ANTI-LAG-3 BINDING PROTEINS

Field of the Invention

The present invention is directed to antigen binding proteins, particularly antibodies that bind Lymphocyte Activation Gene (LAG-3) and cause depletion of activated T cells expressing LAG-3, polynucleotides encoding such antigen binding proteins, pharmaceutical compositions containing said antigen binding proteins, and to the use of said antigen binding proteins in the treatment and/or prevention of diseases associated with the involvement of pathogenic T cells.

Background to the Invention

Lymphocyte Activation Gene-3 (LAG-3) is a negative co-stimulatory receptor that modulates T cell homeostasis, proliferation and activation (Sierro S et al; Expert Opin. Ther. Targets (2010) 15: 91-101). An immunoglobulin superfamily member, LAG-3 is a CD4-like protein which, like CD4, binds to MHC class II molecules, but with two-fold higher affinity and at a distinct site from CD4 (Huard B et al., (1997) Proc Natl Acad Sci USA 94: 5744-9). In addition to exerting very distinct functions (CD4 is a positive co-stimulatory molecule) the two receptors are also differentially regulated. CD4 is constitutively expressed on the surface of all mature CD4+ T cells, with only a small fraction residing intracellularly, whereas a large proportion of LAG-3 molecules are retained in the cell close to the microtubule-organizing centre, and only induced following antigen specific T cell activation (Woo SR et al., (2010) Eur J Immunol 40: 1768-77). The role of LAG-3 as a negative regulator of T cell responses is based on studies with LAG-3 knockout mice and use of blocking anti-LAG-3 antibodies in model *in vitro* and *in vivo* systems (Sierro S et al., Expert Opin. Ther. Targets (2010) 15: 91-101; Hannier S et al (1998), J Immunol 161: 4058-65; Macon-Lemaitre L et al (2005), Immunology 115: 170-8; Workman CJ et al (2003), Eur J Immunol 33:970-9).

At the cell surface, LAG-3 is expressed as a dimer, which is required for formation of stable MHC class II binding sites (Huard B et al. (1997) Proc Natl Acad Sci USA 94: 5744-9). LAG-3, in soluble form, also occurs in serum of healthy donors and patients with tuberculosis and cancer (Lienhardt C et al. (2002), Eur J Immunol 32: 1605-13; Triebel F et al (2006). Cancer Lett 235: 147-53), and this form may correlate with the number of LAG-3+ T cells (Siawaya J et al. (2008). J of Infection 56: 340-7).The key attribute of LAG-3 as a target antigen for an enhanced lymphocyte depletion agent is its relatively selective expression profile when compared with other agents currently in the clinic, i.e. Campath™ (T/B cells), Amevive (most CD45RO+ T-cells) or Rituxan (B-cells). Few molecules have been identified as sustained markers of *in vivo* T cell activation in humans. These include LAG-3, OX40, MHC class II, CD69, CD38, ICOS and CD40L. However, apart from LAG-3 and OX40 the majority of these molecules are also constitutively expressed on human natural T regs or on other cell types. LAG-3 is expressed on a small proportion of T-cells in healthy humans (ca. 1-4%), and in a similar proportion of NK cells (Baixeras E et al. (1992), J Exp Med 176:

327-37; Huard B et al (1994), Immunogenetics 39: 213-7). Upon activation with anti-CD3 ca. 30-80% of both CD4+ and CD8+ T cells express LAG-3 within 24 to 48 h; this percentage is increased in presence of IL2, IL7 and IL12 (Sierro S et al, Expert Opin. Ther. Targets (2010) 15: 91-101; Bruniquel D et al (1998), Immunogenetics 48: 116-24). Following antigen-specific stimulation with recall antigen (i.e. CMV or Tetanus toxoid) the majority of activated T cells are LAG-3+. In addition, in humans, LAG-3 is expressed on a sub-population (1-10%) of CD4+ CD25+ FoxP3+ T regs in healthy human blood. This population appears to be functionally suppressive *in vitro* by cell contact and IL10 dependent mechanisms and therefore may represent a population of recently activated natural or induced T regs [Camisaschi C, Casati C, Rini F et al. (2010). LAG-3 expression defines a subset of CD4+CD25highFox3P + regulatory T cells that are expanded at tumour sites. J. Immunol 184: 6545-51). LAG-3 has been detected on other cell types of hematopoietic lineage, such as plasmacytoid dendritic cells, B-cells, and NKT-cells, but only in the mouse, and mostly following activation (Sierro S, Romero P & Speiser D; Expert Opin. Ther. Targets (2010) 15: 91-101).

Depletion of LAG-3+ T cells may be used to treat or prevent T cell driven immuno-inflammatory disorders. In auto-immune diseases where the majority of auto-reactive cells are chronically activated by self antigens at the disease site and/or re-circulate in the periphery, a short course of a depleting antigen binding protein may selectively deplete this auto-immune T cell repertoire providing long term remission. The precedence for this approach has been demonstrated with the pan-lymphocyte depleting antibody Campath™, in which a single 12mg injection reduced the rate of relapse by 74% compared to standard treatment in a multiple sclerosis trial (The CAMMS223 Trial Investigators (2008), N Engl J Med. 359:1786-801). Due to the more selective expression of LAG-3 compared with CD52, the target for Campath™, the impact on the naïve and resting memory T cell and natural T regs repertoire should be reduced. This is expected to lead to an improved therapeutic index, maintaining efficacy, but with reduced risk of infection and malignancy as well as onset of auto-immunity associated with Campath™. Additionally, in a baboon tuberculin skin challenge model, the LAG-3 targeting chimeric antibody IMP731 mediated depletion of LAG-3+ T-cells, both in the periphery and at the skin challenge site, resulting in a reduction in the tuberculin skin challenge response (Poirier N et al. (2011), Clin Exp Immunol 164: 265-74). In a further study, a LAG-3 polyclonal antibody depleted LAG-3+ infiltrating T-cells from a rat cardiac allograft and prolonged the survival of these grafts (Haudebourg T et al. (2007), Transplantation 84: 1500-1506).

There exists a need in the art for antigen binding proteins, particularly humanised antibodies, that bind LAG-3 and cause deletion of LAG-3+ activated T cells, and which may have use in the treatment of auto-immune diseases, such as psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjögren's syndrome, multiple sclerosis, ulcerative colitis and autoimmune hepatitis; infectious diseases, allergic diseases and cancer.

Summary of the Invention

The present invention is broadly directed to antigen binding proteins, such as humanised antibodies, which bind Lymphocyte Activation Gene 3 (LAG-3) and which may be able to cause depletion of LAG-3+ activated T cells. More particularly, antigen binding proteins of the present invention may comprise CDRL1, CDRL2 and CDRL3 of SEQ ID No. 5.

Antigen binding proteins described herein may have use in the treatment or prevention of diseases associated with the involvement of pathogenic T cells, for example auto-immune diseases, such as psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjögren's syndrome, multiple sclerosis, ulcerative colitis and autoimmune hepatitis; infectious diseases, allergic diseases and cancer. Accordingly, the invention is further directed to pharmaceutical compositions comprising an antigen binding protein according to the invention and optionally one or more pharmaceutically acceptable excipients and/or carriers.

Description of the Figures

Figure 1: Antibody binding to LAG-3 expressing EL4 (A) and activated human CD3+ T cells (B). Synagis, a monoclonal antibody against an unrelated target, was used as negative control.

Figure 2: Effect of afucosylated antibody H5L7BW administered intra-peritoneally on co-administered, activated human PBMCs retrieved from the peritoneal cavity 24 hours post-injection. A) Quantification of human $CD4^+LAG\text{-}3^+$ and $CD8^+LAG\text{-}3^+$ T cells 24 hours after co-administration of 1×10^7 activated human PBMCs and 5mg/kg Control antibody, H5L7BW or Campath™ (Donor A: Control n=2; H5L7BW n=2, MabCampath n=1; Donor B: Control n=2; H5L7BW n=3, Campath™ n=2). B) Quantification of total $CD4^+$ and $CD8^+$ T cells. (*$p<0.001$).

Figure 3: Effect of afucosylated antibody H5L7BW and its non-ADCC enhanced variant H5L7 on activated human PBMCs co-administered intra-peritoneally and retrieved from the peritoneal cavity 5 hours post-injection. A) Quantification of human $CD4^+LAG\text{-}3^+$ and $CD8^+LAG\text{-}3^+$ T cells 5 hours after co-administration of 1×10^7 activated human PBMCs and 5mg/kg Control antibody, H5L7BW or H5L7 (n=3 per group). B) Quantification of total $CD4^+$ and $CD8^+$ T cells. (*$p<0.001$).

Figure 4: Effect of afucosylated antibody H5L7BW administered intravenously 18 hours pre-administration of human activated PBMCs into the peritoneum of SCID mice. A) Quantification of human $CD4^+LAG\text{-}3^+$ and $CD8^+LAG\text{-}3^+$T cells 5 hours after i.p. injection of 5×10^6 (n=1 per group) or 1×10^7 O/N (n=4 per group) activated human PBMCs. B) Quantification of total $CD4^+$ and $CD8^+$ T cells. 5mg/kg H5L7BW or control antibody was injected intravenously 18 hours pre-injection of activated human PBMCs. (*$p<0.001$, # $p=0.0052$).

Figure 5: Effect of H5L7BW, H5L7 or IMP731 (5mg/kg) administered intravenously 18 hours pre-administration of activated human PBMCs into the peritoneum of SCID mice. A) Quantification of human $CD4^+LAG\text{-}3^+$ and $CD8^+LAG\text{-}3^+$T cells 5 hours after i.p. injection of 1×10^7 (n=4 per group) activated human PBMCs. 5mg/kg H5L7BW, H5L7, IMP731 or control antibody were injected

intravenously 18 hours pre injection of human PBMCs. B) Quantification of total $CD4^+$ and $CD8^+$ T cells. 5mg/kg LAG-3 depleting antibodies or control antibody were injected intravenously 18 hours pre-injection of activated human PBMCs. (*$p<0.001$).

Detailed Description of the Invention

The present invention is broadly directed to antigen binding proteins that bind Lymphocyte Activation Gene 3 (LAG-3), and more particularly to antigen binding proteins that may cause depletion of LAG-3+ activated T cells.

The term "antigen binding protein" as used herein refers to antibodies and fragments thereof which are capable of binding to LAG-3. Unless otherwise specified, the term "LAG-3" as used herein refers to Lymphocyte Activation Gene 3. The term "LAG-3" includes within its scope, but is not limited to LAG-3 expressed as a dimer on the surface of, for example, activated T cells, NK cells and B cells (also known in the art as, for example, CD223) and a soluble form of LAG-3 found, for example, in human serum, referred to herein as "sLAG-3".. Unless otherwise specified, references herein to "sLAG-3" and "LAG-3" are to human polypeptides. In a particular embodiment, the present invention provides antigen binding proteins capable of binding the form of LAG-3 expressed as a dimer on the surface of, for example, activated T cells, NK cells and B cells (also known in the art as, for example, CD223). More particularly, the present invention is directed to antigen binding proteins that are capable of binding LAG-3 expressed on activated T-cells and are able to cause depletion of said activated T cells.

In one aspect, the present invention provides an antigen binding protein capable of binding LAG-3 and which comprises CDRL1 from SEQ ID No. 5, wherein position 27E is proline.

In a further aspect, the present invention provides an antigen binding protein, which comprises CDRL1 of SEQ ID NO. 1.

In a further aspect, the present invention provides an antigen binding protein which is capable of binding LAG-3 and which comprises CDRL1 from SEQ ID NO.5, wherein the antigen binding protein further comprises CDRL2 and/or CDRL3 from SEQ ID NO. 5, or a CDR variant thereof.

In a further aspect, the present invention provides an antigen binding protein further comprising CDRL2 of SEQ ID NO. 2 and/or CDRL3 of SEQ ID NO. 3 or a CDR variant thereof.

In a further aspect, the present invention provides an antigen binding protein which is capable of binding LAG-3 and which comprises CDRL1, CDRL2 and CDRL3 from SEQ ID NO.5.

In a further aspect, the present invention provides an antigen binding protein comprising one or more of CDRH1, CDRH2 and CDRH3, or a CDR variant thereof, from SEQ ID NO 10.

In another aspect, the invention provides an antigen binding protein comprising a CDRL1, CDRL2 and CDRL3 from SEQ ID NO:5, and CDRH1, CDRH2 and CDRH3 from SEQ ID NO:10.

In a further aspect, the present invention provides an antigen binding protein comprising one or more CDRs, or a CDR variant thereof, selected from the group comprising CDRH1 of SEQ ID NO. 6, CDRH2 of SEQ ID NO. 7 and CDRH3 of SEQ ID NO. 8.

In a further aspect, the present invention provides an antigen binding protein comprising the following CDRs:

CDRL1: SEQ ID NO. 1

CDRL2: SEQ ID NO. 2

CDRL3: SEQ ID NO. 3

CDRH1: SEQ ID NO. 6

CDRH2: SEQ ID NO. 7

CDRH3: SEQ ID NO. 8.

In another aspect, the invention provides an antigen binding protein comprising a variable light chain comprising CDRL1, CDRL2 and CDRL3 from SEQ ID NO:5, and a variable heavy chain comprising CDRH1, CDRH2 and CDRH3 from SEQ ID NO:10.

In a particular aspect, the antigen binding protein is a humanised antibody, optionally an IgG.

The term "CDR" as used herein, refers to the complementarity determining region amino acid sequences of an antigen binding protein. These are the hypervariable regions of immunoglobulin heavy and light chains. There are three heavy chain and three light chain CDRs (or CDR regions) in the variable portion of an immunoglobulin.

It will be apparent to those skilled in the art that there are various numbering conventions for CDR sequences; Chothia (Chothia et al. (1989) Nature 342: 877-883), Kabat (Kabat et al., Sequences of Proteins of Immunological Interest, 4th Ed., U.S. Department of Health and Human Services, National Institutes of Health (1987)) , AbM (University of Bath) and Contact (University College London). The minimum overlapping region using at least two of the Kabat, Chothia, AbM and contact methods can be determined to provide the "minimum binding unit". The minimum binding unit may be a sub-portion of a CDR. The structure and protein folding of the antibody may mean that other residues are considered part of the CDR sequence and would be understood to be so by a skilled person.

Unless otherwise stated and/or in absence of a specifically identified sequence, references herein to "CDR", "CDRL1", "CDRL2", "CDRL3", "CDRH1", "CDRH2", "CDRH3" refer to amino acid sequences numbered according to any of the known conventions identified in Table 1. In a particular embodiment, the numbering convention utilised is the Kabat convention. References herein to "position 27E" are to the amino acid present at position 27E in the light chain variable domain defined using the Kabat numbering convention. The skilled person will understand that this position has an equivalent under other known conventions, such as, for example, Chothia where position 27E is equivalent to position 30B.

Table 1 below represents one definition using each numbering convention for each CDR or binding unit. It should be noted that some of the CDR definitions may vary depending on the individual publication used.

Table 1

	Kabat CDR	Chothia CDR	AbM CDR	Contact CDR	Minimum binding unit
H1	31-35/35A/ 35B	26-32/33/34	26-35/35A/35B	30-35/35A/35B	31-32
H2	50-65	52-56	50-58	47-58	52-56
H3	95-102	95-102	95-102	93-101	95-101
L1	24-34	24-34	24-34	30-36	30-34
L2	50-56	50-56	50-56	46-55	50-55
L3	89-97	89-97	89-97	89-96	89-96

The term "CDR variant" as used herein, refers to a CDR that has been modified by at least one, for example 1, 2 or 3, amino acid substitution(s), deletion(s) or addition(s), wherein the modified antigen binding protein comprising the CDR variant substantially retains the biological characteristics of the antigen binding protein pre-modification. It will be appreciated that each CDR that can be modified may be modified alone or in combination with another CDR. In one aspect, the modification is a substitution, particularly a conservative substitution, for example as shown in Table 2.

Table 2

Side chain	Members
Hydrophobic	Met, Ala, Val, Leu, Ile
Neutral hydrophilic	Cys, Ser, Thr
Acidic	Asp, Glu
Basic	Asn, Gln, His, Lys, Arg
Residues that influence chain orientation	Gly, Pro
Aromatic	Trp, Tyr, Phe

For example, in a variant CDR, the amino acid residues of the minimum binding unit may remain the same, but the flanking residues that comprise the CDR as part of the Kabat or Chothia definition(s) may be substituted with a conservative amino acid residue.

Such antigen binding proteins comprising modified CDRs or minimum binding units as described above may be referred to herein as "functional CDR variants" or "functional binding unit variants".

Antigen binding proteins of the present invention may be capable of binding sLAG-3. In one aspect, the equilibrium dissociation constant (KD) of the antigen binding protein-sLAG-3 interaction is 10nM or less, such as 1nM or less, for example between 1pM and 300, 400, 500pM or between 500pM and 1nM. A skilled person will appreciate that the smaller the KD numerical value, the stronger the binding. The reciprocal of KD (i.e. 1/KD) is the equilibrium association constant (KA)

having units M^{-1}. A skilled person will appreciate that the larger the KA numerical value, the stronger the binding.

In one aspect, the present invention provides antigen binding proteins that are capable of binding recombinant LAG-3 with a KD of less than 1nM, for example between 1pM and 300pM, when determined by Biacore™ surface Plasmon resonance analysis using recombinant human, or cynomolgus macaque LAG-3 extracellular domains (ECDs) of SEQ ID NOs:51 and 52, respectively.

Furthermore, antigen binging proteins of the present invention may also be capable of binding LAG-3 expressed on, for example, EL4 cells or activated human CD3+ T cells.

Antigen binding proteins of the present invention may also be capable of depleting LAG-3+ activated T cells, in particular, CD4+LAG-3+ and CD8+LAG-3+ T cells. Depletion of LAG-3+ T cells may occur by, for example, antibody dependent cell mediated cytotoxic activity (ADCC) and/or complement-dependent cytotoxic activity (CDC).

In one aspect, the present invention provides antigen binding proteins that are capable of causing greater than 40% depletion of antigen specific CD4 and/or CD8 LAG-3^{+} human T cells by ADCC in an *in-vitro* assay using primary human T cells.

In a further aspect, the present invention provides antigen binding proteins that, at a concentration of 0.1µg/mL, are capable of causing greater than 50% depletion in an in vitro ADCC assay using europium-labelled LAG-3 expressing EL4 cells as target cells and human PBMCs as effector cells, wherein the effector : target ratio is no greater than 50:1 and the assay is run for a period of 2 hours. % cell lysis is calculated based on europium release from LAG-3 expressing EL4 cells.

The interaction between the constant region of an antigen binding protein and various Fc receptors (FcR) including FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) is believed to mediate the effector functions, such as ADCC and CDC, of the antigen binding protein. Significant biological effects can be a consequence of effector functionality. Usually, the ability to mediate effector function requires binding of the antigen binding protein to an antigen and not all antigen binding proteins will mediate every effector function.

Effector function can be measured in a number of ways including for example via binding of the antigen binding protein, for example antibody, of the present invention via FcγRIII to Natural Killer cells or via FcγRI to monocytes/macrophages to measure for ADCC effector function. For example an antigen binding protein of the present invention can be assessed for ADCC effector function in a Natural Killer cell assay. Examples of such assays can be found in Shields et al, 2001 The Journal of Biological Chemistry, Vol. 276, p6591-6604; Chappel et al, 1993 The Journal of Biological Chemistry, Vol 268, p25124-25131; Lazar et al, 2006 PNAS, 103; 4005-4010.

Examples of assays to determine CDC function include thos described in 1995 J Imm Meth 184:29-38.

In one aspect of the present invention, the antigen binding protein is an antibody.

The term "antibody" as used herein refers to molecules with an immunoglobulin-like domain and includes monoclonal (for example IgG, IgM, IgA, IgD or IgE), recombinant, polyclonal, chimeric, humanised, bispecific and heteroconjugate antibodies; a single variable domain (e.g., VL), a domain antibody (dAb®), antigen binding fragments, immunologically effective fragments, Fab, $F(ab')_2$, Fv, disulphide linked Fv, single chain Fv, closed conformation multispecific antibody, disulphide-linked scFv, diabodies, TANDABS™, etc. and modified versions of any of the foregoing (for a summary of alternative "antibody" formats see Holliger and Hudson, Nature Biotechnology, 2005, Vol 23, No. 9, 1126-1136). Alternative antibody formats include alternative scaffolds in which the one or more CDRs of any molecules in accordance with the disclosure can be arranged onto a suitable non-immunoglobulin protein scaffold or skeleton, such as an affibody, a SpA scaffold, an LDL receptor class A domain, an avimer (see, e.g., U.S. Patent Application Publication Nos. 2005/0053973, 2005/0089932, 2005/0164301) or an EGF domain.

In a further aspect, the antigen binding protein is a humanised antibody.

A "humanised antibody" refers to a type of engineered antibody having its CDRs derived from a non-human donor immunoglobulin, the remaining immunoglobulin-derived parts of the molecule being derived from one (or more) human immunoglobulin(s). In addition, framework support residues may be altered to preserve binding affinity (see, e.g., Queen et al., Proc. Natl Acad Sci USA, 86:10029-10032 (1989), Hodgson et al., Bio/Technology, 9:421 (1991)). A suitable human acceptor antibody may be one selected from a conventional database, e.g., the KABAT® database, Los Alamos database, and Swiss Protein database, by homology to the nucleotide and amino acid sequences of the donor antibody. A human antibody characterized by a homology to the framework regions of the donor antibody (on an amino acid basis) may be suitable to provide a heavy chain constant region and/or a heavy chain variable framework region for insertion of the donor CDRs. A suitable acceptor antibody capable of donating light chain constant or variable framework regions may be selected in a similar manner. It should be noted that the acceptor antibody heavy and light chains are not required to originate from the same acceptor antibody. The prior art describes several ways of producing such humanised antibodies – see for example EP-A-0239400 and EP-A-054951.

In yet a further aspect, the humanised antibody has a human antibody constant region that is an IgG1, for example, the heavy chain constant region of SEQ ID No. 46.

It will be understood that the present invention further provides humanised antibodies which comprise a) a light chain sequence of SEQ ID NO. 5 or a light chain sequence with at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to any of SEQ ID NO. 5 and b) a heavy chain sequence of SEQ ID NO. 10 or a heavy chain sequence with at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to any of SEQ ID NO. 10.

In a further aspect, the present invention provides a humanised antibody, which comprises a) a light chain sequence with at least 90% identity to SEQ ID NO. 5, and b) a heavy chain sequence with at least 90% identity to SEQ ID NO. 10.

In a further aspect, the present invention provides a humanised antibody, which comprises a) a light chain sequence with at least 95% identity to SEQ ID NO. 5, and b) a heavy chain sequence with at least 95% identity to SEQ ID NO. 10.

In yet a further aspect, the present invention provides a humanised antibody, which comprises a) a light chain sequence with at least 97% identity to SEQ ID NO. 5, and b) a heavy chain sequence with at least 97% identity to SEQ ID NO. 10.

In yet a further aspect, the present invention provides a humanised antibody, which comprises a) a light chain sequence of SEQ ID NO. 5, and b) a heavy chain sequence of SEQ ID NO. 10.

It will be understood that the present invention further provides humanised antibodies which comprise a) a light chain sequence of SEQ ID NO. 35 or a light chain sequence with at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to any of SEQ ID NO. 35 and b) a heavy chain sequence of SEQ ID NO. 36 or a heavy chain sequence with at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to any of SEQ ID NO. 36.

In a further aspect, the present invention provides antigen binding proteins comprising CDRL1-L3 and CDRH1-H3 of SEQ ID NO: 35 and 36, respectively.

For nucleotide and amino acid sequences, the term "identical" or "identity" indicates the degree of identity between two nucleic acid or two amino acid sequences when optimally aligned and compared with appropriate insertions or deletions.

The percent identity between two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity = number of identical positions/total number of positions multiplied by 100), taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm, as described below.

Percent identity between a query nucleic acid sequence and a subject nucleic acid sequence is the "Identities" value, expressed as a percentage, which is calculated by the BLASTN algorithm when a subject nucleic acid sequence has 100% query coverage with a query nucleic acid sequence after a pair-wise BLASTN alignment is performed. Such pair-wise BLASTN alignments between a query nucleic acid sequence and a subject nucleic acid sequence are performed by using the default settings of the BLASTN algorithm available on the National Center for Biotechnology Institute's website with the filter for low complexity regions turned off. Importantly, a query nucleic acid sequence may be described by a nucleic acid sequence identified in one or more claims herein.

Percent identity between a query amino acid sequence and a subject amino acid sequence is the "Identities" value, expressed as a percentage, which is calculated by the BLASTP algorithm when a subject amino acid sequence has 100% query coverage with a query amino acid sequence after a pair-wise BLASTP alignment is performed. Such pair-wise BLASTP alignments between a query amino acid sequence and a subject amino acid sequence are performed by using the default settings of the BLASTP algorithm available on the National Center for Biotechnology Institute's website with the filter for low complexity regions turned off. Importantly, a query amino acid sequence may be described by an amino acid sequence identified in one or more claims herein.

Production

The antigen binding proteins, for example antibodies, such as humanised antibodies of the present invention may be produced by transfection of a host cell with an expression vector comprising the coding sequence(s) for the antigen binding protein of the invention. An expression vector or recombinant plasmid is produced by placing these coding sequences for the antigen binding protein in operative association with conventional regulatory control sequences capable of controlling the replication and expression in, and/or secretion from, a host cell. Regulatory sequences include promoter sequences, e.g., CMV promoter, and signal sequences which can be derived from other known antibodies. Similarly, a second expression vector can be produced having a DNA sequence which encodes a complementary antigen binding protein light or heavy chain. In certain embodiments this second expression vector is identical to the first except insofar as the coding sequences and selectable markers are concerned, so to ensure as far as possible that each polypeptide chain is functionally expressed. Alternatively, the heavy and light chain coding sequences for the antigen binding protein may reside on a single vector.

A selected host cell is co-transfected by conventional techniques with both the first and second vectors (or simply transfected by a single vector) to create the transfected host cell of the invention comprising both the recombinant or synthetic light and heavy chains. The transfected cell is then cultured by conventional techniques to produce the engineered antigen binding protein of the invention. The antigen binding protein which includes the association of both the recombinant heavy chain and/or light chain is screened from culture by appropriate assay, such as ELISA or RIA. Similar conventional techniques may be employed to construct other antigen binding proteins.

Suitable vectors for the cloning and subcloning steps employed in the methods and construction of the compositions of this invention may be selected by one of skill in the art. For example, the conventional pUC series of cloning vectors may be used. One vector, pUC19, is commercially available from supply houses, such as Amersham (Buckinghamshire, United Kingdom) or Pharmacia (Uppsala, Sweden). Additionally, any vector which is capable of replicating readily, has an abundance of cloning sites and selectable genes (e.g., antibiotic resistance), and is easily

manipulated may be used for cloning. Thus, the selection of the cloning vector is not a limiting factor in this invention.

The expression vectors may also be characterized by genes suitable for amplifying expression of the heterologous DNA sequences, e.g., the mammalian dihydrofolate reductase gene (DHFR). Other preferable vector sequences include a poly A signal sequence, such as from bovine growth hormone (BGH) and the betaglobin promoter sequence (betaglopro). The expression vectors useful herein may be synthesized by techniques well known to those skilled in this art.

The components of such vectors, e.g. replicons, selection genes, enhancers, promoters, signal sequences and the like, may be obtained from commercial or natural sources or synthesized by known procedures for use in directing the expression and/or secretion of the product of the recombinant DNA in a selected host. Other appropriate expression vectors of which numerous types are known in the art for mammalian, bacterial, insect, yeast, and fungal expression may also be selected for this purpose.

The present invention also encompasses a cell line transfected with a recombinant plasmid containing the coding sequences of the antigen binding proteins of the present invention. Host cells useful for the cloning and other manipulations of these cloning vectors are also conventional. However, cells from various strains of E. coli may be used for replication of the cloning vectors and other steps in the construction of antigen binding proteins of this invention.

Suitable host cells or cell lines for the expression of the antigen binding proteins of the invention include mammalian cells such as NS0, Sp2/0, CHO (e.g. DG44), COS, HEK, a fibroblast cell (e.g., 3T3), and myeloma cells, for example it may be expressed in a CHO or a myeloma cell. Human cells may be used, thus enabling the molecule to be modified with human glycosylation patterns. Alternatively, other eukaryotic cell lines may be employed. The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Sambrook et al., cited above.

Bacterial cells may prove useful as host cells suitable for the expression of the recombinant Fabs or other embodiments of the present invention (see, e.g., Plückthun, A., Immunol. Rev., 130:151-188 (1992)). However, due to the tendency of proteins expressed in bacterial cells to be in an unfolded or improperly folded form or in a non-glycosylated form, any recombinant Fab produced in a bacterial cell would have to be screened for retention of antigen binding ability. If the molecule expressed by the bacterial cell was produced in a properly folded form, that bacterial cell would be a desirable host, or in alternative embodiments the molecule may express in the bacterial host and then be subsequently re-folded. For example, various strains of E. coli used for expression are well-known as host cells in the field of biotechnology. Various strains of B. subtilis, Streptomyces, other bacilli and the like may also be employed in this method.

Where desired, strains of yeast cells known to those skilled in the art are also available as host cells, as well as insect cells, e.g. Drosophila and Lepidoptera and viral expression systems.

See, e.g. Miller et al., Genetic Engineering, 8:277-298, Plenum Press (1986) and references cited therein.

The general methods by which the vectors may be constructed, the transfection methods required to produce the host cells of the invention, and culture methods necessary to produce the antigen binding protein of the invention from such host cell may all be conventional techniques. Typically, the culture method of the present invention is a serum-free culture method, usually by culturing cells serum-free in suspension. Likewise, once produced, the antigen binding proteins of the invention may be purified from the cell culture contents according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, gel electrophoresis and the like. Such techniques are within the skill of the art and do not limit this invention. For example, preparations of altered antibodies are described in WO 99/58679 and WO 96/16990.

Yet another method of expression of the antigen binding proteins may utilize expression in a transgenic animal, such as described in U. S. Patent No. 4,873,316. This relates to an expression system using the animals casein promoter which when transgenically incorporated into a mammal permits the female to produce the desired recombinant protein in its milk.

In a further aspect of the invention there is provided a method of producing an antigen binding protein (e.g. a humanised antibody) of the invention which method comprises the step of culturing a host cell transformed or transfected with a vector encoding the light and/or heavy chain of the antibody of the invention and recovering the antigen binding protein thereby produced.

In accordance with the present invention there is provided a method of producing an anti-LAG-3 antigen binding protein (e.g. a humanised antibody) of the present invention which binds to human LAG-3, which method comprises the steps of;

(a) providing a first vector encoding a heavy chain of the antibody;

(b) providing a second vector encoding a light chain of the antibody;

(c) transforming a mammalian host cell (e.g. CHO) with said first and second vectors;

(d) culturing the host cell of step (c) under conditions conducive to the secretion of the antibody from said host cell into said culture media;

(e) recovering the secreted antibody of step (d).

Once expressed by the desired method, the antigen binding protein may then be examined for in vitro activity by use of an appropriate assay, such as Biacore™ surface Plasmon resonance analysis, to assess binding of the antigen binding protein to LAG-3. Additionally, other in vitro and in vivo assays may also be used to determine an antigen binding protein's ability to cause depletion of cells expressing LAG-3, such as activated human T cell populations.

The skilled person will appreciate that, upon production of an antigen binding protein such as an antibody, in particular depending on the cell line used and particular amino acid sequence of the antigen binding protein, post-translational modifications may occur. For example, this may

include the cleavage of certain leader sequences, the addition of various sugar moieties in various glycosylation and phosphorylation patterns, deamidation, oxidation, disulfide bond scrambling, isomerisation, C-terminal lysine clipping, and N-terminal glutamine cyclisation. The present invention encompasses the use of antigen binding proteins which have been subjected to, or have undergone, one or more post-translational modifications. Thus an "antigen binding protein" or "antibody" of the invention includes an "antigen binding protein" or "antibody", respectively, as defined earlier which has undergone a post-translational modification such as described herein.

Glycosylation of antibodies at conserved positions in their constant regions is known to have a profound effect on antibody function, particularly effector functioning, see for example, Boyd et al. (1996) Mol. Immunol. 32: 1311-1318. Glycosylation variants of the antigen binding proteins of the invention wherein one or more carbohydrate moiety is added, substituted, deleted or modified are contemplated. Introduction of an asparagine-X-serine or asparagine-X-threonine motif creates a potential site for enzymatic attachment of carbohydrate moieties and may therefore be used to manipulate the glycosylation of an antibody. In Raju et al. (2001) Biochemistry 40: 8868-8876 the terminal sialyation of a TNFR-IgG immunoadhesin was increased through a process of regalactosylation and/or resialylation using beta-1, 4-galactosyltransferace and/or alpha, 2,3 sialyltransferase. Increasing the terminal sialylation is believed to increase the half-life of the immunoglobulin. Antibodies, in common with most glycoproteins, are typically produced as a mixture of glycoforms. This mixture is particularly apparent when antibodies are produced in eukaryotic, particularly mammalian cells. A variety of methods have been developed to manufacture defined glycoforms, see Zhang et al. (2004) Science 303: 371: Sears et al. (2001) Science 291: 2344; Wacker et al. (2002) Science 298: 1790; Davis et al. (2002) Chem. Rev. 102: 579; Hang et al. (2001) Acc. Chem. Res 34: 727. The antibodies (for example of the IgG isotype, e.g. IgG1) as herein described may comprise a defined number (e.g. 7 or less, for example 5 or less, such as two or a single) of glycoform(s).

Deamidation is an enzymatic reaction primarily converting asparagine (N) to iso-aspartic acid and aspartic acid (D) at approximately 3:1 ratio. To a much lesser degree, deamidation can occur with glutamine residues in a similar manner. Deamidation in a CDR results in a change in charge of the molecule, but typically does not result in a change in antigen binding, nor does it impact on PK/PD.

Oxidation can occur during production and storage (i.e. in the presence of oxidizing conditions) and results in a covalent modification of a protein, induced either directly by reactive oxygen species or indirectly by reaction with secondary by-products of oxidative stress. Oxidation happens primarily with methionine residues, but occasionally can occur at tryptophan and free cysteine residues.

Disulfide bond scrambling can occur during production and basic storage conditions. Under certain circumstances, disulfide bonds can break or form incorrectly, resulting in unpaired cysteine residues (-SH). These free (unpaired) sulfhydryls (-SH) can promote shuffling.

Isomerization typically occurs during production, purification, and storage (at acidic pH) and usually occurs when aspartic acid is converted to isoaspartic acid through a chemical process.

N-terminal glutamine in the heavy chain and/or light chain is likely to form pyroglutamate (pGlu). Most pGlu formation happens in the production bioreactor, but it can be formed non-enzymatically, depending on pH and temperature of processing and storage conditions. pGlu formation is considered as one of the principal degradation pathways for recombinant mAbs.

C-terminal lysine clipping is an enzymatic reaction catalyzed by carboxypeptidases, and is commonly observed in recombinant mAbs. Variants of this process include removal of lysine from one or both heavy chains. Lysine clipping does not appear to impact bioactivity and has no effect on mAb effector function.

Effector Function Enhancement

The interaction between the constant region of an antigen binding protein and various Fc receptors (FcR) including FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) is believed to mediate the effector functions, such as ADCC and CDC, of the antigen binding protein.

The term "Effector Function" as used herein is meant to refer to one or more of Antibody dependant cell mediated cytotoxic activity (ADCC), Complement–dependant cytotoxic activity (CDC) mediated responses, Fc-mediated phagocytosis or antibody dependant cellular phagocytosis (ADCP) and antibody recycling via the FcRn receptor.

The ADCC or CDC properties of antigen binding proteins of the present invention may be enhanced in a number of ways.

Human IgG1 constant regions containing specific mutations or altered glycosylation on residue Asn297 have been shown to enhance binding to Fc receptors. In some cases these mutations have also been shown to enhance ADCC and CDC (Lazar et al. PNAS 2006, 103; 4005-4010; Shields et al. J Biol Chem 2001, 276; 6591-6604; Nechansky et al. Mol Immunol, 2007, 44; 1815-1817).

In one embodiment of the present invention, such mutations are in one or more of positions selected from 239, 332 and 330 (IgG1), or the equivalent positions in other IgG isotypes. Examples of suitable mutations are S239D and I332E and A330L. In one embodiment, the antigen binding protein of the invention herein described is mutated at positions 239 and 332, for example S239D and I332E or in a further embodiment it is mutated at three or more positions selected from 239 and 332 and 330, for example S239D and I332E and A330L. (EU index numbering).

In one embodiment of the present invention, there is provided an antigen binding protein comprising a chimeric heavy chain constant region for example an antigen binding protein

comprising a chimeric heavy chain constant region with at least one CH2 domain from IgG3 such that the antigen binding protein has enhanced effector function, for example wherein it has enhanced ADCC or enhanced CDC, or enhanced ADCC and CDC functions. In one such embodiment, the antigen binding protein may comprise one CH2 domain from IgG3 or both CH2 domains may be from IgG3.

Also provided is a method of producing an antigen binding protein according to the invention comprising the steps of:

a) culturing a recombinant host cell comprising an expression vector comprising an isolated nucleic acid as described herein wherein the expression vector comprises a nucleic acid sequence encoding a Fc region containing domains derived from human germline IgG1 and IgG3 sequences; and

b) recovering the antigen binding protein.

Such methods for the production of antigen binding proteins can be performed, for example, using the COMPLEGENT™ technology system available from BioWa, Inc. (La Jolla, CA, USA) and Kyowa Hakko Kogyo (now, Kyowa Hakko Kirin Co., Ltd.) Co., Ltd. in which a recombinant host cell comprising an expression vector in which a nucleic acid sequence encoding a Fc region containing domains derived from human germline IgG1 and IgG3 sequences is expressed to produce an antigen binding protein having enhanced complement dependent cytotoxicity (CDC) activity that is increased relative to an otherwise identical antigen binding protein lacking such a chimeric Fc domain. Aspects of the COMPLEGENT™ technology system are described in WO2007011041 and US20070148165 each of which are incorporated herein by reference. In an alternative embodiment CDC activity may be increased by introducing sequence specific mutations into the Fc region of an IgG chain. Those of ordinary skill in the art will also recognize other appropriate systems.

In an alternative embodiment of the present invention, there is provided an antigen binding protein comprising a heavy chain constant region with an altered glycosylation profile such that the antigen binding protein has enhanced effector function. For example, wherein the antigen binding protein has enhanced ADCC or enhanced CDC or wherein it has both enhanced ADCC and CDC effector function. Examples of suitable methodologies to produce antigen binding proteins with an altered glycosylation profile are described in WO2003011878, WO2006014679 and EP1229125, all of which can be applied to the antigen binding proteins of the present invention.

The present invention also provides a method for the production of an antigen binding protein according to the invention comprising the steps of:

a) culturing a recombinant host cell comprising an expression vector comprising the isolated nucleic acid as described herein under conditions suitable to express the antigen binding protein, wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase has been inactivated in the recombinant host cell; and

b) isolating the antigen binding protein produced by the recombinant host cell.

The present invention also provides a method for the production of an antigen binding protein according to the invention comprising the steps of:

a) expressing an antigen binding protein according to the invention in a recombinant host cell, wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase is been inactivated in the recombinant host cell; and

b) isolating the antigen binding protein produced by the recombinant host cell.

Such methods for the production of antigen binding proteins can be performed, for example, using the POTELLIGENT™ technology system available from BioWa, Inc. (La Jolla, CA, USA) in which CHOK1SV cells lacking a functional copy of the FUT8 gene produce monoclonal antibodies having enhanced antibody dependent cell mediated cytotoxicity (ADCC) activity that is increased relative to an identical monoclonal antibody produced in a cell with a functional FUT8 gene. Aspects of the POTELLIGENT™ technology system are described in US7214775, US6946292, WO0061739 and WO0231240 all of which are incorporated herein by reference. Those of ordinary skill in the art will also recognize other appropriate systems.

In a further aspect, the present invention provides non-fucosylated antibodies. References herein to "non-fucosylated" or "afucosylated" antibodies refer to antibodies that harbour a tri-mannosyl core structure of complex-type N-glycans of Fc without fucose residue. Non-fucosylated or afucosylated antibodies of the present invention do not comprise fucose on the core carbohydrate structure attached to Asn297. These glycoengineered antibodies that lack core fucose residue from the Fc N-glycans may exhibit stronger ADCC than fucosylated equivalents due to enhancement of FcγRIIIa binding capacity.

It will be apparent to those skilled in the art that such modifications may not only be used alone but may be used in combination with each other in order to further enhance effector function.

In one such embodiment of the present invention there is provided an antigen binding protein comprising a heavy chain constant region which comprises a mutated and chimeric heavy chain constant region. For example, wherein an antigen binding protein comprising at least one CH2 domain from human IgG3 and one CH2 domain from human IgG1, wherein the IgG1 CH2 domain has one or more mutations at positions selected from 239 and 332 and 330 (for example the mutations may be selected from S239D and I332E and A330L) such that the antigen binding protein has enhanced effector function. In this context, enhanced effector function may equate to, for example, having enhanced ADCC or enhanced CDC, for example wherein it has enhanced ADCC and enhanced CDC. In one embodiment the IgG1 CH2 domain has the mutations S239D and I332E.

In an alternative embodiment of the present invention there is provided an antigen binding protein comprising a chimeric heavy chain constant region and which has an altered glycosylation profile. In one such embodiment the heavy chain constant region comprises at least one CH2 domain from IgG3 and one CH2 domain from IgG1 and has an altered glycosylation profile such that the ratio of fucose to mannose is 0.8:3 or less, for example wherein the antigen binding protein is

defucosylated so that said antigen binding protein has an enhanced effector function in comparison with an equivalent antigen binding protein with an immunoglobulin heavy chain constant region lacking said mutations and altered glycosylation profile, for example wherein it has one or more of the following functions, enhanced ADCC or enhanced CDC, for example wherein it has enhanced ADCC and enhanced CDC.

In an alternative embodiment the antigen binding protein has at least one human IgG3 CH2 domain and at least one heavy chain constant domain from human IgG1 wherein both IgG CH2 domains are mutated in accordance with the limitations described herein.

In one aspect of the invention there is provided a method of producing an antigen binding protein according to the invention described herein comprising the steps of:

a) culturing a recombinant host cell containing an expression vector containing an isolated nucleic acid as described herein, said expression vector further comprising a Fc nucleic acid sequence encoding a Fc region containing domains derived from human germline IgG1 and IgG3 sequences , and wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase has been inactivated in the recombinant host cell;and

b) recovering the antigen binding protein.

Such methods for the production of antigen binding proteins can be performed, for example, using the AccretaMab™ technology system available from BioWa, Inc. (La Jolla, CA, USA) which combines the POTELLIGENT™ and COMPLEGENT™ technology systems to produce an antigen binding protein having both ADCC and CDC enhanced activity that is increased relative to an otherwise identical monoclonal antibody lacking a chimeric Fc domain and which has fucose on the oligosaccharide

In yet another embodiment of the present invention there is provided an antigen binding protein comprising a mutated and chimeric heavy chain constant region wherein said antigen binding protein has an altered glycosylation profile such that the antigen binding protein has enhanced effector function, for example wherein it has one or more of the following functions, enhanced ADCC or enhanced CDC. In one embodiment the mutations are selected from positions 239 and 332 and 330, for example the mutations are selected from S239D and I332E and A330L. In a further embodiment the heavy chain constant region comprises at least one CH2 domain from human IgG3 and one Ch2 domain from human IgG1. In one embodiment the heavy chain constant region has an altered glycosylation profile such that the ratio of fucose to mannose is 0.8:3 or less for example the antigen binding protein is defucosylated, so that said antigen binding protein has an enhanced effector function in comparison with an equivalent non-chimeric antigen binding protein or with an immunoglobulin heavy chain constant region lacking said mutations and altered glycosylation profile.

Half-life Extension

Increased half-life, or half-life extension, can be useful in *in vivo* applications of antigen binding proteins, especially antibodies and most especially antibody fragments of small size. Such fragments (Fvs, disulphide bonded Fvs, Fabs, scFvs, dAbs) are generally rapidly cleared from the body. Antigen binding proteins in accordance with the disclosure can be adapted or modified to provide increased serum half-life *in vivo* and consequently longer persistence, or residence, times of the functional activity of the antigen binding protein in the body. Suitably, such modified molecules have a decreased clearance and increased Mean Residence Time compared to the non-adapted molecule. Increased half-life can improve the pharmacokinetic and pharmacodynamic properties of a therapeutic molecule and can also be important for improved patient compliance.

The phrases, "half-life" ("$t_{1/2}$") and "serum half life", refer to the time taken for the serum (or plasma) concentration of an antigen binding protein in accordance with the disclosure to reduce by 50%, *in vivo*, for example due to degradation of the antigen binding protein and/or clearance or sequestration of the antigen binding protein by natural mechanisms.

The antigen binding proteins of the disclosure can be stabilized *in vivo* and their half-life increased by binding to molecules which resist degradation and/or clearance or sequestration ("half-life extending moiety" or "half-life extending molecule"). Half-life extension strategies are reviewed, for example, in *"Therapeutic Proteins: Strategies to Modulate Their Plasma Half-Lives"*, Edited by Roland Kontermann, Wiley-Blackwell, 2012, ISBN: 978-3-527-32849-9. Suitable half-life extension strategies include: PEGylation, polysialylation, HESylation, recombinant PEG mimetics, *N*-glycosylation, *O*-glycosylation, Fc fusion, engineered Fc, IgG binding, albumin fusion, albumin binding, albumin coupling and nanoparticles.

In one embodiment, the half-life extending moiety or molecule is a polyethylene glycol moiety or a PEG mimetic. In one embodiment, the antigen binding protein comprises (optionally consists of) a single variable domain of the disclosure linked to a polyethylene glycol moiety (optionally, wherein said moiety has a size of about 20 to about 50 kDa, optionally about 40 kDa linear or branched PEG). Reference is made to WO04081026 for more detail on PEGylation of domain antibodies and binding moieties. In one embodiment, the antagonist consists of a domain antibody monomer linked to a PEG, wherein the domain antibody monomer is a single variable domain according to the disclosure. Suitable PEG mimetics are reviewed, for example in Chapter 4, pages 63-80, *"Therapeutic Proteins: Strategies to Modulate Their Plasma Half-Lives"* Edited by Roland Kontermann, Wiley-Blackwell, 2012, ISBN: 978-3-527-32849-9.

The interaction between the Fc region of an antibody and various Fc receptors (FcγR) is believed to mediate phagocytosis and half-life/clearance of an antibody or antibody fragment. The neonatal FcRn receptor is believed to be involved in both antibody clearance and the transcytosis across tissues (see Junghans (1997) Immunol. Res 16: 29-57; and Ghetie et al. (2000) Annu. Rev. Immunol. 18: 739-766). In one embodiment, the half-life extending moiety may be an Fc region from an antibody. Such an Fc region may incorporate various modifications depending on the

desired property. For example, a salvage receptor binding epitope may be incorporated into the antibody to increase serum half life, see US 5,739,277.

Human IgG1 residues determined to interact directly with human FcRn includes Ile253, Ser254, Lys288, Thr307, Gln311, Asn434 and His435. Accordingly, substitutions at any of the positions described in this section may enable increased serum half-life and/or altered effector properties of the antibodies.

Half-life extension by fusion to the Fc region is reviewed, for example, in Chapter 9, pages 157-188, *"Therapeutic Proteins: Strategies to Modulate Their Plasma Half-Lives"* Edited by Roland Kontermann, Wiley-Blackwell, 2012, ISBN: 978-3-527-32849-9.

Typically, a polypeptide that enhances serum half-life *in vivo*, i.e. a half-life extending molecule, is a polypeptide which occurs naturally *in vivo* and which resists degradation or removal by endogenous mechanisms which remove unwanted material from the organism (e.g., human). Typically, such molecules are naturally occurring proteins which themselves have a long half-life *in vivo*.

For example, a polypeptide that enhances serum half-life *in vivo* can be selected from proteins from the extracellular matrix, proteins found in blood, proteins found at the blood brain barrier or in neural tissue, proteins localized to the kidney, liver, muscle, lung, heart, skin or bone, stress proteins, disease-specific proteins, or proteins involved in Fc transport. Suitable polypeptides are described, for example, in WO2008/096158.

Such an approach can also be used for targeted delivery of an antigen binding protein, e.g. a single variable domain, in accordance with the disclosure to a tissue of interest. In one embodiment targeted delivery of a high affinity single variable domain in accordance with the disclosure is provided.

In one embodiment, an antigen binding protein, e.g. single variable domain, in accordance with the disclosure can be linked, i.e. conjugated or associated, to serum albumin, fragments and analogues thereof. Half-life extension by fusion to albumin is reviewed, for example in Chapter 12, pages 223-247, *"Therapeutic Proteins: Strategies to Modulate Their Plasma Half-Lives"* Edited by Roland Kontermann, Wiley-Blackwell, 2012, ISBN: 978-3-527-32849-9.

Examples of suitable albumin, albumin fragments or albumin variants are described, for example, in WO2005077042 and WO2003076567.

In another embodiment, a single variable domain, polypeptide or ligand in accordance with the disclosure can be linked, i.e. conjugated or associated, to transferrin, fragments and analogues thereof.

In one embodiment, half-life extension can be achieved by targeting an antigen or epitope that increases half-live *in vivo*. The hydrodynamic size of an antigen binding protein and its serum half-life may be increased by conjugating or associating an antigen binding protein of the disclosure to a binding domain that binds a naturally occurring molecule and increases half-live *in vivo*.

For example, the antigen binding protein in accordance with the invention can be conjugated or linked to an anti-serum albumin or anti-neonatal Fc receptor antibody or antibody fragment, e.g. an anti-SA or anti-neonatal Fc receptor dAb, Fab, Fab' or scFv, or to an anti-SA affibody or anti-neonatal Fc receptor Affibody or an anti-SA avimer, or an anti-SA binding domain which comprises a scaffold selected from, but not limited to, the group consisting of CTLA-4, lipocallin, SpA, an affibody, an avimer, GroEl and fibronectin (see WO2008096158 for disclosure of these binding domains). Conjugating refers to a composition comprising polypeptide, dAb or antagonist of the disclosure that is bonded (covalently or noncovalently) to a binding domain such as a binding domain that binds serum albumin.

In another embodiment, the binding domain may be a polypeptide domain such as an Albumin Binding Domain (ABD) or a small molecule which binds albumin (reviewed, for example in Chapter 14, pages 269-283 and Chapter 15, pages 285-296, *"Therapeutic Proteins: Strategies to Modulate Their Plasma Half-Lives"* Edited by Roland Kontermann, Wiley-Blackwell, 2012, ISBN: 978-3-527-32849-9).

In one embodiment, there is provided a fusion protein comprising an antigen binding protein in accordance with the invention and an anti-serum albumin or anti-neonatal Fc receptor antibody or antibody fragment.

The long half-life of IgG antibodies is reported to be dependent on its binding to FcRn. Therefore, substitutions that increase the binding affinity of IgG to FcRn at pH 6.0 while maintaining the pH dependence of the interaction by engineering the constant region have been extensively studied (Ghetie et al., Nature Biotech. 15: 637-640, 1997; Hinton et al., JBC 279: 6213-6216, 2004; Dall'Acqua et al.,

10 J Immunol 117: 1129-1138, 2006). Another means of modifying antigen binding proteins of the present invention involves increasing the in-vivo half life of such proteins by modification of the immunoglobulin constant domain or FcRn (Fc receptor neonate) binding domain.

In adult mammals, FcRn, also known as the neonatal Fc receptor, plays a key role in maintaining serum antibody levels by acting as a protective receptor that binds and salvages antibodies of the IgG isotype from degradation. IgG molecules are endocytosed by endothelial cells, and if they bind to FcRn, are recycled out into circulation. In contrast, IgG molecules that do not bind to FcRn enter the cells and are targeted to the lysosomal pathway where they are degraded.

The neonatal FcRn receptor is believed to be involved in both antibody clearance and the transcytosis across tissues (see Junghans R.P (1997) Immunol.Res 16. 29-57 and Ghetie et al (2000) Annu.Rev.Immunol. 18, 739-766). Human IgG1 residues determined to interact directly with human FcRn includes Ile253, Ser254, Lys288, Thr307, Gln311, Asn434 and His435. Switches at any of these positions described in this section may enable increased serum half-life and/or altered effector properties of antigen binding proteins of the invention.

Antigen binding proteins of the present invention may have amino acid modifications that increase the affinity of the constant domain or fragment thereof for FcRn. Increasing the half-life of therapeutic and diagnostic IgG's and other bioactive molecules has many benefits including reducing the amount and/or frequency of dosing of these molecules. In one embodiment there is therefore provided an antigen binding according to the invention provided herein or a fusion protein comprising all or a portion (an FcRn binding portion) of an IgG constant domain having one or more of these amino acid modifications and a non-IgG protein or non-protein molecule conjugated to such a modified IgG constant domain, wherein the presence of the modified IgG constant domain increases the in vivo half life of the antigen binding protein.

PCT Publication No. WO 00/42072 discloses a polypeptide comprising a variant Fc region with altered FcRn binding affinity, which polypeptide comprises an amino acid modification at any one or more of amino acid positions 238, 252, 253, 254, 255, 256, 265, 272, 286, 288, 303, 305, 307, 309, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 386,388, 400, 413, 415, 424,433, 434,435, 436, 439, and 447 of the Fc region, wherein the numbering of the residues in the Fc region is that of the EU index (Kabat et al).

PCT Publication No. WO 02/060919 A2 discloses a modified IgG comprising an IgG constant domain comprising one or more amino acid modifications relative to a wild-type IgG constant domain, wherein the modified IgG has an increased half-life compared to the half-life of an IgG having the wild-type IgG constant domain, and wherein the one or more amino acid modifications are at one or more of positions 251, 253, 255, 285-290, 308-314, 385-389, and 428-435.

Shields et al. (2001, J Biol Chem ; 276:6591-604) used alanine scanning mutagenesis to alter residues in the Fc region of a human IgG1 antibody and then assessed the binding to human FcRn. Positions that effectively abrogated binding to FcRn when changed to alanine include I253, S254, H435, and Y436. Other positions showed a less pronounced reduction in binding as follows: E233-G236, R255, K288, L309, S415, and H433. Several amino acid positions exhibited an improvement in FcRn binding when changed to alanine; notable among these are P238, T256, E272, V305, T307, Q311, D312, K317, D376, E380, E382, S424, and N434. Many other amino acid positions exhibited a slight improvement (D265, N286, V303, K360, Q362, and A378) or no change (S239, K246, K248, D249, M252, E258, T260, S267, H268, S269, D270, K274, N276, Y278, D280, V282, E283, H285, T289, K290, R292, E293, E294, Q295, Y296, N297, S298, R301, N315, E318, K320, K322, S324, K326, A327, P329, P331, E333, K334, T335, S337, K338, K340, Q342, R344, E345, Q345, Q347, R356, M358, T359, K360, N361, Y373, S375, S383, N384, Q386, E388, N389, N390, K392, L398, S400, D401, K414, R416, Q418, Q419, N421, V422, E430, T437, K439, S440, S442, S444, and K447) in FcRn binding.

The most pronounced effect was found for combination variants with improved binding to FcRn. At pH 6.0, the E380A/N434A variant showed over 8-fold better binding to FcRn, relative to native IgG1, compared with 2-fold for E380A and 3.5-fold for N434A. Adding T307A to this effected

a 12-fold improvement in binding relative to native IgG1. In one embodiment the antigen binding protein of the invention comprises the E380A/N434A mutations and has increased binding to FcRn.

Dall'Acqua et al. (2002, J Immunol.;169:5171-80) described random mutagenesis and screening of human IgG1 hinge-Fc fragment phage display libraries against mouse FcRn. They disclosed random mutagenesis of positions 251, 252, 254-256, 308, 309, 311, 312, 314, 385-387, 389, 428, 433, 434, and 436. The major improvements in IgG1-human FcRn complex stability occur in substituting residues located in a band across the Fc-FcRn interface (M252, S254, T256, H433, N434, and Y436) and to lesser extend substitutions of residues at the periphery like V308, L309, Q311, G385, Q386, P387, and N389. The variant with the highest affinity to human FcRn was obtained by combining the M252Y/S254T/T256E and H433K/N434F/Y436H mutations and exhibited a 57-fold increase in affinity relative to the wild-type IgG1. The in vivo behaviour of such a mutated human IgG1 exhibited a nearly 4-fold increase in serum half-life in cynomolgus monkey as compared to wild-type IgG1.

The present invention therefore provides a variant of an antigen binding protein with optimized binding to FcRn. In a preferred embodiment, the said variant of an antigen binding protein comprises at least one amino acid modification in the Fc region of said antigen binding protein, wherein said modification is selected from the group consisting of 226, 227, 228, 230, 231, 233, 234, 239, 241, 243, 246, 250, 252, 256, 259, 264, 265, 267, 269, 270, 276, 284, 285, 288, 289, 290, 291, 292, 294, 297, 298, 299, 301, 302, 303, 305, 307, 308, 309, 311, 315, 317, 320, 322, 325, 327, 330, 332, 334, 335, 338, 340, 342, 343, 345, 347, 350, 352, 354, 355, 356, 359, 360, 361, 362, 369, 370, 371, 375, 378, 380, 382, 384, 385, 386, 387, 389, 390, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401 403, 404, 408, 411, 412, 414, 415, 416, 418, 419, 420, 421, 422, 424, 426, 428, 433, 434, 438, 439, 440, 443, 444, 445, 446 and 447 of the Fc region as compared to said parent polypeptide, wherein the numbering of the amino acids in the Fc region is that of the EU index in Kabat.

In a further aspect of the invention the modifications are M252Y/S254T/T256E.

Additionally, various publications describe methods for obtaining physiologically active molecules whose half-lives are modified either by introducing an FcRn-binding polypeptide into the molecules (WO 97/43316; U.S. Patent N° 5,869,046; U.S. Patent N° 5,747,035; WO 96/32478; WO 91/14438) or by fusing the molecules with antibodies whose FcRn-binding affinities are preserved but affinities for other Fc receptors have been greatly reduced (WO 99/43713) or fusing with FcRn binding domains of antibodies (WO 00/09560; U.S. Patent N°4,703,039).

Although substitutions in the constant region are able to significantly improve the functions of therapeutic IgG antibodies, substitutions in the strictly conserved constant region have the risk of immunogenicity in human (Presta, supra, 2008; De Groot and Martin, Clin Immunol 131: 189-201, 2009) and substitution in the highly diverse variable region sequence might be less immunogenic. Reports concerned with the variable region include engineering the CDR residues to improve binding

affinity to the antigen (Rothe et al., Expert Opin Biol Ther 6: 177-187,2006; Bostrom et al., Methods Mol Bioi 525: 353-376,2009; Thie et al., Methods Mol Biol 525: 309-322, 2009) and engineering the CDR and framework residues to improve stability (Worn and Pluckthun, J Mol Biol 305: 989-1010, 2001; Ewert et al., Methods 34: 184-199, 2004) and decrease immunogenicity risk (De Groot and Martin, supra, 2009; Jones et al., Methods Mol Biol 525: 405-423, xiv, 2009). As reported, improved affinity to the antigen can be achieved by affinity maturation using the phage or ribosome display of a randomized library.

Improved stability can be rationally obtained from sequence- and structure-based rational design. Decreased immunogenicity risk (deimmunization) can be accomplished by various humanization methodologies and the removal of T-cell epitopes, which can be predicted using in silico technologies or determined by in vitro assays. Additionally, variable regions have been engineered to lower pI. A longer half life was observed for these antibodies as compared to wild type antibodies despite comparable FcRn binding. Engineering or selecting antibodies with pH dependent antigen binding to modify antibody and/or antigen half life eg IgG2 antibody half life can be shortened if antigen-mediated clearance mechanisms normally degrade the antibody when bound to the antigen. Similarly, the antigen:antibody complex can impact the half-life of the antigen, either extending half-life by protecting the antigen from the typical degradation processes, or shortening the half-life via antibody-mediated degradation. One embodiment relates to antibodies with higher affinity for antigen at pH 7.4 as compared to endosomal pH (i.e., pH 5.5-6.0) such that the KD ratio at pH5.5/ pH 7.4 or at pH 6.0/ pH 7.4 is 2 or more. For example to enhance the pharmacokinetic (PK) and pharmacodynamic (PD) properties of the antibody, it is possible to engineer pH-sensitive binding to the antibody by introducing histidines into CDR residues.

Pharmaceutical Compositions

The antigen binding proteins of the present invention will normally, but not necessarily, be formulated into pharmaceutical compositions prior to administration to a patient. Accordingly, in another aspect of the invention there is provided a pharmaceutical composition comprising an antigen binding protein according to the invention and one or more pharmaceutically acceptable excipients and/or carriers.

Methods for the preparation of such pharmaceutical compositions are well known to those skilled in the art (e.g. Remingtons Pharmaceutical Sciences, 16th edition (1980) Mack Publishing Co and Pharmaceutical Biotechnology; Plenum publishing corporation; Volumes 2, 5 and 9).

The antigen binding proteins of the present invention may be formulated for administration in any convenient way. Pharmaceutical compositions may, for example, be administered by injection or continuous infusion (examples include, but are not limited to, intravenous, intraperitoneal, intradermal, subcutaneous, intramuscular and intraportal). In one embodiment, the composition is suitable for subcutaneous injection.

Pharmaceutical compositions may be suitable for topical administration (which includes, but is not limited to, epicutaneous, inhaled, intranasal or ocular administration) or enteral administration (which includes, but is not limited to, oral or rectal administration).

Pharmaceutical compositions may comprise between 0.0001 mg/kg to 10 mg/kg of antigen binding protein, for example between 0.1 mg/kg and 5 mg/kg of antigen binding protein. Alternatively, the composition may comprise between 1.0 mg/kg and 3.0 mg/kg.

Pharmaceutical compositions may comprise, in addition to an antigen binding protein of the present invention, one or more other therapeutic agents. Additional therapeutic agents that may be combined with an antigen binding protein of the present invention include, but are not limited to, anti-CTLA-4 (e.g. ipilimumab and tremelimumab), anti-TIM-3, anti-OX40, anti-OX40L, anti-PD1 (e.g nivolumab, lambrolizumab), anti-PD1L, anti-GITR, anti-IL-5 (e.g. mepolizumab), anti-B-Lymphocyte cell activating (BLyS) factor (e.g. belimumab), anti-GITRL, anti-IL-7, anti-IL-7R, anti-CD20, anti-CCL20, anti-TNFα, anti-OSM and anti-IL-6 antibodies, as well as inhibitors of JAK, CCR9, RIP kinases, BET proteins, RORγ1 and thiopurines.

The antigen binding proteins of the present invention and one or more other therapeutic agents for combination therapy may be formulated together in the same composition or presented in separate compositions. Separately presented compositions may be administered simultaneously or sequentially.

Methods of Use

The antigen binding proteins described herein may have use in therapy. Antigen binding proteins of the present invention that bind Lymphocyte Activation Gene 3 (LAG-3) and cause depletion of LAG-3+ activated T cells may have use in the treatment or prevention of diseases associated with the involvement of pathogenic T cells, such as auto-immune diseases, infectious diseases, allergic diseases and cancer.

Examples of disease states in which the antigen binding proteins have potentially beneficial effects include auto-immune diseases including, but not limited to psoriasis, inflammatory bowel disease (for example Crohn's disease and/or ulcerative colitis), rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjögren's syndrome, multiple sclerosis, autoimmune hepatitis, uveitis, type I diabetes ankylosing spondylitis, psoriatic arthritis, Grave's disease, graft versus host disease, treatment and/or prevention of organ transplant rejection, e.g. renal or liver transplant rejection, primary sclerosing cholangitis, sarcoidosis, vasculitis, nephritis, autoimmune thrombocytopenic purpura, systemic sclerosis, celiac disease, anti-phosopholipid antibody syndrome, alopecia areata and myasthenia gravis; infectious diseases including, but not limited to, hepatitis C, hepatitis B, HIV, tuberculosis and malaria; and allergic diseases including, but not limited to, asthma, atopic dermatitis and COPD.

The antigen binding proteins of the present invention may also have use in the treatment of cancer, including, but not limited to ovarian cancer, melanoma (e.g. metastatic malignant melanoma), prostate cancer, bowel cancer (e.g. colon cancer and cancer of the small intestine), stomach cancer, oesophageal cancer, breast cancer, lung cancer, renal cancer (e.g. clear cell carcinoma), pancreatic cancer, uterine cancer, liver cancer, bladder cancer, cervical cancer, oral cancer, brain cancer, testicular cancer, skin cancer, thyroid cancer, and haematological malignancies including myelomas and chronic and acute leukaemias.

It will be appreciated by those skilled in the art that references herein to "treatment" or "therapy" may, depending on the condition, extend to prophylaxis in addition to the treatment of an established condition.

There is thus provided as a further aspect of the invention an antigen binding protein of the present invention for use in therapy.

There is also therefore provided an antigen binding protein of the present invention for use in the treatment of psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, SLE, Sjögren's syndrome, multiple sclerosis, ulcerative colitis or autoimmune hepatitis.

In a further embodiment, there is provided an antigen binding protein of the present invention for use in the treatment of psoriasis.

In a further embodiment, there is provided an antigen binding protein of the present invention for use in the treatment of Crohn's disease.

In a further embodiment, there is provided an antigen binding protein of the present invention for use in the treatment of ulcerative colitis.

There is further provided the use of an antigen binding protein of the present invention in the manufacture of a medicament for the treatment of psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjögren's syndrome, multiple sclerosis, ulcerative colitis or autoimmune hepatitis.

In a further embodiment, there is provided the use of an antigen binding protein of the present invention in the manufacture of a medicament for the treatment of psoriasis.

In a further embodiment, there is provided the use of an antigen binding protein of the present invention in the manufacture of a medicament for the treatment of Crohn's disease.

In a further embodiment, there is provided the use of an antigen binding protein of the present invention in the manufacture of a medicament for the treatment of ulcerative colitis.

There is further provided a method of treatment of a human or animal subject, which method comprises administering a therapeutically effective amount of an antigen binding protein of the present invention.

There is further provided a method of treatment of a disease associated with the involvement of pathogenic T cells in a human or animal subject comprising administering a therapeutically effective amount of an antigen binding protein of the present invention.

There is further provided a method of treatment of psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjögren's syndrome, multiple sclerosis, ulcerative colitis or autoimmune hepatitis, which method comprises administering to a human subject in need thereof, a therapeutically effective amount of an antigen binding protein of the present invention.

In a further embodiment, there is provided a method of treatment of psoriasis, which method comprises administering to a human subject in need thereof, a therapeutically effective amount of an antigen binding protein of the present invention.

In a further embodiment, there is provided a method of treatment of Crohn's disease, which method comprises administering to a human subject in need thereof, a therapeutically effective amount of an antigen binding protein of the present invention.

In a further embodiment, there is provided a method of treatment of ulcerative colitis, which method comprises administering to a human subject in need thereof, a therapeutically effective amount of an antigen binding protein of the present invention.

The phrase "therapeutically effective amount" as used herein is an amount of an antigen binding protein of the present invention required to ameliorate or reduce one or more symptoms of, or to prevent or cure, the disease.

Examples

The following Examples illustrate but do not limit the invention.

Example 1: Biacore™ SPR analysis of purified anti-LAG-3 humanised antibodies

A9H12 (IMP731), as disclosed in WO 2008/132601, was humanised by grafting murine CDRs onto two heavy and two light chain human acceptor frameworks. A number of heavy and light chain humanised anti-LAG-3 variants were prepared, containing human to murine back mutations and CDR modifications. Heavy chain variants were numbered H0 to H8, and J0, J7 to J13 and light chain variants were numbered L0 to L10 and M0 to M1. Tissue culture supernatants containing all combinations of heavy and light chain humanised anti_LAG-3 variants were analysed for binding to Fc-tagged recombinant soluble LAG-3 (IMP321). The data was analysed using a 1:1 model inherent to the Biacore™ 4000 software. Antibodies were selected based on calculated affinities and also by visual comparison of binding sensorgrams with the chimeric antibody IMP731. A total of 54 constructs that exhibited equivalent or improved binding for IMP321 were identified for re-analysis

using a Biacore™ 3000. Data was fitted to both the 1:1 and bivalent models, inherent to the BiaCore 3000 analysis software, and binding data was compared by normalising the binding curves at maximal association and comparing off-rates against IMP731 visually. This enabled antibodies that demonstrated improved off-rates in comparison to IMP731 to be discerned. A total of 18 humanised anti-LAG-3 antibodies were selected for further analysis on the basis of either equivalent or improved binding kinetics to recombinant sLAG-3 in comparison to IMP731. These 18 humanised antibodies were re-expressed and analysed as follows:

Anti-LAG-3 humanised antibodies were expressed in HEK 293 6E cells and purified by affinity chromatography as follows:

100ml scale HEK 293 6E expression

Expression plasmids encoding heavy and light chains of the humanised antibodies identified in Table 3 were transiently co-transfected into HEK 293 6E cells and expressed at 100ml scale to produce antibody.

Purification of humanised antibodies

The expressed antibody molecules were purified by affinity chromatography. Protein A sepharose beads (GE Healthcare Cat No 17-5280-04), were added to the cell culture supernatants and mixed at room temperature for 30-60 minutes. The protein A sepharose beads were then centrifuged and washed in PBS. The mixture was then added into a 10ml disposable column (Pierce Cat No: 29924) and the PBS allowed to drain. The column was washed 3 times with 10ml PBS before elution of the antibody with IgG Elution buffer (Pierce Cat No: 21009). The antibody eluted was immediately neutralized using 1M Trizma® hydrochloride buffer (T2819) and was then buffer exchanged into PBS with a Vivaspin 6 mwco 5000 column (Cat. No.: FDP-875-105D). The yield was determined by measurement of absorbance at 280nm. The level of aggregated protein in the purified sample was determined by size exclusion chromatography.

Binding Kinetics

The binding kinetics of the purified antibodies for a sLAG-3 molecule were assessed by SPR using a Biacore™ 3000. A goat anti-human kappa antibody (Southern Biotech, Catalogue No. 2060-01) was immobilised on a CM5 chip by primary amine coupling. Humanised anti-LAG3 antibodies were captured on this surface and the LAG3-Ig molecule IMP321 (Chrystelle Brignone, Caroline Grygar, Manon Marcu, Knut Schakel, Frederic Triebel, The Journal of Immunology, 2007, 179: 4202-4211) used as the analyte at 64nM with a buffer injection (i.e. 0nM) used to double reference the binding curves. Regeneration was with 10mM Glycine, pH1.5. The run was carried out on the Biacore™ 3000, using HBS-EP as running buffer and at 25°C. Sensorgrams were normalised for

binding at maximal association and off-rates compared against IMP731 by visual inspection of the sensorgram profiles.

The results show that the purified humanised anti-LAG-3 antibodies can be categorised into 3 groups; group 1 with humanised variants that appear to be better at binding to IMP32 1than the chimeric IMP731, group 2 with variants that appear to bind in a very similar manner to IMP731 and group 3 with variants that demonstrate worse binding than IMP731.

10 humanised variants fall within group 1 and demonstrate improved (i.e. reduced) off-rates when compared to IMP731 by visual inspection of the Biacore™ sensorgrams. All of these molecules contained the L7 light chain, which contains a glycine to proline substitution at position 27e in light chain CDR1. This data indicates that proline at position 27e improves the off-rate for IMP321 of the humanised anti-LAG-3 antibodies when paired with numerous humanised heavy chains.

Of the remaining antibodies tested, 4 molecules fall within group 2 and had similar off-rates to the chimeric IMP731 antibody, while 4 other molecules fall within group 3 and exhibit worse off-rates than IMP731. Table 3 provides an approximate ranking of those molecules in comparison to IMP731. H5L7 exhibits the best off-rate (i.e. lowest) in this experiment by visual inspection of the Biacore™ sensorgrams.

Table 3: Comparison of off-rates with IMP731

Humanised Variant	Off-rate comparison with IMP731	Rank order of off-rates
H5L7	better	1
H1L7	better	2
J7L7	better	3
H4L7	better	4
J11L7	better	5
H2L7	better	6
J13L7	better	7
H7L7	better	8
J0L7	better	9
H0L7	better	10
H1L1	same	
H5L1	same	
J7L1	same	
J11L1	same	
J13L1	worse	
H7L1	worse	
J0L1	worse	
H0L1	worse	

Example 2: Binding analysis of wild type fucosylated and afucosylated humanised anti-LAG-3 antibodies for binding to recombinant human LAG-3-His using the Biacore™T100

Afucosylated antibody H5L7BW was generated by expression of plasmids encoding H5L7 in the BioWa POTELLIGENT® (FUT8 knock-out CHO) cell line. Afucosylated antibodies produced using POTELLIGENT® technology have been shown to exhibit increased antibody dependent cell-mediated cytotoxicity (ADCC) compared to equivalent highly-fucosylated conventional antibodies through increased affinity to FcγRIIIa (CD16).

Wild type fucosylated and afucosylated antibodies were compared for their ability to bind to recombinant human LAG-3 ECD with a C-terminal His6 (SEQ ID NO:51) using the Biacore™ T100 (GE Healthcare™). Protein A was immobilised on a CM5 chip by primary amine coupling. This surface was then used to capture the humanised antibodies. Recombinant human LAG-3 ECD-His6 was then passed over the captured antibodies at 32, 8, 2, 0.5 and 0.125nM and regeneration was carried out using 50mM NaOH. The binding curves were double referenced with buffer injection (i.e. 0nM) and the data was fitted to the T100 analysis software using the 1:1 model. The run was carried out at 25°c, using HBS-EP as the running buffer.

In order to investigate the statistical significance of this kinetic data, this experiment was repeated 3 times with the same batch of the four antibodies and the chimeric control. KD, ka and kd parameters were each log (base 10) transformed prior to separate statistical analyses. For each parameter, a mixed model analysis of variance ('Anova') was performed on transformed data, including terms for Run (random block effect) and Antibody.

From the Anova, geometric means were predicted for each antibody, along with statistically plausible ranges (95% confidence intervals) for each mean. Planned comparisons of antibodies were performed within the Anova. Comparisons are presented as ratios of the two antibodies compared, again with 95% confidence intervals and p values. The ratios may also be interpreted as a fold change, e.g. a ratio of 0.1 corresponds to a 90% decrease.

Geometric means were derived for each of the humanised antibodies and the chimeric control IMP731 for the binding affinity (KD), shown in Table 4. The mean KD for H5L7 was 0.2075nM, a significant decrease of 92% (i.e. 10 fold decrease) with $p<0.0001$ when compared with IMP731. IMP731 exhibited a mean KD of 2.76nM. Afucosylated H5L7BW exhibits equivalent binding as fucosylated H5L7, with a geometric KD of 0.2179nM, with no significant difference ($p=0.1790$).

The improvement in affinity observed for H5L7 in comparison to IMP731 is predominantly driven by differences in the off-rates of the antibodies for LAG-3-ECD-His6, shown in Table 5. There is an approximate 85% decrease (i.e. almost 10 fold decrease) in kd for H5L7 in comparison IMP731 which is highly statistically significant. There is no significant difference between afucosylated H5L7BW and H5L7 ($p=0.4408$).

Table 4: Statistical evaluation for the KD of fucosylated and afucosylated anti-LAG-3 variants binding to recombinant human LAG-3-His

Geometric Means for KD (nM)				
Antibody	*Batch No*	*Geometric mean*	*Lower 95% CI*	*Upper 95% CI*
H5L7	GRITS42382	2.08E-10	1.89E-10	2.28E-10
H5L7BW	GRITS42760	2.18E-10	1.98E-10	2.40E-10
IMP731	020909	2.76E-09	2.51E-09	3.04E-09

Comparisons of KD				
KD comparison	*Ratio*	*Lower 95% CI*	*Upper 95% CI*	*P value*
H5L7BW-H5L7	1.0502	0.97268	1.13389	0.179
H5L7-IMP731	0.07736	0.0715	0.0837	<.0001

Table 5: Statistical evaluation for the kd of fucosylated and afucosylated anti-LAG-3 variants binding to recombinant human LAG-3-His

Geometric Means for kd (1/s)				
Antibody	*Batch No*	*Geometric mean*	*Lower 95% CI*	*Upper 95% CI*
H5L7	GRITS42382	3.95E-03	3.16E-03	4.94E-03
H5L7BW	GRITS42760	4.41E-03	3.53E-03	5.51E-03
IMP731	020909	2.75E-02	2.20E-02	3.44E-02

Comparisons of kd				
KD comparison	*Ratio*	*Lower 95% CI*	*Upper 95% CI*	*P value*
H5L7BW-H5L7	1.11715	0.81531	1.53073	0.4408
H5L7-IMP731	0.15478	0.11157	0.21471	<.0001

Example 3: Evaluation of the LAG-3-His binding epitope of anti-LAG-3 humanised variants in comparison with chimeric antibody IMP731 using the ProteOn™

An epitope binning experiment was performed with H5L7 to evaluate whether the LAG-3 epitope within which IMP731 binds was conserved upon humanisation. Furthermore, the binding epitope of fucosylated and afucosylated humanised variants was also compared.

Epitope binding was evaluated using the ProteOn™ XPR36 (BioRad™) biosensor machine, by assessing whether anti-LAG-3 antibodies were able to simultaneously bind to LAG-3-His in complex with antibody captured on the ProteOn™ chip surface. IMP731 and non-competitive murine antibody 17B4 were utilised as controls in this assay.

The antibodies to be tested were biotinylated using Ez-Link-sulfo-NHS biotinylation kit. Each biotinylated antibody was captured on a separate flow cell on a neutravidin NLC chip using a vertical

injection. After antibody capture, the surface was blocked with biocytin at 2.5mg/ml. Using the co-inject facility inherent to the ProteOn run software, LAG-3 ECD-His6 was injected over the coupled antibodies at 100nM, followed by the un-biotinylated antibodies at 100nM with both injections being horizontal so that the LAG-3-His and the antibodies cross all 6 neutravidin captured antibodies. The assay was run at 25°c and in HBS-EP on the ProteOn XPR36 Protein Interaction Array System.

Data analysis was carried out using report points taken after the LAG-3-His injection and report points taken after the un-biotinylated antibody analyte injection. The overall response was calculated by subtracting the response seen with the antibody binding from the response seen with LAG-3 ECD-His6 binding. A positive resonance unit (RU) value meant that antibody analyte injection had bound to LAG-3 ECD-His6 complexed with the biotinylated antibody on the neutravidin capture surface, indicative of binding at non-competitive epitopes. No response or a negative response meant that antibody analyte injection had not bound to LAG-3 ECD-His6 complexed with the biotinylated antibody on the neutravidin capture surface, indicating antibodies bind at competitive epitopes.

Anti-LAG-3 humanised variants (fucosylated and afucosylated) are unable to bind to human LAG-3 ECD-His6 in complex with IMP731, indicative that the epitope for LAG-3 ECD-His6 is shared and thus conserved. Murine antibody 17B4 is able to bind to human LAG-3 ECD-His6 in complex with IMP731 substantiating that this antibody is non-competitive for LAG-3 ECD-His6 binding with IMP731. Conversely, the humanised antibodies are able to bind to human LAG-3 ECD-His6 in complex with 17B4.

The results confirm that there has been no alteration in epitope between the chimeric IMP731 and the humanised variant of IMP731 tested in this experiment. The experiment also shows that there is no difference between fucosylated and afucosylated antibodies for binding.

Example 4: Binding analysis of anti-LAG-3 humanised antibodies to recombinant cynomolgus macaque and baboon LAG-3 ECD-His6 using the Biacore™T100

The binding cross reactivity of anti-LAG-3 humanised antibodies for both cynomolgus macaque (cyno) and baboon recombinant LAG-3 ECD-His6 (SEQ ID NOs 52 and 53, respectively) was assessed using the Biacore™ T100 (GE Healthcare™).

Protein A was immobilised on a CM5 chip by primary amine coupling. This surface was then used to capture the humanised antibodies. In-house generated recombinant cynomolgus macaque and baboon LAG-3 ECD-His6 were then passed over the captured antibodies and regeneration was carried out using 50mM NaOH. LAG-3 ECD-His6 was passed over at 16, 4, 1, 0.25 and 0.0625nM. The binding curves were double referenced with buffer injection (i.e. 0nM) and the data was fitted to the T100 analysis software using the 1:1 model. The run was carried out at 37°c using HBS-EP as the running buffer.

H5L7, H5L7BW and IMP731 bind with comparable affinity to both cynomolgus macaque and baboon recombinant LAG-3 ECD-His6. Data was generated from separate experiments, however chimeric antibody IMP731 was utilised as a control between experiments.

This data indicates that both non-human primate recombinant LAG-3 orthologues bind to the H5L7 derived antibodies with a 10 fold improvement in affinity in comparison with human recombinant LAG-3 ECD-His6 (SEQ ID NO: 51) (H5L7: human LAG-3 0.208nM, cyno LAG-3 0.017nM and baboon LAG-3 0.022nM; H5L7BW human LAG-3 0.218nM, cyno LAG-3 0.021nM and baboon LAG-3 0.024nM). Whilst both non-human primate recombinant LAG-3 orthologues bind to IMP731 derived antibodies with an improvement in affinity of approximately 100 fold in comparison with human recombinant LAG-3 ECD-His6 (SEQ ID NO: 51) (IMP731: human LAG-3 2.76nM, cyno LAG-3 0.021nM and baboon LAG-3 0.019nM).

Example 5: Binding profiles of H5L7BW, H5L7 and IMP731 to human LAG-3 expressing EL4 cells, and human primary activated CD3+ T cells

Human LAG-3 expressing EL4 cells were incubated with either IMP731, H5L7 or H5L7BW Alexa647-conjugated antibodies at varying concentrations of up to 50µg/ml for 30 minutes at room temperature. Cells were washed with FACS buffer (PBS+0.5% BSA) to remove unbound antibody.

$CD3^+$ T cells were prepared from PBMCs by negative selection using Untouched Human T cell Dynal beads. $CD3^+$ T cells were activated by incubation with immobilised anti-CD3 and anti-CD28 and soluble recombinant human IL-12 for 3 days at 37°C. Activated cells were incubated with Alexa 647-conjugated antibodies of varying concentrations up to 3µg/ml for 30 minutes at room temperature. Cells were washed with FACS buffer (PBS+0.5% BSA).

EL4 cells and $CD3^+$ T cells were analysed by FACS using a Beckman Coulter FC 500 flow cytometer. FACS raw data were analysed using CXP Analysis software (Beckman Coulter). The data was initially plotted on a forward-scatter versus side-scatter plot and the population of cells of interest were gated. This gated population was then plotted as a histogram displaying fluorescence intensity and the mean fluorescence intensity (MFI) calculated. MFI values were then plotted in GraphPad Prism 5 software to generate dose response curves.

Binding profiles of H5L7BW, H5L7 and IMP731 to human LAG-3 expressing EL4 cells, and human primary activated CD3+ T cells are shown in Fig. 1. The three antibodies exhibited similar binding characteristics to human LAG-3 expressing EL4 cells (Fig. 1A) and activated human CD3+ T cells (Fig. 1B).

Example 6: Assessment of the depleting activity of H5L7BW and H5L7 by antibody dependent cellular cytotoxicity (ADCC) in primary human T cells

The donors used in these experiments were screened for re-call responses to the CD4 antigens present in Revaxis, (Diptheria, Tetanus and Poliomyelitis) and to either a CMVpp65 peptide pool or to a CD8 peptide pool, which contained peptide epitopes to CMV, EBV and Influenza. The antigen used to perform initial studies was the CMVpp65 peptide pool. However, due to the limited number of donors that demonstrated a re-call response to this antigen, Revaxis and the CD8 peptide pool were the antigens used to generate the majority of the potency data for the anti-LAG3 antibodies.

Peripheral blood was collected from healthy human volunteers on day 0 (25mL) and day 5 (75mL) of the experiment and was used to prepare mononuclear cells by ficollplaque density gradient centrifugation. The PBMCs prepared on day 0 were labeled using the CellTrace™ Violet Cell Proliferation Kit, in accordance with the manufacturer's instructions, after which they were washed, seeded in 24-well flat bottomed tissue culture plates at a density of 2x106/mL in medium and stimulated with antigen (Revaxis and the CD8 peptide pool were used at a dilution of 1 in 1000; the CMVpp65 peptide was used at a dilution of 1 in 100). The PBMCs were incubated for 5 days at 37°C in a 5% CO2 humidified incubator.

Autologous donor NK cells were purified from the PBMCs prepared on day 5 of the experiment by negative selection using kits from either Invitrogen or Miltenyi Biotec in accordance with the specific instructions of each manufacturer. The purified NK cells were counted and diluted to a density of 1.3x106/mL in medium.

The cells that had been stimulated with antigen for 5 days were washed, counted and diluted to a density of 2x106/viable cells/mL in medium.

Autologous donor NK cells (80µL) and antigen activated cells (100µL) were pipetted into round-bottomed 5mL polystyrene FACS tubes with test antibody or medium (20µL). The final concentrations of the anti LAG-3 antibodies tested ranged from 1000 to 0.015ng/mL. The samples were incubated for 18 h at 37°C in a 5% CO2 humidified incubator. After 18 h the ADCC assay samples were analysed for the presence of antigen specific LAG-3 positive T cells using flow cytometry. Briefly, the samples were washed in FACS buffer, blocked with human IgG (3µg/tube), and incubated with mouse anti-human CD4, CD8, CD337, CD25 and LAG-3 flurochrome conjugated antibodies for 30 minutes in the dark at room temperature. After a further wash step in PBS the cells were incubated in the presence of a fixable green dead cell for 30 minutes in the dark at room temperature. The samples were finally washed with PBS, fixed and analysed by flow cytometry using a 60 second acquisition time at a flow rate of 1µL per second.

All sample data were acquired using the BD FACSCanto II Flow Cytometer with FACS Diva software version 6.1.3 (BD BioSciences). The Live/Dead fixable green dead cell stain was used as a dead cell exclusion marker and appropriate isotype and FMO-1 controls were used to define negative populations. Briefly dead cells were omitted from the analysis using a plot of forward scatter (FSC-A) against fluorescence in FL1 (Green dead cell stain). Doublets were then excluded from the analysis by using a plot of FSC-W against FSC-H. Viable single lymphocytes were

subsequently identified and gated using a plot of forward scatter (FSC-A) against side scatter (SSC-A). CD4 antigen specific T cells were identified from this gated population of cells using plots of CD4 fluorescence against SSC-A and Violet Dye fluorescence against CD4 fluorescence respectively. Antigen specific CD4 T cells were identified by a reduction of Violet Dye fluorescence. A further plot of CD25 fluorescence against LAG-3 fluorescence was drawn to confirm the activation state of this population of cells and that they expressed LAG-3. Similar plots were drawn to identify antigen specific CD8 T cells.

The percentages of antigen specific CD4 and CD8 T cells present in each sample (as a percentage of the viable lymphocyte population) were recorded. Nonlinear variable slope curve-fits of these data were plotted and EC50 values were generated using GraphPad Prism software (v5.03).

To calculate the maximum level of depletion observed in an assay, at the highest concentration of antibody tested, the following formula was used: (1-(% Antigen specific T cells remaining after antibody treatment)/(% Antigen specific T cells remaining in the absence of antibody))*100.

Potency data for the depletion of LAG3 positive antigen specific CD8 and CD4 T cells by H5L7BW and H5L7 was generated using the *in vitro* assay system detailed above. H5L7BW induced depletion of LAG3 positive antigen specific CD4 and CD8 T cells by ADCC in six of the seven donors studied for disappearance of the respective cell types. The potency of H5L7BW in antigen specific CD4 T cells, as quantified by EC50 values, ranged from 14pg/mL to 3.4ng/mL with maximum levels of depletion ranging from 44 to 78%. The potency of this antibody in antigen specific LAG-3 positive CD8 T cells ranged from 122pg/mL to 17.5ng/mL, with maximum levels of depletion ranging from 39 to 87%. H5L7 mediated low levels of depletion, or was inactive, in the donors studied.

Example 7: Assessment of the depleting activity of H5L7BW and H5L7 in an *in-vivo* human PBMC/mouse SCID xenograft model

This assay describes the use of a human PBMC/mouse SCID xenograft model to assess *in vivo* depletion efficacy of the monoclonal, fully humanised, afucosylated LAG-3 depleting antibody H5L7BW on activated human T cells. Healthy volunteer peripheral blood mononuclear cells (PBMCs) were isolated and stimulated overnight (anti-CD3, IL-12) to induce LAG-3 expression prior to injection into the peritoneum of immuno-compromised SCID mice. LAG-3 depleting or control antibodies were either co-administered into the peritoneum or injected intravenously.

Depletion of LAG-3 positive cells was assessed by flow cytometry in peritoneal lavage samples 5 or 24 hours after cell injection.

Mice were injected with activated huPBMCs (4 x 106- 2 x 107cells in 0.4ml of PBS) by the intraperitoneal route. Depending on the particular study route, LAG-3 antibodies or huIgG1 BioWa controls were either co-administered i.p. with the huPBMCs or mice were pre-treated intravenously 18h prior to huPBMC injection. 5 or 24 hours post-cell injection, mice were euthanized, a peritoneal

lavage was performed and the cellular content of the lavage buffer analysed by flow cytometry. Briefly, peritoneal lavage involved 3 x 5ml washes of the intact peritoneal cavity using cold PBS containing 3mM EDTA.

All sample data were acquired using the BD FACSCanto II Flow Cytometer with FACS Diva software version 6.1.3 (BD BioSciences). Approximately 1 x 106 cells (where possible) were added per FACS tube, the cell suspensions centrifuged at 1500 rpm for 10 minutes, and the pellet then re-suspended in 3ml PBS. The supernatants were then carefully decanted and the cell pellets re-suspended in 100µl cold FACS wash buffer. 15µl FcR Blocking Reagent was then added per tube and the cells incubated for 10 minutes at room temperature. 5µl of each staining antibody (10µl of 1:100 pre-diluted anti-LAG-3 blocking/detection antibody 17B4-PE) or isotype control were then added respectively and incubated for 20 minutes at room temperature protected from light. The cells were subsequently washed by addition of 4 ml FACS buffer per tube and centrifugation at 1500 rpm for 5 minutes after which the supernatant was carefully decanted. This washing step was repeated. Finally the cells were re-suspended in 300µl FACS buffer and analysed by flow cytometry. In addition to LAG-3 detection by use of the fluorescently labeled LAG-3 blocking antibody 17B4-PE, the following T cell and activation markers were used for T cell phenotyping: CD45, CD4, CD8, and CD25. Percentages of CD4 and CD8 T cells were expressed as percentage of CD45 positive cells. LAG-3 positive T cell populations were expressed as percentages of their parent populations CD4 and CD8.

FACS Diva software version 6.1.3 was used to generate batch analyses of individual cell counts/events and cell population percentages. Data were analysed with SAS version 9.2.2 software using a generalized linear model for binomial data. This analysis directly models the cell count as a proportion of the parent population. In this way, the size of the parent population is taken into account during the analysis. Means were calculated for proportions of target cell type for each treatment, along with 95% confidence intervals. These were expressed as percentages.

Planned comparisons of treatments versus Control were made using odds ratios. This expresses the odds of having a target cell type in one treatment as a ratio to the odds of having the target cell type on control treatment. An odds ratio < 1 would indicate a reduced odds of having the cell type in the treatment of interest compared to the control. An odds ratio < 1 would indicate a reduced odds of having the cell type in the treatment of interest compared to the control.

All experiments were performed using PBMCs from individual healthy blood donors and due to the large blood volumes required per experiment, no donor was used more than once. LAG-3 expression levels after overnight stimulation varied greatly between donors (ranging from 2-73% cell surface expression) but these differences in expression levels had no effect on the highly significant depletion efficacy of the tested antibodies.

The human PBMC/mouse SCID *in vivo* model was successfully used to show depletion of activated human, LAG-3 expressing T cells in the peritoneum of immunocompromised SCID mice. Depending on donor, route of administration and time point of analysis, between 84.22-99.71% of

LAG-3 positive human CD4 T cells and between 84.64-99.62% of LAG-3 positive human CD8 T cells were depleted. As shown in Figure 2, co-administration of 5mg/kg H5L7BW to activated human PBMCs in the peritoneum of SCID mice led to highly significant depletion of LAG-3 positive CD4 and CD8 positive T cells 24 hours after injection compared to Control IgG injected animals.

Figure 3 highlights the comparison between 5mg/kg H5L7BW and H5L7 5 hours after co-i.p. administration to activated human PBMCs as described before. Both antibodies induced highly significant depletion of LAG-3 positive CD4 and CD8 T cells (Figure 3A).

As shown in Figure 4, administration of 5mg/kg H5L7BW via the intra-venous route resulted in a highly statistically significant depletion of LAG-3 positive T cells after 5 hours (Figure 4A), similar to what was observed in the experiments with i.p. co-administered LAG-3 depletion antibodies. The comparison between i.v. administered H5L7BW, H5L7 and IMP731 (all at 5mg/kg) 5 hours after i.p. administration of activated human PBMCs revealed very similar depletion efficacies between the 3 molecules compared to control treated animals (Figure 5). Each of the 3 tested LAG-3 depleting antibodies caused highly significant reduction in the number of LAG-3 positive CD4 and CD8 T cells (Figure 5A) with H5L7BW demonstrating greater depletion capacity compared to H5L7 or IMP731.

Example 8: Binding analysis of anti-LAG-3 humanised antibodies to recombinant soluble human Fc gamma receptors using the ProteOn™

Human FcγRIIIa binding was investigated in order to assess the ability of H5L7 and H5L7BW to induce antibody dependent cell-mediated cytotoxicity (ADCC). H5L7 and H5L7BW anti-LAG-3 antibodies were assessed for binding to recombinant soluble human FcγRIIIa in addition to FcγRI and FcγRII receptors using the ProteOn™ XPR36 (BioRad™) biosensor machine, and were compared against chimeric antibody IMP731.

A goat anti-poly-histidine IgG was immobilised on a GLM biosensor chip by primary amine coupling. This surface was used as a capture surface for the poly-histidine tagged human Fc gamma receptors. Antibodies to be tested were used as the analyte and passed over at 2048nM, 512nM, 128nM, 32nM and 8nM with an injection of 0nM (i.e. buffer alone) used to double reference the binding curves. The goat anti-poly-histidine IgG surface was regenerated with 100mM phosphoric acid between interactions. The run was carried out on the ProteOn XPR36 Protein Array Interaction System at 25°c and using HBS-EP as running buffer. Data was analysed for each receptor separately, setting a global R-max and using the Equilibrium Model inherent to the ProteOn's analysis software. Control molecules were run at the beginning and the end of the set of samples to be tested to ensure comparability of results. Data was compared from two experiments and hybrid control antibodies used as controls between experiments.

The results show that H5L7BW bound both polymorphisms of FcγRIIIa (valine V158 and phenylalanine F158) with an improved affinity of approximately 10 fold in comparison to H5L7 (see

Table 6). Fucosylated antibody H5L7 bound to FcγRIIIa with a similar affinity as chimeric antibody IMP731.

No significant changes were observed between the binding of the humanised fucosylated and afucosylated anti-LAG-3 antibodies for the FcγRI or FcγRIIa receptors.

Table 6: Binding of H5L7 and H5L7BW to human Fc gamma receptors

Antibody	FcγRI (nM)	FcγRIIa R131 (nM)	FcγRIIa H131 (nM)	FcγRIIIa V158 (nM)	FcγRIIIa F158 (nM)
IMP731	39.0	2620.0	1280.0	406.0	1750.0
H5L7	26.3	792.0	638.0	236.0	752.0
H5L7BW	26.4	1490.0	1430.0	21.8	81.1

Sequences

Table 7: Sequence Summary

Sequence	Sequence Identifier (SEQ ID No.)	
	Amino acid Sequence	Polynucleotide Sequence
H5L7, CDRL1 (Kabat defined)	1	57
H5L7, CDRL2 (Kabat defined)	2	58
H5L7, CDRL3 (Kabat defined)	3	59
H5L7, VL	4	60
H5L7, light chain humanised construct	5	61
H5L7, CDRH1 (Kabat defined)	6	62
H5L7, CDRH2 (Kabat defined)	7	63
H5L7, CDRH3 (Kabat defined)	8	64
H5L7, VH	9	65
H5L7, heavy chain humanised construct	10	66
H1L7, light chain humanised construct	11	67
H1L7, heavy chain humanised construct	12	68
J7L7, light chain humanised construct	13	69
J7L7, heavy chain humanised construct	14	70
H4L7, light chain humanised construct	15	71
H4L7, heavy chain humanised construct	16	72
J11L7, light chain humanised construct	17	73
J11L7, heavy chain humanised construct	18	74

H2L7, light chain humanised construct	19	75
H2L7, heavy chain humanised construct	20	76
J13L7, light chain humanised construct	21	77
J13L7, heavy chain humanised construct	22	78
H7L7, light chain humanised construct	23	79
H7L7, heavy chain humanised construct	24	80
J0L7, light chain humanised construct	25	81
J0L7, heavy chain humanised construct	26	82
H0L7, light chain humanised construct	27	83
H0L7, heavy chain humanised construct	28	84
H1L1, light chain humanised construct	29	85
H1L1, heavy chain humanised construct	30	86
H5L1, light chain humanised construct	31	87
H5L1, heavy chain humanised construct	32	88
J7L1, light chain humanised construct	33	89
J7L1, heavy chain humanised construct	34	90
J11L1, light chain humanised construct	35	91
J11L1, heavy chain humanised	36	92

construct		
J13L1, light chain humanised construct	37	93
J13L1, heavy chain humanised construct	38	94
H7L1, light chain humanised construct	39	95
H7L1, heavy chain humanised construct	40	96
J0L1, light chain humanised construct	41	97
J0L1, heavy chain humanised construct	42	98
H0L1, light chain humanised construct	43	99
H0L1, heavy chain humanised construct	44	100
Human kappa chain constant region	45	101
Human IgG1 constant region	46	102
IMP731, VH	47	103
IMP731, VL	48	104
IMP731, heavy chain sequence	49	105
IMP731, light chain sequence	50	106
Recombinant human LAG-3-ECD-His6	51	107
Recombinant cynomolgus macaque LAG-3 ECD-His6	52	108
Recombinant baboon LAG-3 ECD-His6	53	109
Leader sequence used for humanised variant heavy and light chain constructs	54	110
IMP731 Leader sequence	55	111
Leader sequence used for	56	112

soluble LAG-3 constructs		

SEQ ID NO. 1

KSSQSLLNPSNQKNYLA

SEQ ID NO.2

FASTRDS

SEQ ID NO.3

LQHFGTPPT

SEQ ID NO.4

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNPSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
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SEQ ID NO.5

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SEQ ID NO. 6

AYGVN

SEQ ID NO. 7

MIWDDGSTDYDSALKS

SEQ ID NO. 8

EGDVAFDY

SEQ ID NO. 9

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SEQ ID NO. 10

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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
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SEQ ID NO.11

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SEQ ID NO.12

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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
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SEQ ID NO.13

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SEQ ID NO.14

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SEQ ID NO.15

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SEQ ID NO.16

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SEQ ID NO.17

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SEQ ID NO.18

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SEQ ID NO.19

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SEQ ID NO.20

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SEQ ID NO.21

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SEQ ID NO.22

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SEQ ID NO.23

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SEQ ID NO.25

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SEQ ID NO.26

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SEQ ID NO.27

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SEQ ID NO.29

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SEQ ID NO.30

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SEQ ID NO.31

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FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.33

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNGSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCLQHFGTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.34

QVQLVQSGAEVKKPGSSVKVSCKASGFSLTAYGVNWVRQAPGQGLEWMGMIWDDGSTDYNSALKSRVTITADKS
TSTAYMELSSLRSEDTAVYYCAREGDVAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.35

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNGSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCLQHFGTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.36

QVQLVQSGAEVKKPGSSVKVSCKASGFSLTAYGVNWVRQAPGQGLEWMGMIWDDGSTDYDSALKSRVTITADKS
TSTAYMELSSLRSEDTAVYYCAREGDVAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.37

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNGSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCLQHFGTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.38

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSAYGVNWVRQAPGQGLEWMGMIWDDGSTDYDSALKSRVTITADKS
TSTAYMELSSLRSEDTAVYYCAREGDVAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.39

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNGSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCLQHFGTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.40

QVQLQESGPGLVKPSETLSLTCTVSGGSISAYGVNWIRQPPGKGLEWIGMIWDDGSTDYDSALKSRVTISVDTS
KNQFSLKLSSVTAADTAVYYCAREGDVAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.41

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNGSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCLQHFGTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.42

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSAYGVNWVRQAPGQGLEWMGMIWDDGSTDYNSALKSRVTITADKS
TSTAYMELSSLRSEDTAVYYCAREGDVAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG

FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.43

DIQMTQSPSSLSASVGDRVTITCKSSQSLLNGSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCLQHFGTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.44

QVQLQESGPGLVKPSETLSLTCTVSGGSISAYGVNWIRQPPGKGLEWIGMIWDDGSTDYNSALKSRVTISVDTS
KNQFSLKLSSVTAADTAVYYCAREGDVAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.45

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS
KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.46

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO.47

QVQLKESGPGLVAPSQSLSITCTVSGFSLTAYGVNWVRQPPGKGLEWLGMIWDDGSTDYNSALKSRLSISKDNS
KSQVFLKMNSLQTDDTARYYCAREGDVAFDYWGQGTTLTVSS

SEQ ID NO.48

DIVMTQSPSSLAVSVGQKVTMSCKSSQSLLNGSNQKNYLAWYQQKPGQSPKLLVYFASTRDSGVPDRFIGSGSG
TDFTLTISSVQAEDLADYFCLQHFGTPPTFGGGTKLEIKR

SEQ ID NO.49 (Note different leader sequence used for chimeric antibodies)

QVQLKESGPGLVAPSQSLSITCTVSGFSLTAYGVNWVRQPPGKGLEWLGMIWDDGSTDYNSALKSRLSISKDNS
KSQVFLKMNSLQTDDTARYYCAREGDVAFDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

SEQ ID NO.50

DIVMTQSPSSLAVSVGQKVTMSCKSSQSLLNGSNQKNYLAWYQQKPGQSPKLLVYFASTRDSGVPDRFIGSGSG
TDFTLTISSVQAEDLADYFCLQHFGTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO.51

LQPGAEVPVVWAQEGAPAQLPCSPTIPLQDLSLLRRAGVTWQHQPDSGPPAAAPGHPLAPGPHPAAPSSWGPRP
RRYTVLSVGPGGLRSGRLPLQPRVQLDERGRQRGDFSLWLRPARRADAGEYRAAVHLRDRALSCRLRLRLGQAS
MTASPPGSLRASDWVILNCSFSRPDRPASVHWFRNRGQGRVPVRESPHHHLAESFLFLPQVSPMDSGPWGCILT
YRDGFNVSIMYNLTVLGLEPPTPLTVYAGAGSRVGLPCRLPAGVGTRSFLTAKWTPPGGGPDLLVTGDNGDFTL
RLEDVSQAQAGTYTCHIHLQEQQLNATVTLAIITVTPKSFGSPGSLGKLLCEVTPVSGQERFVWSSLDTPSQRS
FSGPWLEAQEAQLLSQPWQCQLYQGERLLGAAVYFTELSSPHHHHHH

SEQ ID NO.52

PQPGAEISVVWAQEGAPAQLPCSPTIPLQDLSLLRRAGVTWQHQPDSGPPAPAPGHPPAPGHRPAAPYSWGPRP
RRYTVLSVGPGGLRSGRLPLQPRVQLDERGRQRGDFSLWLRPARRADAGEYRATVHLRDRALSCRLRLRVGQAS
MTASPPGSLRTSDWVILNCSFSRPDRPASVHWFRSRGQGRVPVQGSPHHHLAESFLFLPHVGPMDSGLWGCILT
YRDGFNVSIMYNLTVLGLEPATPLTVYAGAGSRVELPCRLPPAVGTQSFLTAKWAPPGGGPDLLVAGDNGDFTL
RLEDVSQAQAGTYICHIRLQGQQLNATVTLAIITVTPKSFGSPGSLGKLLCEVTPASGQEHFVWSPLNTPSQRS
FSGPWLEAQEAQLLSQPWQCQLHQGERLLGAAVYFTELSSPHHHHHH

SEQ ID NO.53

PQPGAEISVVWAQEGAPAQLPCSPTIPLQDLSLLRRAGVTWQHQPDSGPPAPAPGHPPAPGHRPAAPYSWGPRP
RRYTVLSVGPGGLRSGRLPLQPRVQLDERGRQRGDFSLWLRPARRADAGEYRATVHLRDRALSCRLRLRVGQAS
MTASPPGSLRTSDWVILNCSFSRPDRPASVHWFRSRGQGQVPVQESPHHHLAESFLFLPHVGPMDSGLWGCILT
YRDGFNVSIMYNLTVLGLEPTTPLTVYAGAGSRVELPCRLPPAVGTQSFLTAKWAPPGGGPDLLVVGDNGNFTL
RLEDVSQAQAGTYICHIRLQGQQLNATVTLAIITVTPKSFGSPGSLGKLLCEVTPASGQERFVWSPLNTPSQRS
FSGPWLEAQEAQLLSQPWQCQLHQGERLLGAAVYFTELSSPHHHHHH

SEQ ID NO.54

MGWSCIILFLVATATGVHS

SEQ ID NO.55

MESQTQVLMFLLLWVSGACA

SEQ ID NO.56

MPLLLLLPLL WAGALA

SEQ ID NO. 57

AAGAGCAGCCAGAGCCTGCTGAACCCCAGCAACCAGAAGAACTACCTGGCC

SEQ ID NO. 58

TTCGCCTCTACCAGGGATTCC

SEQ ID NO. 59

CTGCAGCACTTCGGCACCCCTCCCACT

SEQ ID NO. 60

GACATCCAGATGACCCAGAGCCCCTCTAGCCTCAGCGCCAGCGTGGGCGACAGGGTGACCATCACCTGCAAGAG
CAGCCAGAGCCTGCTGAACCCCAGCAACCAGAAGAACTACCTGGCCTGGTACCAGCAGAAACCCGGCAAGGCCC
CCAAGCTGCTGGTCTACTTCGCCTCTACCAGGGATTCCGGCGTCCCCAGCAGGTTCAGCGGCAGCGGCAGCGGC
ACCGACTTCACACTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCTGCAGCACTTCGG
CACCCCTCCCACTTTTGGCCAGGGCACCAAGCTGGAGATTAAGCGT

SEQ ID NO. 61

GACATCCAGATGACCCAGAGCCCCTCTAGCCTCAGCGCCAGCGTGGGCGACAGGGTGACCATCACCTGCAAGAG
CAGCCAGAGCCTGCTGAACCCCAGCAACCAGAAGAACTACCTGGCCTGGTACCAGCAGAAACCCGGCAAGGCCC
CCAAGCTGCTGGTCTACTTCGCCTCTACCAGGGATTCCGGCGTCCCCAGCAGGTTCAGCGGCAGCGGCAGCGGC
ACCGACTTCACACTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCTGCAGCACTTCGG
CACCCCTCCCACTTTTGGCCAGGGCACCAAGCTGGAGATTAAGCGTACGGTGGCCGCCCCCAGCGTGTTCATCT
TCCCCCCCAGCGATGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGG
GAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
ACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGC

SEQ ID NO. 62

GCCTACGGCGTCAAC

SEQ ID NO. 63

ATGATCTGGGACGACGGCAGCACCGACTACGACAGCGCCCTGAAGAGC

SEQ ID NO. 64

GAGGGCGACGTGGCCTTCGATTAC

SEQ ID NO. 65

CAGGTGCAGCTCCAGGAGAGCGGCCCCGGCCTGGTGAAGCCTAGCGAGACCCTGAGCCTGACCTGCACCGTGAG
CGGCTTCTCCCTGACCGCCTACGGCGTCAACTGGATCAGGCAGCCCCCCGGCAAAGGCCTGGAGTGGATTGGGA
TGATCTGGGACGACGGCAGCACCGACTACGACAGCGCCCTGAAGAGCAGGGTGACCATCAGCGTGGACACCAGC
AAGAACCAGTTCAGCCTGAAGCTGAGCAGCGTGACTGCCGCCGACACCGCCGTCTATTACTGCGCCAGGGAGGG
CGACGTGGCCTTCGATTACTGGGGCCAGGGCACACTAGTGACCGTGTCCAGC

SEQ ID NO. 66

CAGGTGCAGCTCCAGGAGAGCGGCCCCGGCCTGGTGAAGCCTAGCGAGACCCTGAGCCTGACCTGCACCGTGAG
CGGCTTCTCCCTGACCGCCTACGGCGTCAACTGGATCAGGCAGCCCCCCGGCAAAGGCCTGGAGTGGATTGGGA
TGATCTGGGACGACGGCAGCACCGACTACGACAGCGCCCTGAAGAGCAGGGTGACCATCAGCGTGGACACCAGC
AAGAACCAGTTCAGCCTGAAGCTGAGCAGCGTGACTGCCGCCGACACCGCCGTCTATTACTGCGCCAGGGAGGG
CGACGTGGCCTTCGATTACTGGGGCCAGGGCACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGGCCCCAGCG
TGTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGGGCTGCCTGGTGAAGGACTAC
TTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGACCAGCGGCGTGCACACCTTCCCCGCCGTGCT
GCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACCGTGCCCAGCAGCAGCCTGGGCACCCAGACCTACA
TCTGTAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACC
CACACCTGCCCCCCCTGCCCTGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCTAA
GGACACCCTGATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCACGAGGACCCTGAGG
TGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACCAAGCCCAGGGAGGAGCAGTACAAC
AGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCTGAACGGCAAGGAGTACAAGTGTAA
GGTGTCCAACAAGGCCCTGCCTGCCCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCC
AGGTGTACACCCTGCCCCCTAGCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGC
TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCC
TGTGCTGGACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCA
ACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGAGCCTGAGCCTGTCCCCT
GGCAAG

SEQ ID NO. 67

GACATCCAGATGACCCAGAGCCCCTCTAGCCTCAGCGCCAGCGTGGGCGACAGGGTGACCATCACCTGCAAGAG
CAGCCAGAGCCTGCTGAACCCCAGCAACCAGAAGAACTACCTGGCCTGGTACCAGCAGAAACCCGGCAAGGCCC
CCAAGCTGCTGGTCTACTTCGCCTCTACCAGGGATTCCGGCGTCCCCAGCAGGTTCAGCGGCAGCGGCAGCGGC
ACCGACTTCACACTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCTGCAGCACTTCGG

CACCCCTCCCACTTTTGGCCAGGGCACCAAGCTGGAGATTAAGCGTACGGTGGCCGCCCCCAGCGTGTTCATCT
TCCCCCCCAGCGATGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGG
GAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
ACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGC

SEQ ID NO. 68

CAGGTGCAGCTCCAGGAGAGCGGCCCCGGCCTGGTGAAGCCTAGCGAGACCCTGAGCCTGACCTGCACCGTGAG
CGGCTTCTCCCTGACCGCCTACGGCGTCAACTGGATCAGGCAGCCCCCCGGCAAAGGCCTGGAGTGGATTGGGA
TGATCTGGGACGACGGCAGCACCGACTACAACAGCGCCCTGAAGAGCAGGGTGACCATCAGCGTGGACACCAGC
AAGAACCAGTTCAGCCTGAAGCTGAGCAGCGTGACTGCCGCCGACACCGCCGTCTATTACTGCGCCAGGGAGGG
CGACGTGGCCTTCGATTACTGGGGCCAGGGCACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGGCCCCAGCG
TGTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGGGCTGCCTGGTGAAGGACTAC
TTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGACCAGCGGCGTGCACACCTTCCCCGCCGTGCT
GCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACCGTGCCCAGCAGCAGCCTGGGCACCCAGACCTACA
TCTGTAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACC
CACACCTGCCCCCCCTGCCCTGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCTAA
GGACACCCTGATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCACGAGGACCCTGAGG
TGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACCAAGCCCAGGGAGGAGCAGTACAAC
AGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCTGAACGGCAAGGAGTACAAGTGTAA
GGTGTCCAACAAGGCCCTGCCTGCCCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCC
AGGTGTACACCCTGCCCCCTAGCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGC
TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCC
TGTGCTGGACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCA
ACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGAGCCTGAGCCTGTCCCCT
GGCAAG

SEQ ID NO. 69

GACATCCAGATGACCCAGAGCCCCTCTAGCCTCAGCGCCAGCGTGGGCGACAGGGTGACCATCACCTGCAAGAG
CAGCCAGAGCCTGCTGAACCCCAGCAACCAGAAGAACTACCTGGCCTGGTACCAGCAGAAACCCGGCAAGGCCC
CCAAGCTGCTGGTCTACTTCGCCTCTACCAGGGATTCCGGCGTCCCCAGCAGGTTCAGCGGCAGCGGCAGCGGC
ACCGACTTCACACTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCTGCAGCACTTCGG
CACCCCTCCCACTTTTGGCCAGGGCACCAAGCTGGAGATTAAGCGTACGGTGGCCGCCCCCAGCGTGTTCATCT
TCCCCCCCAGCGATGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGG
GAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
ACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGC

SEQ ID NO. 70

CAGGTGCAGCTCGTGCAGAGCGGGGCCGAAGTCAAGAAACCCGGCAGCTCCGTGAAGGTGAGCTGCAAGGCCAG
CGGCTTCTCTCTCACTGCCTACGGCGTGAACTGGGTGAGGCAGGCTCCCGGCCAGGGCCTGGAGTGGATGGGCA
TGATCTGGGACGACGGCAGCACCGACTACAACAGCGCCCTGAAGAGCAGGGTGACCATCACCGCCGACAAGAGC
ACCAGCACCGCCTACATGGAACTGAGCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCGCCAGGGAGGG
CGACGTGGCCTTCGATTACTGGGGCCAGGGCACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGGCCCCAGCG
TGTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGGGCTGCCTGGTGAAGGACTAC
TTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGACCAGCGGCGTGCACACCTTCCCCGCCGTGCT
GCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACCGTGCCCAGCAGCAGCCTGGGCACCCAGACCTACA
TCTGTAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACC
CACACCTGCCCCCCCTGCCCTGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCTAA
GGACACCCTGATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCACGAGGACCCTGAGG
TGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACCAAGCCCAGGGAGGAGCAGTACAAC
AGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCTGAACGGCAAGGAGTACAAGTGTAA
GGTGTCCAACAAGGCCCTGCCTGCCCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCC
AGGTGTACACCCTGCCCCCTAGCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGC
TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCC
TGTGCTGGACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCA
ACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGAGCCTGAGCCTGTCCCCT
GGCAAG

SEQ ID NO. 71

GACATCCAGATGACCCAGAGCCCCTCTAGCCTCAGCGCCAGCGTGGGCGACAGGGTGACCATCACCTGCAAGAG
CAGCCAGAGCCTGCTGAACCCCAGCAACCAGAAGAACTACCTGGCCTGGTACCAGCAGAAACCCGGCAAGGCCC
CCAAGCTGCTGGTCTACTTCGCCTCTACCAGGGATTCCGGCGTCCCCAGCAGGTTCAGCGGCAGCGGCAGCGGC
ACCGACTTCACACTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCTGCAGCACTTCGG
CACCCCTCCCACTTTTGGCCAGGGCACCAAGCTGGAGATTAAGCGTACGGTGGCCGCCCCCAGCGTGTTCATCT
TCCCCCCCAGCGATGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGG
GAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
ACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGC

SEQ ID NO. 72

CAGGTGCAGCTCCAGGAGAGCGGCCCCGGCCTGGTGAAGCCTAGCGAGACCCTGAGCCTGACCTGCACCGTGAG
CGGCTTCTCCCTGACCGCCTACGGCGTCAACTGGATCAGGCAGCCCCCCGGCAAAGGCCTGGAGTGGCTGGGGA
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SEQ ID NO. 73

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ACCGACTTCACACTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCTGCAGCACTTCGG
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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 74

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SEQ ID NO. 75

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SEQ ID NO. 76

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SEQ ID NO. 77

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 78

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GGCAAG

SEQ ID NO. 79

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 80

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GGCAAG

SEQ ID NO. 81

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SEQ ID NO. 82

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SEQ ID NO. 83

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 84

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GGCAAG

SEQ ID NO. 85

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 86

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SEQ ID NO. 87

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 88

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GGCAAG

SEQ ID NO. 89

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SEQ ID NO. 90

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GGCAAG

SEQ ID NO. 91

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SEQ ID NO. 92

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GGCAAG

SEQ ID NO. 93

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SEQ ID NO. 94

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GGCAAG

SEQ ID NO. 95

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 96

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SEQ ID NO. 97

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SEQ ID NO. 98

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SEQ ID NO. 99

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CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT
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SEQ ID NO. 100

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GGCAAG

SEQ ID NO. 101

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SEQ ID NO. 102

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SEQ ID NO. 103

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SEQ ID NO. 104

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SEQ ID NO. 105

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GGTAAA

SEQ ID NO. 106

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SEQ ID NO. 107

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SEQ ID NO. 109

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SEQ ID NO. 110

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SEQ ID NO. 111

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SEQ ID NO. 112

ATGCCGCTGC TGCTACTGCT GCCCCTGCTG TGGGCAGGGG CGCTAGCT

Claims

1. An antigen binding protein which is capable of binding Lymphocyte Activation Gene 3 (LAG-3) and which comprises CDRL1, CDRL2 and CDRL3 from SEQ ID No. 5 and CDRH1, CDRH2 and CDRH3 from SEQ ID NO. 10.
2. An antigen binding protein according to claim 1, which comprises the following CDRs:

   CDRL1: SEQ ID NO. 1

   CDRL2: SEQ ID NO. 2

   CDRL3: SEQ ID NO. 3

   CDRH1: SEQ ID NO. 6

   CDRH2: SEQ ID NO. 7

   CDRH3: SEQ ID NO. 8
3. An antigen binding protein according to claim 1 or 2, which comprises a) the variable light chain (VL) of SEQ ID NO. 4 and b) the variable heavy chain (VH) of SEQ ID No. 9.
4. An antigen binding protein according to any of claims 1 to 3, wherein the antigen binding protein is capable of binding LAG-3 expressed on activated T-cells.
5. An antigen binding protein according to any of claims 1 to 4, wherein the antigen binding protein is capable of depleting LAG-3+ activated human T cells.
6. An antigen binding protein according to any of claims 1 to 5, wherein the antigen binding protein is a humanised antibody.
7. A humanised antibody according to claim 6, wherein the humanised antibody comprises a human IgG1 constant region.
8. A humanised antibody according to claim 7, which comprises a) a light chain sequence with at least 97% identity to SEQ ID NO. 5, and b) a heavy chain sequence with at least 97% identity to SEQ ID NO. 10, wherein the humanised antibody comprises CDRL1, CDRL2 and CDRL3 from SEQ ID No. 5 and CDRH1, CDRH2 and CDRH3 from SEQ ID NO. 10.
9. A humanised antibody according to claim 8, which comprises a) a light chain sequence of SEQ ID NO. 5, and b) a heavy chain sequence of SEQ ID NO. 10.
10. A humanised antibody according to any of claims 7 to 9, which is non-fucosylated.
11. A humanised antibody comprising the variable light chain (VL) of SEQ ID NO. 4 and the variable heavy chain (VH) of SEQ ID NO. 9, wherein the antibody does not comprise fucose on the core carbohydrate structure attached to Asn297.
12. An isolated nucleic acid molecule which encodes an antigen binding protein according to any of claims 1 to 6 or a humanised antibody according to any of claims 7 to 11.
13. An expression vector comprising a nucleic acid molecule according to claim 12.

14.A host cell comprising an expression vector according to claim 13.

15.A host cell comprising an expression vector according to claim 13, wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase has been inactivated in the host cell.

16.An antigen binding protein according to any of claims 1 to 6 or a humanised antibody according to any of claims 7 to 11 as produced by the host cell of claim 14 or 15.

17.A method of producing an antigen binding protein according to any of claims 1 to 6 or a humanised antibody according to any of claims 7 to 11, comprising a) culturing a host cell according to claim 14 under conditions suitable to express the antigen binding protein or antibody and b) isolating the antigen binding protein or antibody.

18. A method of producing a humanised antibody according to claim 10 or 11, comprising a) culturing a host cell according to claim 15 under conditions suitable to express the antigen binding protein or antibody, wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase has been inactivated in the recombinant host cell, and b) isolating the antibody.

19.A pharmaceutical composition comprising a) an antigen binding protein according to any of claims 1 to 6 or an antibody according to any of claims 7 to 11, and b) a pharmaceutically acceptable carrier.

20.An antigen binding protein as defined in any of claims 1 to 6 or a humanised antibody as defined in any of claims 7 to 11, for use in therapy.

21.An antigen binding protein as defined in any of claims 1 to 6 or a humanised antibody as defined in any of claims 7 to 11 for use in the treatment of an autoimmune disease selected from the group consisting of psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjogren's syndrome, multiple sclerosis, ulcerative colitis and autoimmune hepatitis.

22.Use of an antigen binding protein as defined in any of claims 1 to 6 or a humanised antibody as defined in any of claims 7 to 11 in the manufacture of a medicament for the treatment of an autoimmune disease selected from the group consisting of psoriasis, Crohn's disease, rheumatoid arthritis, primary biliary cirrhosis, systemic lupus erythematosus (SLE), Sjogren's syndrome, multiple sclerosis, ulcerative colitis and autoimmune hepatitis.