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(54) Title: IL22 IMMUNOCONJUGATES

(57) Abstract: The application relates to a conjugate comprising interleukin-22 (IL22) and an antibody molecule. The antibody molecule preferably binds an antigen associated with angiogenesis, such as the ED-A isoform of fibronectin. In particular, the application relates to the therapeutic use of such conjugates in the treatment of a disease/disorder, such as autoimmune diseases, including inflammatory bowel disease (IBD).

IL22 Immunoconjugates

Field of the Invention

The present invention relates to a conjugate comprising interleukin-22 (IL22) and an antibody molecule. The antibody molecule preferably binds an antigen associated with angiogenesis, such as the ED-A isoform of fibronectin. In particular, the present invention relates to the therapeutic use of such conjugates in the treatment of a disease/disorder, such as autoimmune diseases, including inflammatory bowel disease (IBD).

Background to the Invention

Cytokines are key mediators of innate and adaptive immunity. Many cytokines have been used for therapeutic purposes in patients, such as those with advanced cancer, but their administration is typically associated with severe toxicity, hampering dose escalation to therapeutically active regimens and their development as anticancer drugs, for example. To overcome these problems, the use of 'immunocytokines' (i.e. cytokines fused to antibodies or antibody fragments) has been proposed, with the aim to concentrate the immune-system stimulating activity at the site of disease while sparing normal tissues (Savage *et al.*, 1993; Schrama *et al.*, 2006; Neri *et al.* 2005; Dela Cruz *et al.*, 2004; Reisfeld *et al.*, 1997; Konterman *et al.*, 2012).

For example, several pro-inflammatory immunocytokines (e.g., those based on IL2, IL12, IL15, TNF) have been shown to display a potent anti-tumoural effect in mouse models of cancer (Borsi *et al.* 2003; Carnemolla *et al.*, 2002; Frey *et al.*, 2010; Kaspar *et al.*, 2007; Pasche *et al.*, 2012). In contrast, anti-inflammatory immunocytokines (e.g., those based on IL10) have been shown to be capable of conferring a therapeutic benefit in mouse models of chronic inflammatory conditions (rheumatoid arthritis, endometriosis [Schwager *et al.* 2011; Schwager *et al.*, 2009]) but have no impact on tumour growth.

Antibodies specific to splice-isoforms of fibronectin and of tenascin-C have been described as vehicles for pharmacodelivery applications, as these antigens are virtually undetectable in the normal healthy adult (with the exception of the placenta, endometrium and some vessels in the ovaries) while being strongly expressed in the majority of solid tumours and lymphomas, as well as other diseases (Brack *et al.*, 2006; Pedretti *et al.*, 2009; Schliemann *et al.* 2009). For example, antibodies F8 and L19, specific to the alternatively-spliced EDA

and EDB domains of fibronectin, respectively, and anti-tenascin C antibody F16 (Brack *et al.* 2006, Villa *et al.*, 2008, Viti *et al.*, 1999), have been employed for the development of armed antibodies, some of which have begun clinical testing in oncology and in rheumatology (Eigentler *et al.*, 2011; Papadia *et al.*, 2012). The tumour targeting properties of these antibodies have also been documented in mouse models of cancer and in patients

Interleukin 22 (IL22) is a 17 kDa globular cytokine belonging to the IL-10 family, which is mainly secreted by NK cells, dendritic cells and T-cells (Murphy 2012). It contains two intramolecular disulfide bonds and three N-linked glycosylation sites. Biological functions of IL22 include involvement in tissue protection, autoimmunity and inflammation. Secreted by lamina propria effector T-cells in the intestine, it induces mucin production, antimicrobial, proliferative and antiapoptotic pathways, which prevent tissue damage and promote epithelial repair.(Li et al. 2014). We investigated whether IL22 could be successfully fused to a vascular targeting antibody.

Cytokines can be conjugated to antibody molecules to produce immunocytokines as mentioned above. However, not all immunocytokines retain, for example, the *in vivo* targeting properties of the parental antibody (Pasche & Neri 2012) or expected activities. The preparation of immunocytokines with therapeutic effects, such as anti-inflammatory activity, is therefore far from straightforward.

The preparation of conjugates comprising a mouse IgG1 Fc fused to the N-terminus or C-terminus of mouse IL-22 is described in Smith et al. 2013. These conjugates were prepared with a view to providing a more potent and longer-lasting IL-22R agonist compared with rIL-22. The purpose of the Fc region in this instance was therefore not to target IL22 to regions of disease as was the case with the immunocytokines described in the preceding paragraph.

Statements of Invention

The present inventors have shown that IL22 can be conjugated to antibodies, which bind ED-A, while retaining not only the targeting properties of the unconjugated antibody but also the biological activity of IL22.

In one aspect, the present invention therefore relates to a conjugate comprising interleukin-22 (IL22) and an antibody molecule, or antigen-binding fragment thereof, which binds an antigen associated with angiogenesis. The present invention also relates to a nucleic acid

molecule encoding such a conjugate, as well as an expression vector comprising such a nucleic acid. A host cell comprising such a vector is also contemplated.

The present invention also relates to a conjugate of the invention for use in a method for treatment of the human body by therapy. For example, the invention relates to a conjugate of the invention for use in a method of treating an autoimmune disease in a patient and to a conjugate of the invention for use in delivering IL22 to sites of autoimmune disease in a patient is also contemplated. A method of treating of an autoimmune disease in a patient, the method comprising administering a therapeutically effective amount of a conjugate of the invention to the patient also forms part of the inventions, as does a method of delivering IL22 to sites of autoimmune disease in a patient comprising administering the conjugate of the invention to the patient.

The present invention further relates to a conjugate of the invention for use in a method of treating an inflammation in a patient and to a conjugate of the invention for use in delivering IL22 to sites of inflammation in a patient is also contemplated. A method of treating inflammation in a patient, the method comprising administering a therapeutically effective amount of a conjugate of the invention to the patient also forms part of the inventions, as does a method of delivering IL22 to sites of inflammation in a patient comprising administering the conjugate of the invention to the patient. The inflammation is preferably the result of an inflammatory disease and/or disorder.

Brief Description of the Figures

Figure 1 shows a schematic diagram of the mammalian cell expression vectors used to express the mulL22-F8 (**Figure 1A**) and F8-mulL22 conjugates (**Figure 1B**).

Figure 2 A and **B** show the results of an SDS-PAGE analysis of the mulL22-F8 and F8-mulL22 conjugates, respectively, under reducing and non-reducing conditions (lanes 1 and 2, respectively), and in the presence of PNGase F (lanes 3 and 4, respectively). **C** and **D** show the results of size exclusion chromatography of the mulL22-F8 and F8-mulL22 conjugates, respectively. The fact that only single peaks were visible confirms the homogeneity of the conjugate preparations.

Figure 3 A and B, respectively, show the results of surface plasmon resonance (Biacore) using an ED-A coated chip and the mulL22-F8 and F8-mulL22 fusion proteins, respectively,

and demonstrate that the mulL22-F8 and F8-mulL22 fusion proteins are capable of binding ED-A. C and D, respectively, show the results of an ELISA using ED-A coated wells and the mulL22-F8 and F8-mulL22 fusion proteins, respectively, and further confirms that the mulL22-F8 and F8-mulL22 fusion proteins are capable of binding ED-A.

Figure 4 shows the results of a bioactivity assay using the F8-mulL22 and mulL22-F8 fusion proteins and demonstrates that the mulL22 in the F8-mulL22 and mulL22-F8 fusion proteins retains the ability to induce phosphorylation of STAT3 upon binding to the receptor on colon carcinoma cells. The concentration of the fusion proteins employed in the experiments (5 µg/ml, 0.5 µg/ml, and 0.05 µg/ml) is indicated at the top of the figure. "O" indicates the lanes comprising negative controls. The location of the band corresponding to phosphorylated STAT3 is indicated.

Figure 5 shows the results of tumour targeting studies using the mulL22-F8 and F8-mulL22 fusion proteins in F9 tumour-bearing mice. The fusion proteins primarily localized to the tumour tissue, which is known to express ED-A in the tumour neovasculature, with minimal amounts of fusion protein found in other (healthy) tissues of the mice, which are not expected to express ED-A. The y-axis shows the percentage of the injected dose of the fusion protein per gram of tissue (%ID/g).

Detailed Description

Antibody Molecule

This describes an immunoglobulin whether natural or partly or wholly synthetically produced. The term also relates to any polypeptide or protein comprising an antibody antigen-binding site. It must be understood here that the antibody molecules may have been isolated or obtained by purification from natural sources, or else obtained by genetic recombination, or by chemical synthesis, and that they can contain unnatural amino acids.

As antibodies can be modified in a number of ways, the term "antibody molecule" should be construed as covering any specific binding member or substance having an antibody antigen-binding site with the required specificity and/or binding to antigen. Thus, this term covers antibody fragments, in particular antigen-binding fragments, and derivatives, including any polypeptide comprising an antibody antigen-binding site, whether natural or wholly or partially synthetic. Chimeric molecules comprising an antibody antigen-binding

site, or equivalent, fused to another polypeptide (e.g. belonging to another antibody class or subclass) are therefore included. Cloning and expression of chimeric antibodies are described in EP-A-0120694 and EP-A-0125023, and a large body of subsequent literature.

As mentioned above, fragments of a whole antibody can perform the function of binding antigens. Examples of binding fragments are (i) the Fab fragment consisting of VL, VH, CL and CH1 domains; (ii) the Fd fragment consisting of the VH and CH1 domains; (iii) the Fv fragment consisting of the VL and VH domains of a single antibody; (iv) the dAb fragment (Ward *et al.* (1989) Nature 341, 544-546; McCafferty *et al.*, (1990) Nature, 348, 552-554; Holt *et al.* (2003) Trends in Biotechnology 21, 484-490), which consists of a VH or a VL domain; (v) isolated CDR regions; (vi) F(ab')2 fragments, a bivalent fragment comprising two linked Fab fragments (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by an amino acid linker which allows the two domains to associate to form an antigen binding site (Bird *et al.* (1988) Science, 242, 423-426; Huston *et al.* (1988) PNAS USA, 85, 5879-5883); (viii) bispecific single chain Fv dimers (PCT/US92/09965) and (ix) "diabodies", multivalent or multispecific fragments constructed by gene fusion (WO94/13804; Holliger *et al.* (1993a), Proc. Natl. Acad. Sci. USA 90 6444-6448). Fv, scFv or diabody molecules may be stabilized by the incorporation of disulphide bridges linking the VH and VL domains (Reiter *et al.* (1996), Nature Biotech, 14, 1239-1245). Minibodies comprising a scFv joined to a CH3 domain may also be made (Hu *et al.* (1996), Cancer Res., 56(13):3055-61). Other examples of binding fragments are Fab', which differs from Fab fragments by the addition of a few residues at the carboxyl terminus of the heavy chain CH1 domain, including one or more cysteines from the antibody hinge region, and Fab'-SH, which is a Fab' fragment in which the cysteine residue(s) of the constant domains bear a free thiol group.

The half-life of antibody molecules for use in the present invention, or conjugates of the invention, may be increased by a chemical modification, especially by PEGylation, or by incorporation in a liposome.

An antibody molecule for use in the present invention preferably is, or comprises, an scFv. Diabodies, for example, comprise two scFv molecules. Most preferably, the antibody molecule for use in the present invention is a diabody. Diabodies and scFvs do not comprise an antibody Fc region, thus potentially reducing the effects of anti-idiotypic reactions.

Where the antibody molecule is a diabody, the VH and VL domains are preferably linked by a 5 to 12 amino acid linker. A diabody comprises two VH-VL molecules which associate to form a dimer. The VH and VL domains of each VH-VL molecule are preferably linked by a 5 to 12 amino acid linker. For example, the VH and VL domains may be linked by an amino acid linker which is 5, 6, 7, 8, 9, 10, 11, or 12 amino acid in length. Preferably, the amino acid linker is 5 amino acids in length. Suitable linker sequences are known in the art and include the linker sequence set forth in SEQ ID NO: 9.

Where the antibody molecule is an scFv, the VH and VL domains of the antibody are preferably linked by a 14 to 20 amino acid linker. For example, the VH and VL domains may be linked by an amino acid linker which is 14, 15, 16, 17, 18, 19, or 20 amino acid in length. Suitable linker sequences are known in the art and include the linker sequence set forth in SEQ ID NO: 43.

The present inventors have shown that a conjugate comprising IL22 and an antibody molecule which binds the Extra-Domain A (ED-A) of fibronectin can successfully, and specifically, target tumour tissue *in vivo*. The ED-A isoform of fibronectin is known to be expressed in neovasculature, such as the neovasculature found in tumours, but not in healthy tissues. This data therefore provides evidence that a conjugate comprising IL22 and an antibody molecule which binds the ED-A of fibronectin can be used to target sites of angiogenesis. IL22 conjugates therefore are suitable for treating inflammation and autoimmune diseases in an individual. Many autoimmune diseases, as well as diseases associated with inflammation, are known to involve and/or be characterised by angiogenesis.

It is expected that other conjugates comprising IL22 and an antibody molecule which binds an antigen associated with angiogenesis will similarly be suitable to target IL22 to sites of angiogenesis and thus find application in the treatment of autoimmune diseases and/or inflammation. Many such antigens are known in the art, as are antibodies capable of binding such antigens. In additions, antibodies against a given antigen can be generated using well-known methods such as those described in the present application. In one example, the antigen may be an extra-cellular matrix component associated with angiogenesis, such as a fibronectin, including the Extra-Domain A (ED-A) isoform of fibronectin (A-FN), the Extra-Domain B (ED-B) isoform of fibronectin (B-FN), tenascin C, the ED-A of fibronectin, the ED-B of fibronectin, or the A1 Domain of Tenascin C. Antibodies which bind the ED-A of fibronectin, and thus also A-FN, are known in the art and include antibody F8. Antibodies which bind the ED-B of fibronectin, or the A1 Domain of Tenascin C (and thus also the B-FN

and tenascin C) are also known in the art and include antibodies L19 and F16, respectively. Antibodies which bind the ED-B of fibronectin, or the A1 Domain of Tenascin C, including antibodies L19 and F16, have been shown to be capable of specifically targeting neovasculature *in vivo*. It is thus expected that conjugates comprising IL22 and an antibody molecule which binds B-FN, tenascin C, the ED-B of fibronectin, or the A1 Domain of Tenascin C, will be capable of targeting IL22 to neovasculature, in the same way as a conjugate comprising IL22 and an antibody molecule which binds A-FN, as demonstrated using antibody F8 herein and thus find application in the treatment of autoimmune diseases and/or inflammation.

Thus an antibody molecule for use in the invention binds an antigen associated with angiogenesis. Preferably, antibody molecule for use in the invention binds an extra-cellular matrix component associated with angiogenesis, such as A-FN, B-FN, tenascin C, the ED-A of fibronectin, the ED-B of fibronectin, or the A1 Domain of Tenascin C. More preferably, an antibody molecule for use in the invention binds the A-FN or the ED-A of fibronectin. Most preferably, an antibody molecule for use in the invention binds the ED-A of fibronectin.

In a preferred embodiment, an antibody molecule for use in the invention may have the CDRs and/or the VH and/or VL domains of antibodies F8, L19 or F16 described herein. An antibody molecule for use in the invention preferably has the CDRs of antibody F8 set forth in SEQ ID NOs 1-6. More preferably, an antibody for use in the invention comprises the VH and/or VL domains of antibody F8 set forth in SEQ ID NOs 7 and 8. Yet more preferably, an antibody for use in the invention comprises the VH and VL domains of antibody F8 set forth in SEQ ID NOs 7 and 8. The F8 antibody is preferably in diabody or scFv format, most preferably in diabody format. Where the F8 antibody is in diabody format, the antibody molecule for use in the invention preferably has the amino acid sequence set forth in SEQ ID NO: 10.

An antibody molecule for use in the invention may bind the A-FN and/or the ED-A of fibronectin, with the same affinity as anti-ED-A antibody F8 e.g. in diabody format, or with an affinity that is better. An antibody molecule for use in the invention may bind the B-FN and/or the ED-B of fibronectin, with the same affinity as anti-ED-B antibody L19 e.g. in diabody format, or with an affinity that is better. An antibody molecule for use in the invention may bind the Tenascin C and/or the A1 domain of tenascin C, with the same affinity as anti-ED-A antibody F16 e.g. in diabody format, or with an affinity that is better.

An antibody molecule for use in the invention may bind to the same epitope on A-FN and/or the ED-A of fibronectin as anti-ED-A antibody F8. An antibody molecule for use in the invention may bind to the same epitope on B-FN and/or the ED-B of fibronectin as anti-ED-A antibody L19. An antibody molecule for use in the present invention may bind to the same epitope on tenascin C and/or the A1 domain of tenascin C as antibody F16.

Variants of antibody molecules disclosed herein may be produced and used in the present invention. The techniques required to make substitutions within amino acid sequences of CDRs, antibody VH or VL domains, in particular the framework regions of the VH and VL domains, and antibody molecules generally are available in the art. Variant sequences may be made, with substitutions that may or may not be predicted to have a minimal or beneficial effect on activity, and tested for ability to bind A-FN and/or the ED-A of fibronectin, B-FN and/or the ED-B of fibronectin, tenascin C and/or the A1 domain of tenascin C, and/or for any other desired property.

It is contemplated that from 1 to 5, e.g. from 1 to 4, including 1 to 3, or 1 or 2, or 3 or 4, amino acid alterations (addition, deletion, substitution and/or insertion of an amino acid residue) may be made in one or more of the CDRs and/or the VH and/or the VL domain of an antibody molecule as described herein. Thus, an antibody molecule which binds the FN-A, FN-B, or tenascin C, may comprise the CDRs and/or the VH and/or the VL domain of antibody F8, L19, or F16 described herein with 5 or fewer, for example, 5, 4, 3, 2 or 1 amino acid alterations within the CDRs and/or the VH and/or the VL domain. For example, an antibody molecule which binds the FN-A, FN-B, or tenascin C, may comprise the VH and/or the VL domain of antibody F8, L19, or F16 described herein with 5 or fewer, for example, 5, 4, 3, 2 or 1 amino acid alterations within the framework region of the VH and/or VL domain. An antibody molecule that binds the FN-A or ED-A of fibronectin, as referred to herein, thus may comprise the VH domain shown in SEQ ID NO: 7 and/or the VL domain set forth in SEQ ID NO: 8 with 5 or fewer, for example, 5, 4, 3, 2 or 1 amino acid alterations within the framework region of the VH and/or VL domain. Such an antibody molecule may bind the ED-A isoform or ED-A of fibronectin with the same or substantially the same, affinity as an antibody molecule comprising the VH domain set forth in SEQ ID NO: 7 and the VL domain shown in SEQ ID NO: 8 or may bind the ED-A isoform or ED-A of fibronectin with a higher affinity than an antibody molecule comprising the VH domain set forth in SEQ ID NO: 7 and the VL domain set forth in SEQ ID NO: 8.

An antibody molecule for use in the invention may comprise a VH and/or VL domain that has at least 70%, more preferably one of at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, sequence identity to the VH and/or VL domain, as applicable, of antibody F8, L19, or F16 set forth in SEQ ID NOs 7, 8, 31, 32, 40, and 41. An antibody molecule for use in the invention may have at least 70%, more preferably one of at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, sequence identity to the amino acid sequence of the F8, L19, or F16 antibodies set forth in SEQ ID NOs 10, 33, and 42, respectively.

Sequence identity is commonly defined with reference to the algorithm GAP (Wisconsin GCG package, Accelerys Inc, San Diego USA). GAP uses the Needleman and Wunsch algorithm to align two complete sequences that maximizes the number of matches and minimizes the number of gaps. Generally, default parameters are used, with a gap creation penalty = 12 and gap extension penalty = 4. Use of GAP may be preferred but other algorithms may be used, e.g. BLAST (which uses the method of Altschul et al. (1990) J. Mol. Biol. 215: 405-410), FASTA (which uses the method of Pearson and Lipman (1988) PNAS USA 85: 2444-2448), or the Smith-Waterman algorithm (Smith and Waterman (1981) J. Mol Biol. 147: 195-197), or the TBLASTN program, of Altschul et al. (1990) supra, generally employing default parameters. In particular, the psi-Blast algorithm (Nucl. Acids Res. (1997) 25 3389-3402) may be used.

Antigen-binding site

This describes the part of a molecule that binds to and is complementary to all or part of the target antigen. In an antibody molecule it is referred to as the antibody antigen-binding site, and comprises the part of the antibody that binds to and is complementary to all or part of the target antigen. Where an antigen is large, an antibody may only bind to a particular part of the antigen, which part is termed an epitope. An antibody antigen-binding site may be provided by one or more antibody variable domains. An antibody antigen-binding site preferably comprises an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH).

An antigen binding site may be provided by means of arrangement of complementarity determining regions (CDRs). The structure for carrying a CDR or a set of CDRs will generally be an antibody heavy or light chain sequence or substantial portion thereof in which the CDR or set of CDRs is located at a location corresponding to the CDR or set of CDRs of naturally occurring VH and VL antibody variable domains encoded by rearranged

immunoglobulin genes. The structures and locations of immunoglobulin variable domains may be determined by reference to Kabat *et al.* (1987) (Sequences of Proteins of Immunological Interest. 4th Edition. US Department of Health and Human Services.), and updates thereof, now available on the Internet (at immuno.bme.nwu.edu or find "Kabat" using any search engine).

By CDR region or CDR, it is intended to indicate the hypervariable regions of the heavy and light chains of the immunoglobulin as defined by Kabat *et al.* (1987) Sequences of Proteins of Immunological Interest, 4th Edition, US Department of Health and Human Services (Kabat *et al.*, (1991a), Sequences of Proteins of Immunological Interest, 5th Edition, US Department of Health and Human Services, Public Service, NIH, Washington, and later editions). An antibody typically contains 3 heavy chain CDRs and 3 light chain CDRs. The term CDR or CDRs is used here in order to indicate, according to the case, one of these regions or several, or even the whole, of these regions which contain the majority of the amino acid residues responsible for the binding by affinity of the antibody for the antigen or the epitope which it recognizes.

Among the six short CDR sequences, the third CDR of the heavy chain (HCDR3) has a greater size variability (greater diversity essentially due to the mechanisms of arrangement of the genes which give rise to it). It can be as short as 2 amino acids although the longest size known is 26. Functionally, HCDR3 plays a role in part in the determination of the specificity of the antibody (Segal *et al.*, (1974), PNAS, 71:4298-4302; Amit *et al.*, (1986), Science, 233:747-753; Chothia *et al.*, (1987), J. Mol. Biol., 196:901-917; Chothia *et al.*, (1989), Nature, 342:877-883; Caton *et al.*, (1990), J. Immunol., 144:1965-1968; Sharon *et al.*, (1990a), PNAS, 87:4814-4817; Sharon *et al.*, (1990b), J. Immunol., 144:4863-4869; Kabat *et al.*, (1991b), J. Immunol., 147:1709-1719).

An antigen binding site forming part of an antibody molecule for use in the invention preferably has the CDRs of antibody F8 set forth in SEQ ID NOs 1-6, the CDRs of antibody L19 set forth in SEQ ID NOs 25-30, or the CDRs of antibody F16 set forth in SEQ ID NOs 34-39. Most preferably, an antigen binding site forming part of an antibody molecule for use in the invention has the CDRs of antibody F8 set forth in SEQ ID NOs 1-6.

Preparation and Selection of Antibody Molecules

Various methods are available in the art for obtaining antibodies molecules against a target antigen. The antibody molecules for use in the present invention are preferably monoclonal antibodies, especially of human, murine, chimeric or humanized origin, which can be obtained according to the standard methods well known to the person skilled in the art. An antibody molecule for use in the present invention is most preferably a human antibody molecule.

It is possible to take monoclonal and other antibodies and use techniques of recombinant DNA technology to produce other antibodies or chimeric molecules that bind the target antigen. Such techniques may involve introducing DNA encoding the immunoglobulin variable region, or the CDRs, of an antibody molecule to the constant regions, or constant regions plus framework regions, of a different immunoglobulin. See, for instance, EP-A-184187, GB 2188638A or EP-A-239400, and a large body of subsequent literature. A hybridoma or other cell producing an antibody may also be subject to genetic mutation or other changes, which may or may not alter the binding specificity of antibodies produced.

Techniques available in the art of antibody engineering have made it possible to isolate human and humanised antibodies. For example, human hybridomas can be made as described by Kontermann & Dubel (2001), S, *Antibody Engineering,* Springer-Verlag New York, LLC; ISBN: 3540413545. Phage display, another established technique for generating specific binding members has been described in detail in many publications such as WO92/01047 (discussed further below) and US patents US5969108, US5565332, US5733743, US5858657, US5871907, US5872215, US5885793, US5962255, US6140471, US6172197, US6225447, US6291650, US6492160, US6521404 and Kontermann & Dubel (2001), S, *Antibody Engineering,* Springer-Verlag New York, LLC; ISBN: 3540413545. Transgenic mice in which the mouse antibody genes are inactivated and functionally replaced with human antibody genes while leaving intact other components of the mouse immune system, can be used for isolating human antibodies (Mendez *et al.*, (1997), Nature Genet, 15(2): 146–156).

In general, for the preparation of monoclonal antibodies or their functional fragments, especially of murine origin, it is possible to refer to techniques which are described in particular in the manual "Antibodies" (Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor N.Y., pp. 726, 1988) or to the technique

of preparation from hybridomas described by Kohler and Milstein, 1975, Nature, 256:495-497.

Monoclonal antibodies can be obtained, for example, from an animal cell immunized against the an antigen associated with angiogenesis, such as A-FN, B-FN, tenascin C, the ED-A of fibronectin, the ED-B of fibronectin, or the A1 Domain of Tenascin C, according to the usual working methods, by genetic recombination starting with a nucleic acid sequence contained in the cDNA sequence coding for A-FN, B-FN, or tenascin C, or fragment thereof, or by peptide synthesis starting from a sequence of amino acids comprised in the peptide sequence of the A-FN, B-FN, or tenascin C, and/or a fragment thereof.

Synthetic antibody molecules may be created by expression from genes generated by means of oligonucleotides synthesized and assembled within suitable expression vectors, for example as described by Knappik *et al.* (2000) J. Mol. Biol. 296, 57-86 or Krebs *et al.* (2001) Journal of Immunological Methods, 254 67–84.

Alternatively, one or more antibody molecules for an antigen associated with angiogenesis, such as the A-FN, the ED-A, B-FN, the ED-B, tenascin C, or the A1 domain of tenascin C may be obtained by bringing into contact a library of antibody molecules and the antigen or a fragment thereof, e.g. a fragment comprising or consisting of ED-A, ED-B, or the A1 domain of tenascin C, or a peptide fragment thereof, and selecting one or more antibody molecules of the library able to bind the antigen.

An antibody library may be screened using Iterative Colony Filter Screening (ICFS). In ICFS, bacteria containing the DNA encoding several binding specificities are grown in a liquid medium and, once the stage of exponential growth has been reached, some billions of them are distributed onto a growth support consisting of a suitably pre-treated membrane filter which is incubated until completely confluent bacterial colonies appear. A second trap substrate consists of another membrane filter, pre-humidified and covered with the desired antigen.

The trap membrane filter is then placed onto a plate containing a suitable culture medium and covered with the growth filter with the surface covered with bacterial colonies pointing upwards. The sandwich thus obtained is incubated at room temperature for about 16 h. It is thus possible to obtain the expression of the genes encoding antibody fragments scFv having a spreading action, so that those fragments binding specifically with the antigen

which is present on the trap membrane are trapped. The trap membrane is then treated to point out bound antibody fragments scFv with colorimetric techniques commonly used to this purpose.

The position of the coloured spots on the trap filter allows one to go back to the corresponding bacterial colonies which are present on the growth membrane and produced the antibody fragments trapped. Such colonies are gathered and grown and the bacteria-a few millions of them are distributed onto a new culture membrane repeating the procedures described above. Analogous cycles are then carried out until the positive signals on the trap membrane correspond to single positive colonies, each of which represents a potential source of monoclonal antibody fragments directed against the antigen used in the selection. ICFS is described in e.g. WO0246455.

A library may also be displayed on particles or molecular complexes, e.g. replicable genetic packages such bacteriophage (e.g. T7) particles, or other *in vitro* display systems, each particle or molecular complex containing nucleic acid encoding the antibody VH variable domain displayed on it, and optionally also a displayed VL domain if present. Phage display is described in WO92/01047 and e.g. US patents US5969108, US5565332, US5733743, US5858657, US5871907, US5872215, US5885793, US5962255, US6140471, US6172197, US6225447, US6291650, US6492160 and US6521404.

Following selection of antibody molecules able to bind the antigen and displayed on bacteriophage or other library particles or molecular complexes, nucleic acid may be taken from a bacteriophage or other particle or molecular complex displaying a said selected antibody molecule. Such nucleic acid may be used in subsequent production of an antibody molecule or an antibody VH or VL variable domain by expression from nucleic acid with the sequence of nucleic acid taken from a bacteriophage or other particle or molecular complex displaying a said selected antibody molecule.

Ability to bind an antigen associated with angiogenesis, such as the A-FN, B-FN, the ED-A, or the ED-B of fibronectin, tenascin C or the A1 domain of tenascin C or other target antigen or isoform may be further tested, e.g. ability to compete with an antibody specific for the A-FN, B-FN, the ED-A, or the ED-B of fibronectin, tenascin C or the A1 domain of tenascin C, such as antibody F8, L19, or F16.

Novel VH or VL regions carrying CDR-derived sequences for use in the invention may be also generated using random mutagenesis of one or more selected VH and/or VL genes to generate mutations within the entire variable domain. In some embodiments one or two amino acid substitutions are made within an entire variable domain or set of CDRs. Another method that may be used is to direct mutagenesis to CDR regions of VH or VL genes.

Variable domains employed in the invention may be obtained or derived from any germ-line or rearranged human variable domain, or may be a synthetic variable domain based on consensus or actual sequences of known human variable domains. A variable domain can be derived from a non-human antibody. A CDR sequence for use in the invention (e.g. CDR3) may be introduced into a repertoire of variable domains lacking a CDR (e.g. CDR3), using recombinant DNA technology. For example, Marks *et al.* (1992) describe methods of producing repertoires of antibody variable domains in which consensus primers directed at or adjacent to the 5' end of the variable domain area are used in conjunction with consensus primers to the third framework region of human VH genes to provide a repertoire of VH variable domains lacking a CDR3. Marks *et al.* further describe how this repertoire may be combined with a CDR3 of a particular antibody. Using analogous techniques, the CDR3-derived sequences of the present invention may be shuffled with repertoires of VH or VL domains lacking a CDR3, and the shuffled complete VH or VL domains combined with a cognate VL or VH domain to provide antibody molecules for use in the invention. The repertoire may then be displayed in a suitable host system such as the phage display system of WO92/01047, or any of a subsequent large body of literature, including Kay, Winter & McCafferty (1996), so that suitable antibody molecules may be selected. A repertoire may consist of from anything from 10^4 individual members upwards, for example at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9 or at least 10^{10} members.

An antigen associated with angiogenesis, such as the A-FN, B-FN, the ED-A, or the ED-B of fibronectin, tenascin C or the A1 domain of tenascin C may be used in a screen for antibody molecules, e.g. antibody molecules, for use in the invention. The screen may a screen of a repertoire as disclosed elsewhere herein.

Similarly, one or more, or all three CDRs may be grafted into a repertoire of VH or VL domains that are then screened for an antibody molecule or antibody molecules for an antigen associated with angiogenesis, such as A-FN, B-FN, the ED-A, or the ED-B of fibronectin, tenascin C or the A1 domain of tenascin C. One or more of the HCDR1, HCDR2 and HCDR3 of antibody F8, L19, or F16, or the set of HCDRs of antibody F8, L19, or F16

may be employed, and/or one or more of the LCDR1, LCDR2 and LCDR3 of antibody F8, L19, or F16 the set of LCDRs of antibody F8, L19, or F16 may be employed.

A substantial portion of an immunoglobulin variable domain may comprise at least the three CDR regions, together with their intervening framework regions. The portion may also include at least about 50% of either or both of the first and fourth framework regions, the 50% being the C-terminal 50% of the first framework region and the N-terminal 50% of the fourth framework region. Additional residues at the N-terminal or C-terminal end of the substantial part of the variable domain may be those not normally associated with naturally occurring variable domain regions. For example, construction of antibody molecules of the present invention made by recombinant DNA techniques may result in the introduction of N- or C-terminal residues encoded by linkers introduced to facilitate cloning or other manipulation steps. Other manipulation steps include the introduction of linkers to join variable domains disclosed elsewhere herein to further protein sequences including antibody constant regions, other variable domains (for example in the production of diabodies) or detectable/functional labels as discussed in more detail elsewhere herein.

Although antibody molecules may comprise a pair of VH and VL domains, single binding domains based on either VH or VL domain sequences may also be used in the invention. It is known that single immunoglobulin domains, especially VH domains, are capable of binding target antigens in a specific manner. For example, see the discussion of dAbs above.

In the case of either of the single binding domains, these domains may be used to screen for complementary domains capable of forming a two-domain antibody molecule able to bind an antigen associated with angiogenesis, such as A-FN, B-FN, the ED-A, or the ED-B of fibronectin, tenascin C or the A1 domain of tenascin C. This may be achieved by phage display screening methods using the so-called hierarchical dual combinatorial approach as disclosed in WO92/01047, in which an individual colony containing either an H or L chain clone is used to infect a complete library of clones encoding the other chain (L or H) and the resulting two-chain antibody molecule is selected in accordance with phage display techniques such as those described in that reference. This technique is also disclosed in Marks 1992.

Fragments of whole antibodies for use in the invention can be obtained starting from any of the antibody molecules described herein, e.g. antibody molecules comprising VH and/or VL

domains or CDRs of any of antibodies described herein, by methods such as digestion by enzymes, such as pepsin or papain and/or by cleavage of the disulfide bridges by chemical reduction. In another manner, antibody fragments may be obtained by techniques of genetic recombination likewise well known to the person skilled in the art or else by peptide synthesis by means of, for example, automatic peptide synthesizers such as those supplied by the company Applied Biosystems, etc., or by nucleic acid synthesis and expression.

Conjugate

A conjugate according to the present invention comprises IL22 and an antibody molecule which binds an antigen associated with angiogenesis, as described herein. The antibody molecule is preferably a diabody or an scFv, most preferably a diabody, as described herein.

The IL22 is preferably human IL22. Typically, IL22 has at least 70%, more preferably one of at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, sequence identity to the amino acid sequence set forth in SEQ ID NO: 11. IL22 in conjugates of the invention retains a biological activity of human IL22, e.g. the ability to inhibit inflammation. Most preferably, the IL22 comprises or consist of the sequence set forth in SEQ ID NO: 11.

The inventors expect that IL22 is glycosylated at the asparagine residues at positions 21, 35 and 64 in SEQ ID NO:11. Two glycosylation sites have been described for insect cell based production (Acta Crystallogr D Biol Crystallogr. 2005 Jul;61(Pt 7):942-50. Epub 2005 Jun 24.) The third one was obtained using sequence analysis. The inventors also predict that substitution of the asparagine residues at positions 21, 35 and 64 with glutamine will prevent glycosylation of IL22 at these residues. It is generally preferable to avoid glycosylation, as glycosylation may interfere with conjugate production, including batch consistency, and result in more rapid clearance of the conjugate from the patient's body. Preferably, a conjugates of the present invention, and in particular the IL22 present in a conjugate of the present invention, is not glycosylated. Thus, IL22 may comprise or consist of the sequence shown in SEQ ID NO: 11, except that the residue at position 21, and/or position 35, and/or position 64 of SEQ ID NO: 11 is a glutamine residue rather than an asparagine residue.

Preferably, the antibody molecule is connected to the IL22 through a linker, preferably an amino acid linker. Alternatively, the antibody molecule and IL22 may be connected directly, e.g. through a chemical bond.

Where the antibody molecule is a two-chain or multi-chain molecule, IL22 may be connected to one or more polypeptide chains in the antibody molecule by means of an amino acid linker, or connected directly to one or more polypeptide chains in the antibody molecule.

The chemical bond may be, for example, a covalent or ionic bond. Examples of covalent bonds include peptide bonds (amide bonds) and disulphide bonds. The antibody molecule and IL22 may be covalently linked, for example by peptide bonds (amide bonds).

Where the antibody molecule is linked to IL22 by means of an amino acid linker, the conjugate may be or comprise a fusion protein. By "fusion protein" is meant a polypeptide that is a translation product resulting from the fusion of two or more genes or nucleic acid coding sequences into one open reading frame (ORF). Where the conjugate comprises a diabody, the two scFv molecules making up the diabody (each of which is preferably linked to IL22 via and amino acid linker) may each be expressed as a fusion protein and then allowed to associate to form a dimer.

The amino acid linker connecting the antibody molecule and IL22 may be a flexible amino acid linker. Suitable examples of amino acid linker sequences are known in the art. The linker may be 10-20 amino acids, preferably 10-15 amino acids in length. Most preferably, the linker is 11-15 amino acids in length. The linker may have the sequence set forth in SEQ ID NO: 12.

In the conjugate employed in the present examples, IL22 from mus musculus (muIL22) was conjugated via an amino acid linker to either the VH domains or the VL domains of two scFv molecules making up a diabody, as shown in SEQ ID NOs 23 and 24. Both conjugates were shown to be capable of specifically targeting neovasculature. Thus, where the antibody molecule is, or comprises, an scFv, IL22 may be linked to the N-terminus of the VH domain of the scFv via an amino acid linker or to the C-terminus of the VL domain of the scFv via an amino acid linker.

The conjugate of the present invention may comprise or consist of the sequence shown in SEQ ID NO: 16 or 17. The conjugate may have at least 70%, more preferably one of at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, sequence identity to the amino acid sequence shown in SEQ ID NO: 16 or 17.

The conjugate of the present invention may be deglycosylated. Methods for deglycosylating a polypeptide are known in the art and include treatment with Peptide-N-Glycosidase F (PNGase F).

Nucleic acids

Also provided is an isolated nucleic acid molecule encoding a conjugate according to the present invention. Nucleic acid molecules may comprise DNA and/or RNA and may be partially or wholly synthetic. Reference to a nucleotide sequence as set out herein encompasses a DNA molecule with the specified sequence, and encompasses a RNA molecule with the specified sequence in which U is substituted for T, unless context requires otherwise.

Further provided are constructs in the form of plasmids, vectors (e.g. expression vectors), transcription or expression cassettes which comprise such nucleic acids. Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, marker genes and other sequences as appropriate. Vectors may be plasmids e.g. phagemid, or viral e.g. 'phage, as appropriate. For further details see, for example, Sambrook & Russell (2001) Molecular Cloning: a Laboratory Manual: 3rd edition, Cold Spring Harbor Laboratory Press. Many known techniques and protocols for manipulation of nucleic acid, for example in the preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in Ausubel et al. (1999) 4th eds., Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology, John Wiley & Sons.

Host Cells

A recombinant host cell that comprises one or more constructs as described above is also provided. Suitable host cells include bacteria, mammalian cells, plant cells, filamentous fungi, yeast and baculovirus systems and transgenic plants and animals.

A conjugate according to the present invention may be produced using such a recombinant host cell. The production method may comprise expressing a nucleic acid or construct as described above. Expression may conveniently be achieved by culturing the recombinant host cell under appropriate conditions for production of the conjugate. Following production

the conjugate may be isolated and/or purified using any suitable technique, and then used as appropriate. The conjugate may be formulated into a composition including at least one additional component, such as a pharmaceutically acceptable excipient.

Systems for cloning and expression of a polypeptide in a variety of different host cells are well known. The expression of antibodies, including conjugates thereof, in prokaryotic cells is well established in the art. For a review, see for example Plückthun (1991), Bio/Technology 9: 545-551. A common bacterial host is *E.coli*.

Expression in eukaryotic cells in culture is also available to those skilled in the art as an option for production of conjugates for example Chadd et al. (2001), Current Opinion in Biotechnology 12: 188-194); Andersen et al. (2002) Current Opinion in Biotechnology 13: 117; Larrick & Thomas (2001) Current Opinion in Biotechnology 12:411-418. Mammalian cell lines available in the art for expression of a heterologous polypeptide include Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney cells, NS0 mouse melanoma cells, YB2/0 rat myeloma cells, human embryonic kidney cells, human embryonic retina cells and many others.

A method comprising introducing a nucleic acid or construct disclosed herein into a host cell is also described. The introduction may employ any available technique. For eukaryotic cells, suitable techniques may include calcium phosphate transfection, DEAE-Dextran, electroporation, liposome-mediated transfection and transduction using retrovirus or other virus, e.g. vaccinia or, for insect cells, baculovirus. Introducing nucleic acid in the host cell, in particular a eukaryotic cell may use a viral or a plasmid based system. The plasmid system may be maintained episomally or may be incorporated into the host cell or into an artificial chromosome. Incorporation may be either by random or targeted integration of one or more copies at single or multiple loci. For bacterial cells, suitable techniques may include calcium chloride transformation, electroporation and transfection using bacteriophage.

The nucleic acid may or construct be integrated into the genome (e.g. chromosome) of the host cell. Integration may be promoted by inclusion of sequences that promote recombination with the genome, in accordance with standard techniques.

Isolated

This refers to the state in which conjugates of the invention, antibodies for use in the invention, or nucleic acid encoding such conjugates, will generally be in accordance with the present invention. Thus, conjugates of the present invention, antibodies for use in the invention, or nucleic acid encoding such conjugates may be provided in isolated and/or purified, e.g. from the environment in which they are prepared (such as cell culture), in substantially pure or homogeneous form, or, in the case of nucleic acid, free or substantially free of nucleic acid other than the sequence encoding a polypeptide with the required function. Isolated members and isolated nucleic acids will be free or substantially free of material with which they are found in the environment in which they are prepared (e.g. cell culture) when such preparation is by recombinant DNA technology practised *in vitro* or *in vivo*. Specific conjugates and nucleic acids may be formulated with diluents or adjuvants and still for practical purposes be isolated - for example the members may be mixed with pharmaceutically acceptable carriers or diluents when used in therapy. Specific conjugates may be glycosylated, either naturally or by systems of heterologous eukaryotic cells (e.g. CHO or NS0 (ECACC 85110503) cells, or they may be (for example if produced by expression in a prokaryotic cell) unglycosylated.

Heterogeneous preparations of conjugates may also be used in the invention. For example, such preparations may be mixtures of conjugates comprising antibody molecules with full-length heavy chains and heavy chains lacking the C-terminal lysine, with various degrees of glycosylation and/or with derivatized amino acids, such as cyclization of an N-terminal glutamic acid to form a pyroglutamic acid residue.

Fibronectin

Fibronectin is an antigen subject to alternative splicing, and a number of alternative isoforms of fibronectin are known, including alternatively spliced isoforms A-FN and B-FN, comprising domains ED-A or ED-B respectively, which are known markers of angiogenesis. An antibody molecule, as referred to herein, may selectively bind to isoforms of fibronectin selectively expressed in the neovasculature. An antibody molecule may bind fibronectin isoform A-FN, e.g. it may bind domain ED-A (extra domain A). An antibody molecule may bind ED-B (extra domain B).

Fibronectin Extra Domain-A (ED-A or ED-A) is also known as ED, extra type III repeat A (EIIIA) or EDI. The sequence of human ED-A has been published by Kornblihtt *et al.* (1984), Nucleic Acids Res. 12, 5853-5868 and Paolella *et al* . (1988), Nucleic Acids Res. 16, 3545-3557. The sequence of human ED-A is also available on the SwissProt database as amino acids 1631-1720 (Fibronectin type-III 12; extra domain 2) of the amino acid sequence deposited under accession number P02751. The sequence of mouse ED-A is available on the SwissProt database as amino acids 1721-1810 (Fibronectin type-III 13; extra domain 2) of the amino acid sequence deposited under accession number P11276.

The ED-A isoform of fibronectin (A-FN) contains the Extra Domain-A (ED-A). The sequence of the human A-FN can be deduced from the corresponding human fibronectin precursor sequence which is available on the SwissProt database under accession number P02751. The sequence of the mouse A-FN can be deduced from the corresponding mouse fibronectin precursor sequence which is available on the SwissProt database under accession number P11276. The A-FN may be the human ED-A isoform of fibronectin. The ED-A may be the Extra Domain-A of human fibronectin.

ED-A is a 90 amino acid sequence which is inserted into fibronectin (FN) by alternative splicing and is located between domain 11 and 12 of FN (Borsi *et al.* (1987), *J. Cell. Biol.*, 104, 595-600). ED-A is mainly absent in the plasma form of FN but is abundant during angiogenesis, embryogenesis, tissue remodelling, fibrosis, cardiac transplantation and solid tumour growth.

Fibronectin isoform B-FN is one of the best known markers angiogenesis (US 10/382,107, WO01/62298). An extra domain "ED-B" of 91 amino acids is found in the B-FN isoform and is identical in mouse, rat, rabbit, dog and man. B-FN accumulates around neovascular structures in aggressive tumours and other tissues undergoing angiogenesis, such as the endometrium in the proliferative phase and some ocular structures in pathological conditions, but is otherwise undetectable in normal adult tissues.

Tenascin C

Tenascin-C is a large hexameric glycoprotein of the extracellular matrix which modulates cellular adhesion. It is involved in processes such as cell proliferation and cell migration and is associated with changes in tissue architecture as occurring during morphogenesis and embryogenesis as well as under tumourigenesis or angiogenesis. Several isoforms of

tenascin-C can be generated as a result of alternative splicing which may lead to the inclusion of (multiple) domains in the central part of this protein, ranging from domain AI to domain D (Borsi L *et al* Int J Cancer 1992; 52:688-692, Carnemolla B *et al.* Eur J Biochem 1992; 205:561-567, WO2006/050834). An antibody molecule, as referred to herein, may bind tenascin-C. An antibody molecule may bind tenascin-C domain A1.

Autoimmune diseases

An autoimmune disease is preferably associated with and/or characterised by angiogenesis. An autoimmune disease may be an autoimmune disease characterised by angiogenesis, wherein the neovasculature expresses the ED-A isoform of fibronectin, the ED-B isoform of fibronectin and/or tenascin C. The autoimmune disease may be an inflammatory autoimmune disease, i.e. an autoimmune disease associated with and/or characterised by inflammation.

The conjugate used in the treatment of an autoimmune disease, or delivery of IL22 to sites of autoimmune disease in a patient, may be selected based on the expression of the ED-A isoform of fibronectin, ED-B isoform of fibronectin and/or tenascin C in said autoimmune disease. The autoimmune disease may be selected from the group consisting of: inflammatory bowel disease (IBD), atherosclerosis, rheumatoid arthritis (RA), multiple sclerosis (MS), endometriosis, autoimmune diabetes (such as diabetes mellitus type 1), psoriasis, psoriatic arthritis, and periodontitis. Preferably, the autoimmune disease is IBD.

IBD is a group of inflammatory conditions that affect the colon and small intestine. The major types of IBD are Crohn's disease (CD) and ulcerative colitis (UC), while other types of IBD include collagenous colitis, lymphocytic colitis, ischaemic colitis, diversion colitis, Behçet's disease and indeterminate colitis. CD can affect any part of the gastrointestinal tract, whereas UC is typically restricted to the colon and rectum.

IBD, as referred to herein, may be CD, UC, collagenous colitis, lymphocytic colitis, ischaemic colitis, diversion colitis, Behçet's disease or indeterminate colitis. In particular, the terms CD, UC, collagenous colitis, lymphocytic colitis, ischaemic colitis, diversion colitis, Behçet's disease and indeterminate colitis, as used herein, may refer to active CD, active UC, active collagenous colitis, active lymphocytic colitis, active ischaemic colitis, active diversion colitis, and active indeterminate colitis, respectively. In one embodiment, the IBD may be CD or UC.

Inflammatory Diseases and/or Disorders

"Inflammatory disease and/or disorder" refers to disease and/or disorders which are accompanied and/or characterised by inflammation. An inflammatory disease and/or disorder is preferably associated with and/or characterised by angiogenesis. An inflammatory disease and/or disorder may be an inflammatory disease and/or disorder characterised by angiogenesis, wherein the neovasculature expresses the ED-A isoform of fibronectin, the ED-B isoform of fibronectin and/or tenascin C.

The conjugate used in the treatment of an inflammatory disease and/or disorder, or delivery of IL22 to sites of an inflammatory disease and/or disorder in a patient, may be selected based on the expression of the ED-A isoform of fibronectin, ED-B isoform of fibronectin and/or tenascin C in said inflammatory disease and/or disorder. The inflammatory disease and/or disorder may be selected from the group consisting of: graft versus host disease; wound healing; and ulcers, in particular diabetic foot ulcers.

Treatment

It is expected that the conjugates of the invention will have anti-inflammatory activity and thus find application in the treatment of inflammation and/or autoimmune diseases. Without being limited by any theoretical explanation, it is expected that the conjugates of the invention will show potent anti-inflammatory activity as a result of excellent targeting of neovasculature, as demonstrated in the examples. The conjugates of the present invention are thus designed to be used in methods of treatment of patients, preferably human patients.

Accordingly, the invention provides methods of treatment comprising administration of a conjugate according to the present invention, pharmaceutical compositions comprising such conjugates, and use of such a conjugates in the manufacture of a medicament for administration, for example in a method of making a medicament or pharmaceutical composition comprising formulating the conjugate with a pharmaceutically acceptable excipient. Pharmaceutically acceptable vehicles are well known and will be adapted by the person skilled in the art as a function of the nature and of the mode of administration of the active compound(s) chosen.

Conjugates according to the present invention will usually be administered in the form of a pharmaceutical composition, which may comprise at least one component in addition to the antibody molecule. Thus, pharmaceutical compositions described herein, and for use in accordance with the present invention, may comprise, in addition to active ingredient, a pharmaceutically acceptable excipient, carrier, buffer, stabilizer or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The precise nature of the carrier or other material will depend on the route of administration, which may be by injection, e.g. intravenous or subcutaneous. Preferably, the conjugate of the present invention is administered intravenously.

Liquid pharmaceutical compositions generally comprise a liquid carrier such as water, petroleum, animal or vegetable oils, mineral oil or synthetic oil. Physiological saline solution, dextrose or other saccharide solution or glycols such as ethylene glycol, propylene glycol or polyethylene glycol may be included.

For intravenous injection, or injection at the site of affliction, the active ingredient will be in the form of a parenterally acceptable aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of relevant skill in the art are well able to prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's Injection, Lactated Ringer's Injection. Preservatives, stabilizers, buffers, antioxidants and/or other additives may be employed, as required. Many methods for the preparation of pharmaceutical formulations are known to those skilled in the art. See e.g. Robinson ed., Sustained and Controlled Release Drug Delivery Systems, Marcel Dekker, Inc., New York, 1978.

A composition comprising a conjugate according to the present invention may be administered alone or in combination with other treatments, concurrently or sequentially or as a combined preparation with another therapeutic agent or agents, for the treatment of inflammation and/or an autoimmune disease. For example, a conjugate of the invention may be used in combination with an existing therapeutic agent for inflammation and/or an autoimmune disease.

A conjugate according to the invention may be used in the manufacture of a medicament. The medicament may be for separate or combined administration to an individual, and accordingly may comprise the conjugate and the additional component as a combined

preparation or as separate preparations. Separate preparations may be used to facilitate separate and sequential or simultaneous administration, and allow administration of the components by different routes.

In accordance with the present invention, compositions provided may be administered to mammals, preferably humans. Administration may be in a "therapeutically effective amount", this being sufficient to show benefit to a patient. Such benefit may be at least amelioration of at least one symptom. Thus "treatment" of a specified disease refers to amelioration of at least one symptom. The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of what is being treated, the particular patient being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the composition, the type of conjugate, the method of administration, the scheduling of administration and other factors known to medical practitioners. Prescription of treatment, e.g. decisions on dosage etc., is within the responsibility of general practitioners and other medical doctors, and may depend on the severity of the symptoms and/or progression of a disease being treated. Appropriate doses of antibody are well known in the art (Ledermann et al. (1991) Int. J. Cancer 47: 659-664; and Bagshawe et al. (1991) Antibody, Immunoconjugates and Radiopharmaceuticals 4: 915-922). Specific dosages indicated herein, or in the Physician's Desk Reference (2003) as appropriate for the type of medicament being administered, may be used. A therapeutically effective amount or suitable dose of a conjugate for use in the invention can be determined by comparing its *in vitro* activity and *in vivo* activity in an animal model. Methods for extrapolation of effective dosages in mice and other test animals to humans are known. The precise dose will depend upon a number of factors, including whether the antibody is for diagnosis, prevention or for treatment, the size and location of the area to be treated, the precise nature of the conjugate. A typical conjugate dose will be in the range 100 µg to 1 g for systemic applications. An initial higher loading dose, followed by one or more lower doses, may be administered. This is a dose for a single treatment of an adult patient, which may be proportionally adjusted for children and infants, and also adjusted according to conjugate format in proportion to molecular weight. Treatments may be repeated at daily, twice-weekly, weekly or monthly intervals, at the discretion of the physician. Treatments may be every two to four weeks for subcutaneous administration and every four to eight weeks for intravenous administration. In some embodiments of the present invention, treatment is periodic, and the period between administrations is about two weeks or more, e.g. about three weeks or more, about four weeks or more, or about once a month. In other

embodiments of the invention, treatment may be given before, and/or after surgery, and may be administered or applied directly at the anatomical site of surgical treatment.

Further aspects and embodiments of the invention will be apparent to those skilled in the art given the present disclosure including the following experimental exemplification.

All documents mentioned in this specification are incorporated herein by reference in their entirety.

"and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. For example "A and/or B" is to be taken as specific disclosure of each of (i) A, (ii) B and (iii) A and B, just as if each is set out individually herein.

Unless context dictates otherwise, the descriptions and definitions of the features set out above are not limited to any particular aspect or embodiment of the invention and apply equally to all aspects and embodiments which are described.

Certain aspects and embodiments of the invention will now be illustrated by way of example and with reference to the figures described above.

Examples

Materials and Methods

Cloning of fusion proteins comprising IL22 and anti-ED-A antibody F8

The genes encoding the antibody fusion proteins comprising mulL22 (from mus musculus) and anti-ED-A antibody F8 were generated using PCR assembly. The sequence encoding IL22 (lacking the signal peptide sequence) was linked via a sequence encoding a 15 amino acid glycine-serine-linker [$(G_4S)_3$] either to the C-terminus (F8-IL22) or the N-terminus (IL22-F8) of the gene encoding the F8 antibody in diabody format (heavy chain and light connected via a GGSGG-linker). A sequence encoding an IgG-derived signal peptide was added at the N-terminus to enable high yield production of the encoded fusion proteins. Using engineered NheI and NotI restriction sites, the genes were cloned into the pcDNA 3.1 mammalian cell expression vector. A schematic illustration of the gene assembly is shown in

Figure 1. The sequences of the genes used to encode the mulL22-F8 and F8-mulL22 fusion proteins are shown in SEQ ID NOs: 21 and 22, respectively, while the amino acid sequences of the mature mulL22-F8 and F8-mulL22 fusion proteins employed in the experiments reported below are shown in SEQ ID NOs: 23 and 24, respectively. The signal peptides are cleaved after expression of the fusion proteins and thus are not part of the mature fusion proteins.

The approach described above could also be used to prepare genes encoding antibody fusion proteins comprising human IL22 (hulL22) and anti-ED-A antibody F8. Exemplary sequences which could be used to encode hulL22-F8 and F8-hulL22 fusion proteins are shown in SEQ ID NOs: 14 and 15, respectively, while the amino acid sequences of mature hulL22-F8 and F8-hulL22 fusion proteins are shown in SEQ ID NOs: 16 and 17, respectively. As explained above, the signal peptides encoded by the nucleic acid sequences shown in SEQ ID NOs 14 and 15 are cleaved after expression of the fusion proteins and thus will not be part of the mature fusion proteins.

Expression of fusion proteins

Fusion proteins comprising mulL22 were expressed transiently in CHO-S cells via PEI mediated transfection. 500 x 10^6 cells were resuspended in 250 mL of pre-warmed ProCHO-2 medium (supplemented with 10% FBS, 2% HT supplement, 4% Ultraglutamine, 1% antibiotics-antimycotics solution). 625 µg of plasmid containing the gene encoding the fusion protein was diluted with a sterile 150 mM solution of NaCl to reach a total volume of 12.5 ml. 2.5 mL of sterile PEI solution (polyethylenimine, 1g/L linear, MW 25'000) in filtered water was mixed with 10 ml sterile 150 mM NaCl. The PEI mixture was added to the plasmid mixture and incubated for 10 minutes at room temperature. After the required incubation time, the mixture was added to the prepared cells and the cells were placed on a 37°C shaker at 160 rpm for 4 hours. After 4 hours 250 mL of prewarmed PowerCHO-2 medium (supplemented with 10% FBS, 2% HT supplement, 4% Ultraglutamine, 1% antibiotics-antimycotics solution) was added and the cells were placed on a 31°C shaker at 140 rpm for 6 days. This was followed by purification of the fusion protein. The same methodology could be employed to express fusion proteins comprising hulL22.

Purification of fusion proteins using protein A resin

500 mL of transfected CHO-S cell suspension was centrifuged for 20 minutes at 7000 rpm at 4 °C. The supernatant was decanted into a flask and stored at 4°C and the pellet discarded. The supernatant was loaded over a column containing gel filtration medium (SephadexTM G-25 Medium, GE Healthcare, #17-0033-02) onto a column containing protein A resin (protein A agarose beads / resin, Sino Biological Inc.), using a pump of which the flow rate had been adjusted to a maximum of 2 mL/ minute using PBS. The gel filtration resin was subsequently discarded. The protein A column was washed with 400 mL of "wash A" (100 mM NaCl (Sodium chloride for analysis, Emsure™, 7547-14-5), 0.5 mM EDTA pH 8.0 (kindly provided by Franziska Bootz), 0.1% Tween 20 (Polyoxyethylenesorbitan monolaurate, Sigma-Aldrich™, #SZBA3190V) in PBS) until the optical density of the wash as determined with a spectrophotometer (NanoDrop 2000c, witec ag, OD280nm) was below 0.1 and then washed with 400 mL of "wash B" (100 mM NaCl 0.5 mM EDTA in PBS) until the optical density at 280nm of the wash as determined with the spectrophotometer NanoDrop was below 0.05. The fusion protein comprising mulL22 was eluted by gravity flow with 10 mL of 0.1 M glycine (pH3, Fluka™, #BCBB2819). The fractions were collected as 1 mL aliquots in 1.5 mL Eppendorf tubes and immediately put on ice. Fractions containing the fusion protein, as confirmed by UV spectrometry, were pooled, transferred into a dialysis membrane (Spectra/Por™ Dialysis Membrane, MWCO 12'000-14'000, Spectrum laboratories) and dialysed overnight in 3-4 L of PBS. The next day the fusion protein solution was transferred to an Eppendorf tube and stored at 4°C for 1-2 days for further analysis or snap frozen in liquid nitrogen and transferred to a -80°C freezer. The same method could be used to purify fusion proteins comprising hulL22.

Deglycosylation of fusion proteins

Deglycosylation of fusion proteins comprising mulL22 was performed using Peptide-N-Glycosidase F (PNGase F, NEB P0704S) to remove complex oligosaccharides from N-linked glycoproteins. Under denaturing conditions 15 µg of fusion protein were incubated with 10x Glycoprotein Denaturing Buffer (NEB) in a total volume of 30 µl for 10 minutes at 99°C. The denatured fusion protein was mixed with 6 µl 10x Glycobuffer 2 (NEB), 6 µl of 10 % NP-40 and deionized water in a total volume of 60 µl. After addition of 3 µl PNGase F the reaction mix was incubated for 4 hours at 37°C. Afterwards all samples were analyzed by SDS-PAGE. The effect of deglycosylation is visible as mobility shift and sharpening of bands

in SDS-PAGE gels. Deglycosylation of fusion proteins comprising hulL22 could be performed in the same way.

Size exclusion chromatography of fusion proteins

Size exclusion chromatography of fusion proteins was performed using a superdex 200 5/150 column (GE healthcare) with phosphate buffered saline as running buffer on a ÄKTA-FPLC system (GE healthcare). 100 µl protein solutions were injected into a loop and automatically injected onto the column. UV absorbance at 280 nm was assessed over time.

Biacore analysis of fusion proteins

Using surface plasmon resonance (Biacore 3000 system, GE Healthcare) the binding affinity of fusion proteins comprising mulL22 to ED-A was analysed. A microsensor chip (CM5, GE Healthcare) was coated with 11A12, a recombinantly expressed ED-A, with 1500 resonance units coating density. For analysis on surface plasmon resonance, proteins were filtered with a syringe driven filter unit (Millex®-GV, Low protein binding durapore membrane, 0.22 µm, #N3HA70695) and their concentration determined with a spectrophotometer (NanoDrop 2000c, witec ag, OD280nm). Biacore analysis of fusion proteins comprising hulL22 could be performed in the same way.

ELISA of fusion proteins

The binding capacity of the antibody moiety was further confirmed by ELISA. Recombinant EDA-domain was immobilized on maxisorp wells (Nunc-Immuno) over night at room temperature. On the day of binding assessment, wells were blocked using 200 µl 4% milk in phosphate buffered saline solution (milk-PBS) for 2 hours at room temperature. After removal of the blocking solution, 200 µl of different antibody concentrations in 2% milk-PBS were added to the wells and incubated for 1 hour at room temperature. Afterwards wells were washed with three times 200µl PBS containing 0.1% Tween-20 and three times PBS. Subsequently, 200 µl 2% milk-PBS containing protein-A HRP (GE healthcare). After 40 minutes incubation at room temperature, POD substrate (Roche) was added. The reaction was stopped using H2SO4 and the read out was obtained measuring absorption at 450nm and 650 nm using a UV spectrophotometer (SpectraMax Paradigm, Molecular Devices)

Bioactivity assay of fusion proteins: IL22 induced phosphorylation of STAT3

The activity of muIL22 in the muIL22 containing fusion proteins was verified by STAT3 phosphorylation in HT29cells. Cells were incubated with the fusion proteins and phosphorylation of STAT3 was quantified by Western Blot analysis.

HT29 cells were seeded with a density of 0.1 x 10^6 cells per well in 300 µl of McCoy's medium (GIBCO, supplemented with 10% FBS and 1% antibiotics-antimycotics solution) in a sterile 96 well plate. When cells were attached to the flask, the medium was replaced by serum-free medium and cells were incubated over night at 37°C. The following day, muIL22 fusion proteins were added in a ten-fold serial dilution and starting with a concentration of 5 µg/ml as shown in **Figure 4**. After an incubation period of 20 minutes at 37°C, cells were washed with wash buffer (10 ml PBS containing 1 tablet protease inhibitor (Roche, Complete Mini EDTA-free protease inhibitor cocktail)) and 20 µl RIPA buffer (25 mM TrisHCl pH7.4, 150 mM NaCl, 1 % NP40, 0.1 % SDS), 1 tablet protease inhibitor was added to the cells for 15 minutes for cell lysis. After centrifugation (2000 rpm, 15 min, 25°C), the cell lysate was used for SDS-PAGE. Afterwards the separated proteins were blotted from the polyacrylamid gel onto a nitrocellulose membrane for 1 h at 30 V and 220 mA. Following this, the membrane was blocked in 4 % milk PBS for 1 h at 25°C. A 1:1000 dilution of the primary antibody, mouse-α-human-phospho-STAT3 (Peprotech, 0.1mg/ml), in 2 % milk PBS was added to the membrane and incubated for 1 h at 25°C on a shaker. Before incubation with the secondary antibody, a washing step was performed. The membrane was incubated three times for 5 minutes in PBS + 0.1 % Tween. The secondary antibody, α-mouse-horseradish peroxidase (Invitrogen), was added to the membrane at a dilution of 1:1000 in 2% milk PBS and incubated for 1 hour at 25°C on a shaker. After incubation with the secondary antibody, a washing procedure was performed with PBS + 0.1 % Tween for 5 minutes two times and afterwards two times with PBS for 5 minutes. For signal detection, the membrane was covered with ECL reagent (Amersham Prime, GE healthcare) and exposed to a film and then developed. The activity of huIL22 in fusion proteins comprising huIL22 could be determined in the same way.

Tumour targeting assessment

The *in vivo* targeting performance of fusion proteins comprising muIL22 was assessed by quantitative biodistribution studies in F9 tumour bearing mice. Proteins were labelled with ^{125}I using the Iodogen method. 15 µg of radioiodinated fusion protein was injected intra venously

(*i.v.*) into the lateral tail vein. Mice were sacrificed 24 h after injection, organs were excised, weighed and radioactivity was measured using a Packard Cobra γ counter. Radioactivity of organs was expressed as percentage of injected dose per gram of tissue (%ID/g ± SEM). The same approach could be used to determine the *in vivo* targeting performance of fusion proteins comprising huIL22.

Results

Characterization of muIL22-F8 and F8-muIL22 fusion proteins

The purified fusion proteins exhibited favourable biochemical properties as confirmed using (1) SDS-PAGE and (2) size exclusion chromatography. SDS-PAGE analysis using coomassie staining revealed broad protein bands slightly higher than the estimated 44kDa (**Figure 2A and B**). This shift was caused by the presence of N-linked glycans, which could be removed using PNGase F, leading to a band shift to the expected size for the fusion proteins (**Figure 2A and B**). Size exclusion chromatography analysis using a Superdex S200 5/150 column further confirmed the homogeneity of the conjugate preparations (**Figure 2C and D**).

After fusion with muIL22, the binding capacity of the F8 moiety to the ED-A of fibronectin was maintained, as confirmed using surface plasmon resonance (Biacore) (**Figure 3 A and B**) and ELISA analysis (**Figure 3 C and D**).

The muIL22 also retained its biological activity after fusion with the F8 antibody in the muIL22-F8 and F8-muIL22 fusion proteins, as determined using western blot analysis on of phosphorylated STAT3 in HT29 cells after induction using the muIL22 fusion proteins (**Figure 4**).

Tissue targeting specificity of the muIL22-F8 and F8-muIL22 fusion proteins

Quantitative biodistribution studies of the muIL22-F8 and F8-muIL22 fusion proteins in F9 tumour bearing mice showed excellent tumour targeting by the fusion proteins. Although the fusion proteins are not intended for use in treating or detecting tumours, this demonstrates that the fusion proteins specifically target tissues expressing ED-A (such as neovasculature, which is known to express ED-A), with very limited presence of the fusion proteins in other

(healthy) tissues. These excellent targeting properties are expected to be useful when employing fusion proteins comprising IL22 for therapeutic applications.

Sequence listing

Amino acid sequences of the F8 CDR's

F8 CDR1 VH – LFT (SEQ ID NO: 1)

F8 CDR2 VH – SGSGGS (SEQ ID NO: 2)

F8 CDR3 VH – STHLYL (SEQ ID NO: 3)

F8 CDR1 VL – MPF (SEQ ID NO: 4)

F8 CDR2 VL – GASSRAT (SEQ ID NO: 5)

F8 CDR3 VL – MRGRPP (SEQ ID NO: 6)

Amino acid sequence of the F8 VH domain (SEQ ID NO: 7)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSLFTMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSTHLYLFDYWGQGTLVTVSS

Amino acid sequence of the F8 VL domain (SEQ ID NO: 8)

EIVLTQSPGTLSLSPGERATLSCRASQSVSMPFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSG
SGTDFTLTISRLEPEDFAVYYCQQMRGRPPTFGQGTKVEIK

Amino acid sequence of the linker linking the F8 VH domain to the F8 VL domain in the F8 diabody (SEQ ID NO: 9)

GGSGG

Amino acid sequence of the F8 diabody (SEQ ID NO: 10)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSLFTMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSTHLYLFDYWGQGTLVTVSSGGSGGEIVLTQSPGT
LSLSPGERATLSCRASQSVSMPFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISR
LEPEDFAVYYCQQMRGRPPTFGQGTKVEIK

Amino acid sequence of human IL22 (huIL22) (SEQ ID NO: 11)

APISSHCRLDKSNFQQPYITNRTFMLAKEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLE
EVLFPQSDRFQPYMQEVVPFLARLSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLL
FMSLRNACI

Amino acid sequence of the linker linking huIL22 to the F8 VH domain in the huIL22-F8 conjugate, and huIL22 to the F8 VL domain in the F8-huIL22 conjugate, respectively (SEQ ID NO: 12)

GGGGSGGGGSGGGGS

Nucleotide sequence encoding hulL22 (SEQ ID NO: 13)

GCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCAACC
GCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTCGTCTCATTGG
GGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAAC
TTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGT
GCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCAT
ATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCA
AAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTAA

Nucleotide sequence encoding the hulL22-F8 conjugate (SEQ ID NO: 14)

The below sequence shows (in order) the sequence encoding: (i) hulL22 [underlined], (ii) a 15 amino acid linker [bold]; (iii) the F8 VH domain [itallics]; (iv) a 5 amino acid linker [bold and underlined]; (v) the F8 VL domain; and (vi) the stop codon [bold]

hulL22 – 15AA Linker – F8V_H – 5AA Linker – F8V_L

GCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCAACC
GCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTCGTCTCATTGG
GGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAAC
TTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGT
GCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCAT
ATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCA
AAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATT**GGTGGAGGCGGT**
TCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCA*GAGGTGCAGCTGTTGGAGTCTGGGGGAGG*
CTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCCTG
TTTACGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGT
GGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACA
ATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTA
CTGTGCGAAAAGTACTCATTTGTATCTTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
*CGAGT***GGCGGTAGCGGAGGG**GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC
CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCATGCCGTTTTTAGCCTG
GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACT
GGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC
TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGATGCGTGGTCGGCCGCCGACGTTCGG
CCAAGGGACCAAGGTGGAAATCAAA

Nucleotide sequence encoding the F8-hulL22 conjugate (SEQ ID NO: 15)

The below sequence shows (in order) the sequence encoding: (i) the F8 VH domain [itallics]; (ii) a 5 amino acid linker [bold and underlined]; (iii) the F8 VL domain; (iv) a 15 amino acid linker [bold]; hulL22 [underlined]; and (vi) the stop codon [bold]

$F8V_H$ – 5AA Linker – $F8V_L$ – 15AA Linker – hulL22

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTAGCCTGTTTACGATGAGCTGGGTCCGCCAGGCTCCAGGGA
AGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
CTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAAGTACTCATTTGTATCTTTTTGACTA
*CTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGT***GGCGGTAGCGGAGGG**GAAATTGTGTTGAC
GCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGT
CAGAGTGTTAGCATGCCGTTTTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCC
TCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTG
GGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAG
CAGATGCGTGGTCGGCCGCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA**GGTGGAGG**
CGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCAGCGCCCATCAGCTCCCACTGCAGGC
TTGACAAGTCCAACTTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCT
AGCTTGGCTGATAACAACACAGACGTTCGTCTCATTGGGGAGAAACTGTTCCACGGAGTCAGTAT
GAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCT
CAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACA
GGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAA
GGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTG
TTTATGTCTCTGAGAAATGCCTGCATT

Amino acid sequence of the hulL22-F8 conjugate (SEQ ID NO: 16)

The below sequence shows (in order) the amino acid sequence of: (i) hulL22 [underlined], (ii) a 15 amino acid linker [bold]; (iii) the F8 VH domain [itallics]; (iv) a 5 amino acid linker [bold and underlined]; and (v) the F8 VL domain.

APISSHCRLDKSNFQQPYITNRTFMLAKEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLE
EVLFPQSDRFQPYMQEVVPFLARLSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLL
FMSLRNACI**GGGGSGGGGSGGGGS***EVQLLESGGGLVQPGGSLRLSCAASGFTFSLFTMSWVRQAP*
GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSTHLYLFDYW

*GQGTLVTVSS***GGSGG**EIVLTQSPGTLSLSPGERATLSCRASQSVSMPFLAWYQQKPGQAPRLLIYGA SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQMRGRPPTFGQGTKVEIK

Amino acid sequence of the F8-hulL22 conjugate (SEQ ID NO: 17)

The below sequence shows (in order) the amino acid sequence of: (i) the F8 VH domain [itallics]; (ii) a 5 amino acid linker [bold and underlined]; (iii) the F8 VL domain; (iv) a 15 amino acid linker [bold]; and hulL22 [underlined].

*EVQLLESGGGLVQPGGSLRLSCAASGFTFSLFTMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSTHLYLFDYWGQGTLVTVSS***GGSGG**EIVLTQSPGT LSLSPGERATLSCRASQSVSMPFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYYCQQMRGRPPTFGQGTKVEIK**GGGGSGGGGSGGGGS**APISSHCRLDKSNFQQPYIT NRTFMLAKEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVP FLARLSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Amino acid sequence of mus musculus IL22 (mulL22) (SEQ ID NO: 18)
LPVNTRCKLEVSNFQQPYIVNRTFMLAKEASLADNNTDVRLIGEKLFRGVSAKDQCYLMKQVLNFTLE DVLLPQSDRFQPYMQEVVPFLTKLSNQLSSCHISGDDQNIQKNVRRLKETVKKLGESGEIKAIGELDLL FMSLRNACV

Amino acid sequence of the linker linking mulL22 to the F8 VH domain in the mulL22-F8 conjugate (SEQ ID NO: 19)
GGGGSGGGGSGGGGS

Amino acid sequence of the linker linking mulL22 to the F8 VL domain in the F8-mulL22 conjugate (SEQ ID NO: 20)
GGGGSGGGGSGGGGS

Nucleotide sequence encoding the mulL22-F8 conjugate (SEQ ID NO: 21)

mulL22 – 15AA Linker – F8V_H – 5AA Linker – F8V_L

The below sequence shows (in order) the sequence encoding: (i) mulL22 [underlined], (ii) a 15 amino acid linker [bold]; (iii) the F8 VH domain [itallics]; (iv) a 5 amino acid linker [bold and underlined]; (v) the F8 VL domain; and (vi) the stop codon [bold]

CTGCCCGTCAACACCCGGTGCAAGCTTGAGGTGTCCAACTTCCAGCAGCCGTACATCGTCAACC GCACCTTTATGCTGGCCAAGGAGGCCAGCCTTGCAGATAACAACACAGATGTCCGGCTCATCGG GGAGAAACTGTTCCGAGGAGTCAGTGCTAAGGATCAGTGCTACCTGATGAAGCAGGTGCTCAAC

TTCACCCTGGAAGACGTTCTGCTCCCCCAGTCAGACAGGTTCCAGCCCTACATGCAGGAGGTGG
TGCCTTTCCTGACCAAACTCAGCAATCAGCTCAGCTCCTGTCACATCAGCGGTGACGACCAGAA
CATCCAGAAGAATGTCAGAAGGCTGAAGGAGACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATC
AAGGCGATTGGGGAACTGGACCTGCTGTTTATGTCTCTGAGAAATGCTTGCGTC**GGTGGAGGCG**
GTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCA*GAGGTGCAGCTGTTGGAGTCTGGGGGA*
GGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCC
TGTTTACGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTA
GTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGA
CAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATAT
TACTGTGCGAAAAGTACTCATTTGTATCTTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGT
*CTCGAGT***GGCGGTAGCGGAGGG**GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCT
CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCATGCCGTTTTTAGCCT
GGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCA
CTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG
ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGATGCGTGGTCGGCCGCCGACGTTC
GGCCAAGGGACCAAGGTGGAAATCAAA

Nucleotide sequence encoding the F8-mulL22 conjugate (SEQ ID NO: 22)

F8V_H – 5AA Linker – F8V_L – 15AA Linker – mulL22

The below sequence shows (in order) the sequence encoding: (i) the F8 VH domain [itallics]; (ii) a 5 amino acid linker [bold and underlined]; (iii) the F8 VL domain; (iv) a 15 amino acid linker [bold]; mulL22 [underlined]; and (vi) the stop codon [bold]

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTAGCCTGTTTACGATGAGCTGGGTCCGCCAGGCTCCAGGGA
AGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
CTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAAGTACTCATTTGTATCTTTTTGACTA
*CTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGT***GGCGGTAGCGGAGGG**GAAATTGTGTTGAC
GCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGT
CAGAGTGTTAGCATGCCGTTTTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCC
TCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTG
GGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAG
CAGATGCGTGGTCGGCCGCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA**GGTGGAGG**
CGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCACTGCCCGTCAACACCCGGTGCAAGC
TTGAGGTGTCCAACTTCCAGCAGCCGTACATCGTCAACCGCACCTTTATGCTGGCCAAGGAGGC
CAGCCTTGCAGATAACAACACAGATGTCCGGCTCATCGGGGAGAAACTGTTCCGAGGAGTCAGT

GCTAAGGATCAGTGCTACCTGATGAAGCAGGTGCTCAACTTCACCCTGGAAGACGTTCTGCTCC
CCCAGTCAGACAGGTTCCAGCCCTACATGCAGGAGGTGGTGCCTTTCCTGACCAAACTCAGCAA
TCAGCTCAGCTCCTGTCACATCAGCGGTGACGACCAGAACATCCAGAAGAATGTCAGAAGGCTG
AAGGAGACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAGGCGATTGGGGAACTGGACCTG
CTGTTTATGTCTCTGAGAAATGCTTGCGTC

Amino acid sequence of the mulL22-F8 conjugate (SEQ ID NO: 23)

The below sequence shows (in order) the amino acid sequence of: (i) mulL22 [underlined], (ii) a 15 amino acid linker [bold]; (iii) the F8 VH domain [itallics]; (iv) a 5 amino acid linker [bold and underlined]; and (v) the F8 VL domain.

LPVNTRCKLEVSNFQQPYIVNRTFMLAKEASLADNNTDVRLIGEKLFRGVSAKDQCYLMKQVLNFTLE
DVLLPQSDRFQPYMQEVVPFLTKLSNQLSSCHISGDDQNIQKNVRRLKETVKKLGESGEIKAIGELDLL
FMSLRNACV**GGGGSGGGGSGGGGS***EVQLLESGGGLVQPGGSLRLSCAASGFTFSLFTMSWVRQA*
PGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSTHLYLFDY
*WGQGTLVTVSS***GGSGG**EIVLTQSPGTLSLSPGERATLSCRASQSVSMPFLAWYQQKPGQAPRLLIY
GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQMRGRPPTFGQGTKVEIK

Amino acid sequence of the F8-mulL22 conjugate (SEQ ID NO: 24)

The below sequence shows (in order) the amino acid sequence of: (i) the F8 VH domain [itallics]; (ii) a 5 amino acid linker [bold and underlined]; (iii) the F8 VL domain; (iv) a 15 amino acid linker [bold]; and mulL22 [underlined].

E*VQLLESGGGLVQPGGSLRLSCAASGFTFSLFTMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKG*
*RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSTHLYLFDYWGQGTLVTVSS***GGSGG**EIVLTQSPGT
LSLSPGERATLSCRASQSVSMPFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISR
LEPEDFAVYYCQQMRGRPPTFGQGTKVEIK**GGGGSGGGGSGGGGS**LPVNTRCKLEVSNFQQPYIV
NRTFMLAKEASLADNNTDVRLIGEKLFRGVSAKDQCYLMKQVLNFTLEDVLLPQSDRFQPYMQEVVP
FLTKLSNQLSSCHISGDDQNIQKNVRRLKETVKKLGESGEIKAIGELDLLFMSLRNACV

Amino acid sequence of L19 CDR's

L19 CDR1 VH - Ser Phe Ser Met Ser (SEQ ID NO: 25)
L19 CDR2 VH - Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys (SEQ ID NO: 26)
L19 CDR3 VH - Pro Phe Pro Tyr Phe Asp Tyr (SEQ ID NO: 27)
L19 CDR1 VL - Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala (SEQ ID NO: 28)
L19 CDR2 VL - Tyr Ala Ser Ser Arg Ala Thr (SEQ ID NO: 29)
L19 CDR3 VL - Gln Gln Thr Gly Arg Ile Pro Pro Thr (SEQ ID NO: 30)

Amino acid sequence of L19 VH domain (SEQ ID NO: 31)

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

Amino acid sequence of L19 VL domain (SEQ ID NO: 32)

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Tyr Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Gly Arg Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

Amino acid sequence of L19 diabody (SEQ ID NO: 33)

The VH and VL domain linker sequence is shown underlined

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Tyr Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Gly Arg Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

Amino acid sequence of F16 CDR's

F16 CDR1 VH – RYGMS (SEQ ID NO: 34)

F16 CDR2 VH – AISGSGGSTYYADSVKG (SEQ ID NO: 35)

F16 CDR3 VH – AHNAFDY (SEQ ID NO: 36)

F16 CDR1 VL – QGDSLRSYYAS (SEQ ID NO: 37)

F16 CDR2 VL – GKNNRPS (SEQ ID NO: 38)

F16 CDR3 VL – NSSVYTMPPVV (SEQ ID NO: 39)

Amino acid sequence F16 VH domain (SEQ ID NO: 40)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAHNAFDYWGQGTLVTVSR

Amino acid sequence F16 VL domain (SEQ ID NO: 41)

SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSG
NTASLTITGAQAEDEADYYCNSSVYTMPPVVFGGGTKLTVL

Amino acid sequence of the F16 diabody (SEQ ID NO: 42)

The VH and VL domain linker sequence is shown underlined

EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAHNAFDYWGQGTLVTVSRGGSGGSSELTQDPAV
SVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGA
QAEDEADYYCNSSVYTMPPVVFGGGTKLTVL

VH and VL domain linker sequence in an scFv molecule (SEQ ID NO: 43)

GGGSGGGSGG

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Claims

1. A conjugate comprising interleukin-22 (IL22) and an antibody molecule, or antigen-binding fragment thereof, which binds an antigen associated with angiogenesis.

2. The conjugate according to claim 1, wherein the antibody molecule, or antigen-binding fragment thereof, is, or comprises, a single chain Fv (scFv).

3. The conjugate according to any one of claims 1 to 2, wherein the antibody molecule, or antigen-binding fragment thereof, is a diabody.

4. The conjugate according to any one of claims 1 to 3, wherein the antibody molecule, or antigen-binding fragment thereof, binds fibronectin.

5. The conjugate according to claim 4, wherein the antibody molecule, or antigen-binding fragment thereof, binds the Extra Domain-A (ED-A) of fibronectin.

6. The conjugate according to claim 5, wherein the antibody molecule, or antigen-binding fragment thereof, comprises an antigen binding site having the complementarity determining regions (CDRs) of antibody F8 set forth in SEQ ID NOs 1-6.

7. The conjugate according to claim 6, wherein the antibody molecule, or antigen-binding fragment thereof, comprises the VH and VL domains of antibody F8 set forth in SEQ ID NOs 7 and 8.

8. The conjugate according to any one of claim 1 to 7, wherein the VH domain and the VL domain of the antibody molecule, or antigen-binding fragment thereof, are linked by a 5 to 12 amino acid linker.

9. The conjugate according to claim 6 to 8, wherein the antibody molecule, or antigen-binding fragment thereof, has, or comprises, the amino acid sequence of F8 set forth in SEQ ID NO: 10.

10. The conjugate according to any one of claims 1 to 9, wherein the IL22 is human IL22.

11. The conjugate according to claim 10, wherein the IL22 comprises, or consists of, the sequence set forth in SEQ ID NO: 11.

12. The conjugate according to any one of claims 1 to 11, wherein the IL22 is linked to the antibody molecule, or antigen-binding fragment thereof, by an amino acid linker.

13. The conjugate according to any one of claims 1 to 12, wherein the antibody molecule, or antigen-binding fragment thereof, is, or comprises, a single chain Fv (scFv) and, wherein the IL22 is linked to the N-terminus of the VH domain of the scFv via an amino acid linker.

14. The conjugate according to any one of claims 1 to 12, wherein the antibody molecule, or antigen-binding fragment thereof, is, or comprises, a single chain Fv (scFv) and, wherein the IL22 is linked to the C-terminus of the VL domain of the scFv via an amino acid linker.

15. The conjugate according to any one of claims 12 to 14, wherein the amino acid linker is 10 to 20 amino acids long.

16. The conjugate according to any one of claims 1 to 13 and 15, wherein the conjugate has, or comprises, the amino acid sequence set forth in SEQ ID NO: 16.

17. The conjugate according to any one of claims 1 to 12 and 14 to 15, wherein the conjugate has, or comprises, the amino acid sequence set forth in SEQ ID NO: 17.

18. A nucleic acid molecule encoding a conjugate according to any one of claims 1 to 17.

19. The nucleic acid molecule according to claim 18, wherein the nucleic acid molecule has, or comprises the nucleotide sequence set forth in SEQ ID NO: 14 or 15.

20. An expression vector comprising the nucleic acid of claim 18 or 19.

21. A host cell comprising the vector of claim 20.

22. A method of producing a conjugate according to any one of claims 1 to 17, the method comprising culturing the host cell of claim 21 under conditions for expression of the conjugate.

23. The method of claim 22 further comprising isolating and/or purifying the conjugate following expression.

24. The conjugate according to any of claims 1 to 17 for use in a method for treatment of the human body by therapy.

25. The conjugate according to any one of claims 1 to 17 for use in a method of treating an autoimmune disease in a patient.

26. The conjugate according to any one of claims 1 to 17 for use in a method of delivering IL22 to sites of autoimmune disease in a patient.

27. A method of treating of an autoimmune disease in a patient, the method comprising administering a therapeutically effective amount of a conjugate according to any one of claims 1 to 17 to the patient.

28. A method of delivering IL22 to sites of autoimmune disease in a patient comprising administering the conjugate according to any one of claims 1 to 17 to the patient.

29. The conjugate for use according to claim 25 or 26, or the method according to claim 27 or 28, wherein the autoimmune disease is selected from the group consisting of: bowel disease (IBD), rheumatoid arthritis (RA), multiple sclerosis (MS), endometriosis, autoimmune diabetes (such as diabetes mellitus type 1), psoriasis, psoriatic arthritis, periodontitis and atherosclerosis.

30. The conjugate for use or a method according to claim 29, wherein the autoimmune disease is bowel disease.

31. The conjugate for use or a method according to claim 30, wherein the bowel disease is ulcerative colitis or Crohn's disease.

32. The conjugate according to any one of claims 1 to 17 for use in a method of treating inflammation in a patient.

33. The conjugate according to any one of claims 1 to 17 for use in a method of delivering IL22 to sites of inflammation in a patient.

34. A method of treating inflammation in a patient, the method comprising administering a therapeutically effective amount of a conjugate according to any one of claims 1 to 17 to the patient.

35. A method of delivering IL22 to sites of inflammation in a patient comprising administering the conjugate according to any one of claims 1 to 17 to the patient.

36. The conjugate for use according to claim 32 or 33, or the method according to claim 34 or 35, wherein the inflammation is the result of an inflammatory disease and/or disorder.

37. The conjugate for use according to claim 36, or the method according to claim 36, wherein the inflammatory disease and/or disorder is selected from the group consisting of: graft versus host disease; wound healing; and ulcers, in particular diabetic foot ulcers.

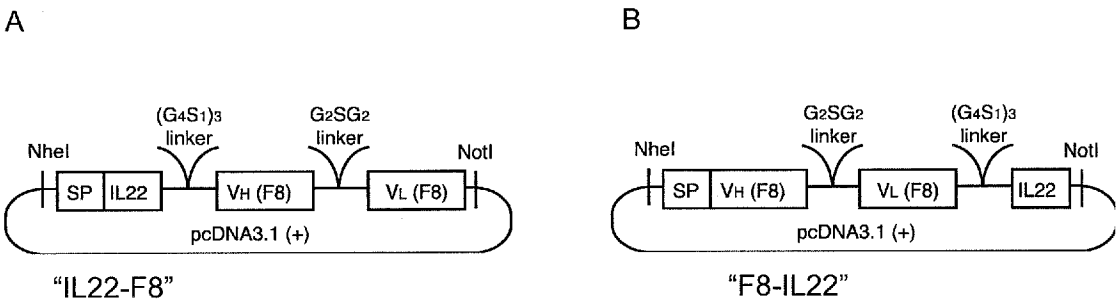
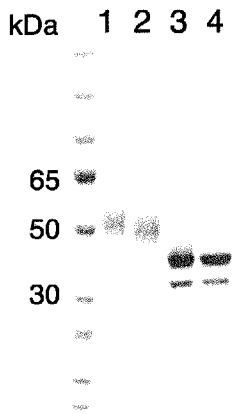

A
(G4S1)3 linker
G2SG2 linker
NheI
NotI
SP
IL22
VH (F8)
VL (F8)
pcDNA3.1 (+)
"IL22-F8"
B
G2SG2 linker
(G4S1)3 linker
NheI
NotI
SP
VH (F8)
VL (F8)
IL22
pcDNA3.1 (+)
"F8-IL22"

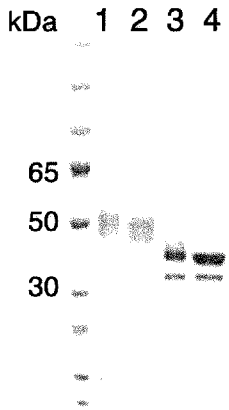
Figure 1

A



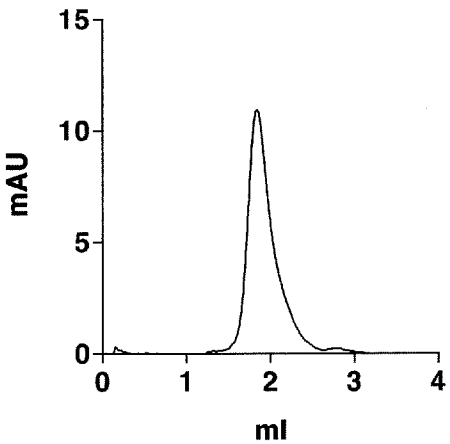
1. F8-IL22 reduced
2. F8-IL22 not reduced
3. F8-IL22 + PNGase reduced
4. F8-IL22 + PNGase not reduced

B



1. IL22-F8 reduced
2. IL22-F8 not reduced
3. IL22-F8 + PNGase reduced
4. IL22-F8 + PNGase not reduced

C



D

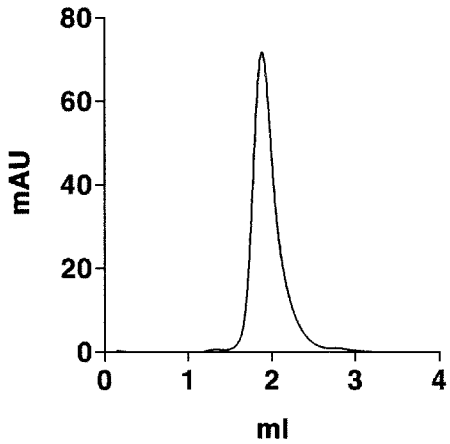
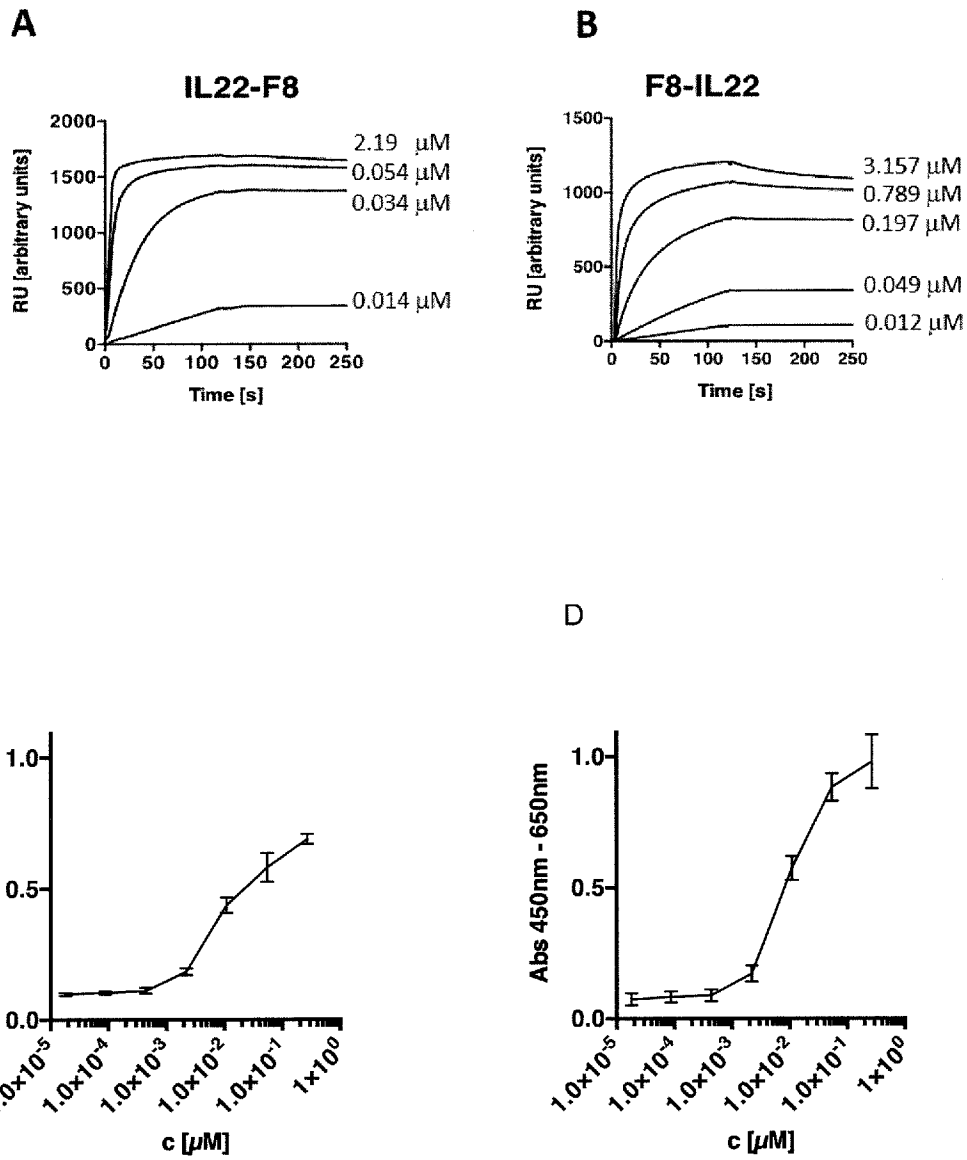


Figure 2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IL22-F8
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1500
1000
500
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0.054 µM
0.034 µM
0.014 µM
0 50 100 150 200 250
Time [s]
B
F8-IL22
RU [arbitrary units]
1500
1000
500
0
3.157 µM
0.789 µM
0.197 µM
0.049 µM
0.012 µM
0 50 100 150 200 250
Time [s]
C
Abs 450nm - 650nm
1.0
0.5
0.0
1.0×10-5
1.0×10-4
1.0×10-3
1.0×10-2
1.0×10-1
1×100
c [µM]
D
Abs 450nm - 650nm
1.0
0.5
0.0
1.0×10-5
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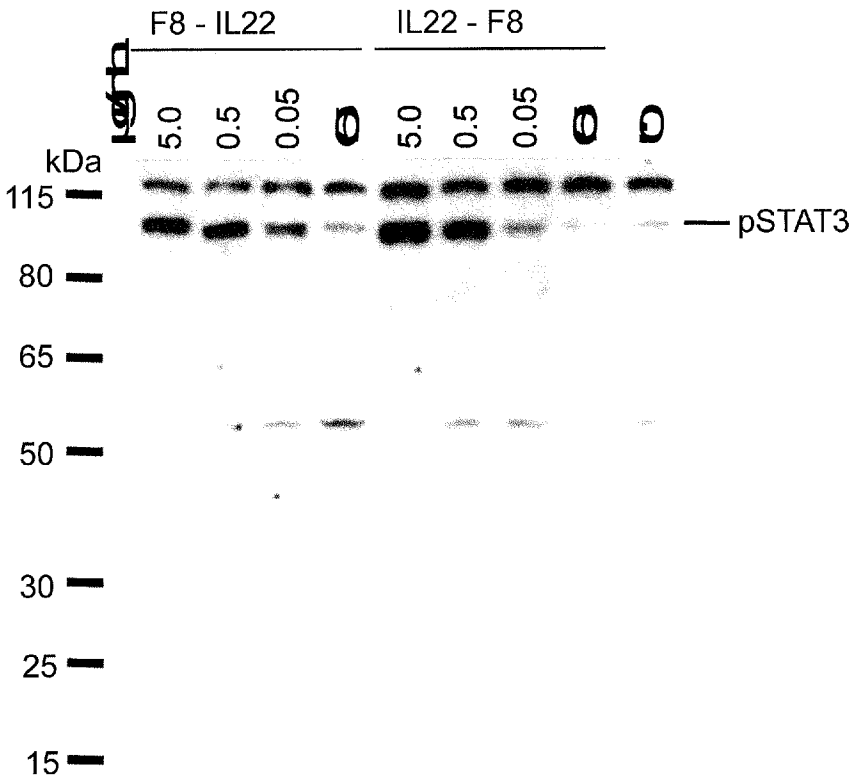
1.0×10-1
1×100
c [µM]

Figure 3


F8 - IL22
IL22 - F8
μg/ml
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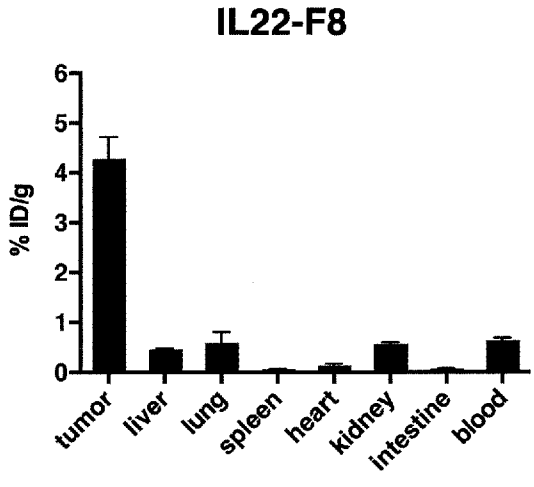
0.5
0.05
0
5.0
0.5
0.05
0
0
kDa
115
80
65
50
30
25
15
pSTAT3

Figure 4

A


IL22-F8
% ID/g
0
1
2
3
4
5
6
tumor
liver
lung
spleen
heart
kidney
intestine
blood

B

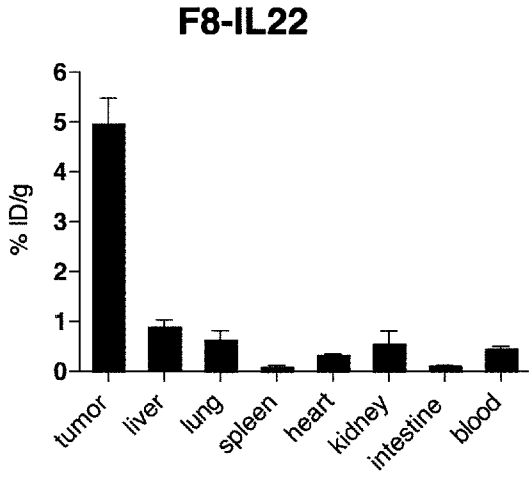

F8-IL22
% ID/g
0
1
2
3
4
5
6
tumor
liver
lung
spleen
heart
kidney
intestine
blood

Figure 5