific, tetravalent single chain Fab
<VEGF-ANG-2> antibody molecule scFab-Avastin-Ang2i-LC06-2641

<400> 114

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 115
<211> 946
<212> PRT
<213> Artificial

<220>
<223> Heavy chain 1 of bispecific, trivalent single chain Fab
<VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab

<400> 115

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

245										250					255				
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val				
			260					265						270					
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val				
		275					280					285							
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser				
	290					295					300								
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu				
305					310					315					320				
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala				
				325					330					335					
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro				
			340					345					350						
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln				
		355					360					365							
Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala				
	370					375					380								
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr				
385					390					395					400				
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu				
				405					410					415					
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser				
			420					425					430						
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser				
		435					440					445							
Leu	Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln				
	450					455						460							
Pro	Gly	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln	Thr				
465					470					475					480				

Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile	Gly	Ser	Lys	Ser	Val	His	
				485					490					495		
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Val	Tyr	Asp	
			500					505					510			
Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Asn	
		515					520					525				
Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Gly	Asp	
	530					535					540					
Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Ser	Ser	Asp	His	Tyr	
545					550					555					560	
Val	Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu	Arg	Thr	Val	Ala	Ala	
				565					570					575		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	
			580					585					590			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	
		595					600					605				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	
	610					615					620					
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	
625					630					635					640	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	
				645					650					655		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	
			660					665					670			
Phe	Asn	Arg	Gly	Glu	Cys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
		675					680					685				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
	690					695					700					

Gly Gly Gly Ser Gly Gly Gln Val Gln Leu Val Glu Ser Gly Ala Glu
705 710 715 720

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
725 730 735

Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly
740 745 750

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr
755 760 765

Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
770 775 780

Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
785 790 795 800

Thr Ala Val Tyr Tyr Cys Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp
805 810 815

Ser Ser Gly Tyr Tyr Tyr Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly
820 825 830

Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
835 840 845

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
850 855 860

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
865 870 875 880

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
885 890 895

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
900 905 910

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
915 920 925

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
930 935 940

Thr His
945

<210> 116
<211> 453
<212> PRT
<213> Artificial

<220>
<223> Heavy chain 2 of bispecific, trivalent single chain Fab
<VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab

<400> 116

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 117

<211> 214

<212> PRT

<213> Artificial

<220>

<223> Light chain of bispecific, trivalent single chain Fab
<VEGF-ANG-2> antibody molecule Avastin-LC06-KiH-C-scFab

<400> 117

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

	100		105		110										
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
145					150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
				165					170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
			180					185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195					200					205			
Phe	Asn	Arg	Gly	Glu	Cys										
	210														

<210> 118
 <211> 698
 <212> PRT
 <213> Artificial

<220>
 <223> Heavy chain 1 of bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS

<400> 118

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Ala	Asp	Phe
	50					55					60				

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
465 470 475 480

Gly Gly Ser Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala
485 490 495

Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser
500 505 510

Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu

515	520	525
Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe		
530	535	540
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val		
545	550	555
Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser		
565	570	575
Ser Asp His Tyr Val Phe Gly Cys Gly Thr Lys Val Thr Val Leu Arg		
580	585	590
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln		
595	600	605
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr		
610	615	620
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser		
625	630	635
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr		
645	650	655
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys		
660	665	670
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro		
675	680	685
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
690	695	

<210> 119

<211> 719

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 2 of bispecific, trivalent <VEGF-ANG-2> antibody molecule Avastin-LC06-C-Fab-6CSS

<400> 119

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

450				455				460							
Gly 465	Gly	Gly	Ser	Gly	Gly 470	Gly	Gly	Ser	Gly	Gly 475	Gly	Gly	Ser	Gly	Gly 480
Gly	Gly	Ser	Gln	Val 485	Gln	Leu	Val	Glu	Ser 490	Gly	Ala	Glu	Val	Lys 495	Lys
Pro	Gly	Ala	Ser 500	Val	Lys	Val	Ser	Cys 505	Lys	Ala	Ser	Gly	Tyr 510	Thr	Phe
Thr	Gly	Tyr 515	Tyr	Met	His	Trp	Val 520	Arg	Gln	Ala	Pro	Gly 525	Gln	Cys	Leu
Glu	Trp 530	Met	Gly	Trp	Ile	Asn 535	Pro	Asn	Ser	Gly	Gly 540	Thr	Asn	Tyr	Ala
Gln 545	Lys	Phe	Gln	Gly	Arg 550	Val	Thr	Met	Thr	Arg 555	Asp	Thr	Ser	Ile	Ser 560
Thr	Ala	Tyr	Met	Glu 565	Leu	Ser	Arg	Leu	Arg 570	Ser	Asp	Asp	Thr	Ala 575	Val
Tyr	Tyr	Cys	Ala 580	Arg	Ser	Pro	Asn	Pro 585	Tyr	Tyr	Tyr	Asp	Ser 590	Ser	Gly
Tyr	Tyr	Tyr 595	Pro	Gly	Ala	Phe	Asp 600	Ile	Trp	Gly	Gln	Gly 605	Thr	Met	Val
Thr	Val 610	Ser	Ser	Ala	Ser	Thr 615	Lys	Gly	Pro	Ser	Val 620	Phe	Pro	Leu	Ala
Pro 625	Ser	Ser	Lys	Ser	Thr 630	Ser	Gly	Gly	Thr	Ala 635	Ala	Leu	Gly	Cys	Leu 640
Val	Lys	Asp	Tyr	Phe 645	Pro	Glu	Pro	Val	Thr 650	Val	Ser	Trp	Asn	Ser 655	Gly
Ala	Leu	Thr	Ser 660	Gly	Val	His	Thr	Phe 665	Pro	Ala	Val	Leu	Gln 670	Ser	Ser
Gly	Leu	Tyr 675	Ser	Leu	Ser	Ser	Val 680	Val	Thr	Val	Pro	Ser 685	Ser	Ser	Leu

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
690 695 700

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
705 710 715

<210> 120

<211> 214

<212> PRT

<213> Artificial

<220>

<223> Light chain of bispecific, trivalent <VEGF-ANG-2> antibody
molecule Avastin-LC06-C-Fab-6CSS

<400> 120

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 121

<211> 459

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 1 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL

<400> 121

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr
100 105 110

Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
210 215 220

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 122

<211> 457

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 2 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL

<400> 122

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Asp Phe Thr His Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe

50						55										60
Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	Lys	Ser	Thr	Ala	Tyr	
65					70					75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Lys	Tyr	Pro	Tyr	Tyr	Tyr	Gly	Thr	Ser	His	Trp	Tyr	Phe	Asp	Val	
			100					105					110			
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Val	Ala	Ala	
		115					120					125				
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	
	130					135					140					
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	
145					150					155					160	
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	
				165					170					175		
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	
			180					185					190			
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	
		195					200					205				
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	
	210					215					220					
Phe	Asn	Arg	Gly	Glu	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
225					230					235					240	
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
				245					250					255		
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
			260					265					270			
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
		275					280					285				

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
290 295 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305 310 315 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
325 330 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
340 345 350

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
355 360 365

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
405 410 415

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 123

<211> 215

<212> PRT

<213> Artificial

<220>

<223> Light chain 1 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL

<400> 123

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 124

<211> 212
<212> PRT
<213> Artificial

<220>
<223> Light chain 2 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-CH1-CL

<400> 124

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Ser Ala Ser Thr
100 105 110

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
115 120 125

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145 150 155 160

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
165 170 175

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
180 185 190

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
195 200 205

Pro Lys Ser Cys
210

<210> 125

<211> 459

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 1 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL

<400> 125

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr
100 105 110

Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

145		150		155		160
Tyr Phe Pro Glu	Pro Val Thr Val Ser	Trp Asn Ser Gly Ala Leu Thr				
	165	170			175	
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr						
	180	185			190	
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln						
	195	200			205	
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp						
	210	215			220	
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro						
	225	230			235	240
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro						
	245	250			255	
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr						
	260	265			270	
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn						
	275	280			285	
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg						
	290	295			300	
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val						
	305	310			315	320
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser						
	325	330			335	
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys						
	340	345			350	
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp						
	355	360			365	
Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe						
	370	375			380	

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 126

<211> 439

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 2 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL

<400> 126

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ala Ser Thr
100 105 110

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
115 120 125

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145 150 155 160

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
165 170 175

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
180 185 190

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
195 200 205

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

325 330 335

Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
340 345 350

Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
370 375 380

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 127
<211> 215
<212> PRT
<213> Artificial

<220>
<223> Light chain 1 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL

<400> 127

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 128

<211> 230

<212> PRT

<213> Artificial

<220>

<223> Light chain 2 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL

<400> 128

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr

[illegible]

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 1 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL-SS

<400> 129

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr
100 105 110

Pro Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
210 215 220

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 130
<211> 439
<212> PRT
<213> Artificial

<220>
<223> Heavy chain 2 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06-VH-VL-SS

<400> 130

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ala Ser Thr
100 105 110

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
115 120 125

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145 150 155 160

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
165 170 175

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
180 185 190

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
195 200 205

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
340 345 350

Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
370 375 380

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 131
<211> 215
<212> PRT
<213> Artificial

<220>
<223> Light chain 1 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL-SS

<400> 131

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Tyr Val Phe Gly Cys Gly Thr Lys Val Thr Val Leu Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 132

<211> 230

<212> PRT

<213> Artificial

<220>

<223> Light chain 2 of bispecific, bivalent domain exchanged
<VEGF-ANG-2> antibody molecule Avastin-LC06- VH-VL-SS

<400> 132

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala
115 120 125

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
130 135 140

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
145 150 155 160

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
165 170 175

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
180 185 190

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
195 200 205

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
210 215 220

Phe Asn Arg Gly Glu Cys
225 230

<210> 133

<211> 706

<212> PRT

<213> Artificial

<220>

<223> Heavy chain 1 of bispecific, bivalent ScFab-Fc fusion
<VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFab

<400> 133

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gln Val Gln Leu Val Glu Ser Gly Ala
245 250 255

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
260 265 270

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
275 280 285

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
290 295 300

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
305 310 315 320

Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp
325 330 335

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr
340 345 350

Asp Ser Ser Gly Tyr Tyr Tyr Pro Gly Ala Phe Asp Ile Trp Gly Gln
355 360 365

Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
370 375 380

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
385 390 395 400

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
405 410 415

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
420 425 430

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
435 440 445

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
450 455 460

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
465 470 475 480

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
485 490 495

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
500 505 510

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
515 520 525

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
530 535 540

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
545 550 555 560

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
565 570 575

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
580 585 590

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
595 600 605

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
610 615 620

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
625 630 635 640

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
645 650 655

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
660 665 670

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
675 680 685

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

690 695 700

Gly Lys
705

<210> 134
<211> 699
<212> PRT
<213> Artificial

<220>
<223> Heavy chain 2 of bispecific, bivalent ScFab-Fc fusion
<VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFab

<400> 134

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	165	170	175
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	180	185	190
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	195	200	205
Phe	Asn	Arg	Gly	Glu	Cys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	210	215	220
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	225	230	235
Gly	Gly	Gly	Ser	Gly	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	245	250	255
Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	260	265	270
Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	275	280	285
Lys	Gly	Leu	Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	290	295	300
Thr	Tyr	Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	305	310	315
Ser	Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	325	330	335
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	Ser	340	345	350
His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	355	360	365
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	370	375	380

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
385 390 395 400

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
405 410 415

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
420 425 430

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
435 440 445

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
450 455 460

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
465 470 475 480

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
485 490 495

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
500 505 510

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
515 520 525

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
530 535 540

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
545 550 555 560

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
565 570 575

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
580 585 590

Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp
595 600 605

Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe

610	615	620
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
625	630	635 640
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
	645	650 655
Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly		
	660	665 670
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
	675	680 685
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	690	695
<210> 135		
<211> 706		
<212> PRT		
<213> Artificial		
<220>		
<223> Heavy chain 1 of bispecific, bivalent ScFab-Fc fusion		
<VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFabSS		
<400> 135		
Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln		
1	5	10 15
Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val		
	20	25 30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr		
	35	40 45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser		
	50	55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly		
	65	70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His		
	85	90 95

Tyr Val Phe Gly Cys Gly Thr Lys Val Thr Val Leu Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gln Val Gln Leu Val Glu Ser Gly Ala
245 250 255

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
260 265 270

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
275 280 285

Gly Gln Cys Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
290 295 300

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
305 310 315 320

Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp
325 330 335

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Pro Asn Pro Tyr Tyr Tyr
340 345 350

Asp Ser Ser Gly Tyr Tyr Tyr Pro Gly Ala Phe Asp Ile Trp Gly Gln
355 360 365

Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
370 375 380

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
385 390 395 400

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
405 410 415

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
420 425 430

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
435 440 445

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
450 455 460

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
465 470 475 480

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
485 490 495

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
500 505 510

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
515 520 525

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
530 535 540

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

545 550 555 560

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
565 570 575

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
580 585 590

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
595 600 605

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
610 615 620

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
625 630 635 640

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
645 650 655

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
660 665 670

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
675 680 685

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
690 695 700

Gly Lys
705

<210> 136
<211> 699
<212> PRT
<213> Artificial

<220>
<223> Heavy chain 2 of bispecific, bivalent ScFab-Fc fusion
<VEGF-ANG-2> antibody molecule Avastin-LC06-N-scFabSS

<400> 136

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Gly Gly Gly Ser Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
260 265 270

Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly
275 280 285

Lys Cys Leu Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro
290 295 300

Thr Tyr Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr
305 310 315 320

Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
325 330 335

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser
340 345 350

His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
355 360 365

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
370 375 380

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
385 390 395 400

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
405 410 415

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
420 425 430

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
435 440 445

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
450 455 460

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro

465				470				475				480			
Cys	Pro	Ala	Pro	Glu 485	Leu	Leu	Gly	Gly	Pro 490	Ser	Val	Phe	Leu	Phe 495	Pro
Pro	Lys	Pro	Lys 500	Asp	Thr	Leu	Met	Ile 505	Ser	Arg	Thr	Pro	Glu 510	Val	Thr
Cys	Val	Val 515	Val	Asp	Val	Ser	His 520	Glu	Asp	Pro	Glu	Val 525	Lys	Phe	Asn
Trp	Tyr 530	Val	Asp	Gly	Val	Glu 535	Val	His	Asn	Ala	Lys 540	Thr	Lys	Pro	Arg
Glu 545	Glu	Gln	Tyr	Asn	Ser 550	Thr	Tyr	Arg	Val	Val 555	Ser	Val	Leu	Thr	Val 560
Leu	His	Gln	Asp	Trp 565	Leu	Asn	Gly	Lys	Glu 570	Tyr	Lys	Cys	Lys	Val 575	Ser
Asn	Lys	Ala	Leu 580	Pro	Ala	Pro	Ile	Glu 585	Lys	Thr	Ile	Ser	Lys 590	Ala	Lys
Gly	Gln	Pro 595	Arg	Glu	Pro	Gln	Val 600	Cys	Thr	Leu	Pro	Pro 605	Ser	Arg	Asp
Glu 610	Leu	Thr	Lys	Asn	Gln	Val 615	Ser	Leu	Ser	Cys	Ala 620	Val	Lys	Gly	Phe
Tyr 625	Pro	Ser	Asp	Ile	Ala 630	Val	Glu	Trp	Glu	Ser 635	Asn	Gly	Gln	Pro	Glu 640
Asn	Asn	Tyr	Lys	Thr 645	Thr	Pro	Pro	Val	Leu 650	Asp	Ser	Asp	Gly	Ser 655	Phe
Phe	Leu	Val	Ser 660	Lys	Leu	Thr	Val	Asp 665	Lys	Ser	Arg	Trp	Gln 670	Gln	Gly
Asn	Val	Phe 675	Ser	Cys	Ser	Val	Met 680	His	Glu	Ala	Leu	His 685	Asn	His	Tyr
Thr	Gln 690	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					

