Title: Human CD3 binding antibody

The invention relates to the field of antibodies, in particular to the field of therapeutic antibodies. The antibodies can be used in the treatment of humans. More in particular the invention relates to antibodies and preferably bispecific antibodies for the treatment of a tumor.

Monoclonal antibodies that bind to human CD3 were among the first antibodies developed for therapeutic use in humans. Monoclonal CD3 binding antibodies are typically used for their immune suppressive qualities, for instance in transplant rejection. Antibodies which are bispecific for CD3 on T cells and for a surface target antigen on cancer cells, are capable of connecting any kind of T cell to a cancer cell, independently of T-cell receptor specificity, costimulation, or peptide antigen presentation. Such bispecific T-cell engaging antibodies show great promise in the treatment of various cancers and neoplastic growths.

WO2014/051433 (incorporated herein by reference) describes CD3 mAbs that are suitable candidates to serve as building block in the generation of bispecific antibodies that act as T-cell engager molecules. These CD3 mAbs are designated 3056 and 3896; the VH and VL sequences of these mAbs are disclosed in figure 22. Both the 3056 and 3896 CD3 mAbs have good properties in terms of functional activity. They bind to cell surface expressed CD3/TCR on human T cell lines with an affinity (KD) that is significantly less than the affinity of the well-known mouse anti-CD3 antibody mOKT3, resulting in a lower mean fluorescence intensity in flow cytometric analysis on $CD3^{POS}$ cells. Similarly, when immobilized on tissue culture plates, they induce T cell proliferation to a lesser extent when compared to mOKT3.

Without being bound by theory it is believed that a CD3 affinity that is significantly less than the affinity of mOKT3 is preferred in a bispecific T-cell engager format. It is preferred that the bispecific antibody binds to CD3 with an affinity that is less than the affinity of binding to the tumor antigen. Without being bound to theory it is believed that this difference in affinity permits preferential opsonization of the tumor cells by the bispecific antibody, thereby labelling them for destruction by immune effector cells including NK and/or T cells present in the vicinity.

The inventors observed that results obtained with the 3056 antibody exhibited batch to batch variation. This surprised the inventors as the variability was not an issue with the antibody 15C3, which has the same VH-sequence as antibody 3056 but a different light chain (described in WO2005/118635).

It is an object of the invention to provide a variant of antibody 3056 with essentially the same CD3 binding properties in kind, not necessarily in amount, with improved characteristics.

SUMMARY OF THE INVENTION

The invention provides an antibody that binds human CD3 which antibody comprises a heavy chain and light chain wherein said heavy chain comprises a variable region that comprises an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A.

The invention further provides a nucleic acid molecule that encodes an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A.

The combination X_1 and X_2 in an antibody as described herein is preferably X_1 = N and X_2 = A.

The invention further provides a cell that expresses the antibody and/or comprises the nucleic acid molecule.

An antibody of the invention is, unless otherwise specifically specified, preferably a bispecific antibody. The bispecific antibody preferably binds at least human CD3. In addition, the bispecific antibody preferably binds at least a surface molecule that is preferentially expressed on human tumor cells. In a preferred embodiment, the bispecific antibody binds to BCMA, CD19, CD20, CD30, CD33, CD38, CD44, CD123, CD138, CEA, CLEC12A, CS-1, EGFR, EGFRvIII, EPCAM, DLL3, LGR5, MSLN, FOLR1, FOLR3, HER2, HM1.24, MCSP, or PSMA. In a more preferred embodiment, the bispecific antibody binds to CLEC12A.

The invention further provides a pharmaceutical composition comprising an antibody according to the invention.

Further provided is an antibody according to the invention that further comprises a label, preferably a label for in vivo imaging.

The invention also provides a method for the treatment of a subject having a tumor or at risk of having a tumor comprising administering to the subject a bispecific antibody according to the invention. Also provided is a bispecific antibody according to the invention for use in the treatment of a subject having a tumor or at risk of a tumor. Further provided is the use of an antibody of the invention for the preparation of a medicament for the treatment of a subject having a tumor or at risk of a tumor. In a preferred embodiment the tumor is a CLEC12A positive tumor.

DETAILED DESCRIPTION OF THE INVENTION

An antibody of the invention is preferably a bispecific antibody. The bispecific antibody preferably binds at least human CD3. In addition, the bispecific antibody preferably binds at least a surface molecule that is expressed on human tumor cells. In a preferred embodiment the bispecific antibody binds to BCMA, CD19, CD20, CD30, CD33, CD38, CD44, CD123, CD138, CEA, CLEC12A,

CS-1, EGFR, EGFRvIII, EPCAM, DLL3, LGR5, MSLN, FOLR1, FOLR3, HER2, HM1.24, MCSP, or PSMA. In a particularly preferred embodiment, the bispecific antibody binds to CLEC12A.

BCMA is also referred to as Tumor Necrosis Factor Receptor Superfamily, Member 17 (TNFRSF17); TNFRSF13A2; B Cell Maturation Antigen; BCM; B-Cell Maturation Factor; B-Cell Maturation Protein; CD269 or CD269 Antigen. Ids: HGNC: 11913; Entrez Gene: 608; Ensembl: ENSG00000048462; OMIM: 109545; UniProtKB: Q02223.

CD19 is also referred to as CD19 Molecule; T-Cell Surface Antigen Leu-12; CD19 Antigen; CVID3; Differentiation Antigen CD19; B4; B-Lymphocyte Surface Antigen B4; B-Lymphocyte Antigen CD19. Ids: HGNC: 1633; Entrez Gene: 930; Ensembl: ENSG00000177455; OMIM: 107265; UniProtKB: P15391.

CD20 is also referred to as Membrane-Spanning 4-Domains, Subfamily A, Member 1 (MS4A1); MS4A2; CD20; S7; Leukocyte Surface Antigen Leu-16; B-Lymphocyte Antigen CD20; Bp35; B-Lymphocyte Cell-Surface Antigen B1; CD20 Antigen; CD20 Receptor; CVID5; B-Lymphocyte Surface Antigen B1; B1; Membrane-Spanning 4-Domains Subfamily A Member 1; LEU-16. Ids: HGNC: 7315; Entrez Gene: 931; Ensembl: ENSG00000156738; OMIM: 112210; UniProtKB: P11836.

CD30 is also referred to as Tumor Necrosis Factor Receptor Superfamily, Member 8 (TNFRSF8); Ki-1 Antigen; CD30; Ki-1; D1S166E; Cytokine Receptor CD30; Lymphocyte Activation Antigen CD30; Tumor Necrosis Factor Receptor Superfamily Member 8; CD30L Receptor; CD30 Antigen. Ids: HGNC: 11923; Entrez Gene: 943; Ensembl: ENSG00000120949; OMIM: 153243; UniProtKB: P28908.

CD33 is also referred to as CD33 Molecule; SIGLEC-3; CD33 Antigen (Gp67); Myeloid Cell Surface Antigen CD33; Sialic Acid Binding Ig-Like Lectin 3; Siglec-3; SIGLEC3; CD33 Antigen and gp67. Ids: HGNC:

1659; Entrez Gene: 945; Ensembl: ENSG00000105383; OMIM: 159590; UniProtKB: P20138.

CD38 is also referred to as CD38 Molecule; T10; CD38 Antigen (P45); CADPr Hydrolase 1; ADP-Ribosyl Cyclase 1; ADP-Ribosyl Cyclase/Cyclic ADP-Ribose Hydrolase; NAD(+) Nucleosidase; EC 3.2.2.5; Cyclic ADP-Ribose Hydrolase 1; CD38 Antigen. Ids: HGNC: 1667; Entrez Gene: 952; Ensembl: ENSG00000004468; OMIM: 107270; UniProtKB: P28907.

CD44 is also referred to as CD44 Molecule (Indian Blood Group); IN; MDU2; CD44 Antigen (Homing Function And Indian Blood Group System); MDU3; CDW44; MIC4; CSPG8; Chondroitin Sulfate Proteoglycan 8; HCELL; Hematopoietic Cell E- And L-Selectin Ligand; MC56; Extracellular Matrix Receptor III; Pgp1; Heparan Sulfate Proteoglycan; Cell Surface Glycoprotein CD44; Hyaluronate Receptor; epican; Phagocytic Glycoprotein 1; Homing Function And Indian Blood Group System; ECMR-III; CDw44; HUTCH-I; Epican; LHR; PGP-1; CD44 Antigen; PGP-I; CP90 Lymphocyte Homing/Adhesion Receptor; Phagocytic Glycoprotein I; Hermes Antigen. Ids: HGNC: 1681; Entrez Gene: 960; Ensembl: ENSG00000026508; OMIM: 107269; UniProtKB: P16070.

CD123 is also referred to as Cell Division Cycle 123; Cell Division Cycle 123 Homolog; C10orf7; Cell Division Cycle Protein 123 Homolog; D123; Protein D123; HT-1080; CCEP123; PZ32; CEP89; Cell Division Cycle 123 Homolog (S. Cerevisiae); FLJ14640; Chromosome 10 Open Reading Frame 7. Ids: HGNC: 16827; Entrez Gene: 8872; Ensembl: ENSG00000151465; OMIM: 615470; UniProtKB: O75794.

CD138 is also referred to as Syndecan 1 (SCD1); CD138; SDC; Heparan Sulfate Proteoglycan Fibroblast Growth Factor Receptor; Syndecan Proteoglycan 1; syndecan; SYND1; syndecan-1; CD138 Antigen. Ids: HGNC: 10658; Entrez Gene: 6382; Ensembl: ENSG00000115884; OMIM: 186355; UniProtKB: P18827.

CEA is also referred to as Carcinoembryonic Antigen-Related Cell Adhesion Molecule 5 (CEACAM5); Meconium Antigen 100; CD66e; Carcinoembryonic Antigen; CD66e Antigen. Ids: HGNC: 1817; Entrez Gene: 1048; Ensembl: ENSG00000105388; OMIM: 114890; UniProtKB: P06731.

CLEC12A is also referred to as C-Type Lectin Domain Family 12, Member A; C-Type Lectin Protein CLL-1; MICL; Dendritic Cell-Associated Lectin 2; C-Type Lectin Superfamily; Myeloid Inhibitory C-Type Lectin-Like Receptor; C-Type Lectin-Like Molecule-1; CLL-1; DCAL2; CLL1; C-Type Lectin-Like Molecule 1; DCAL-2; Killer cell lectin like receptor subfamily L, member 1 (KLRL1); CD371 (Bakker A. et al. Cancer Res. 2004, 64, p8843 50; GenBankTM access.no: AY547296; Zhang W. et al. GenBankTM access.no: AF247788; A.S. Marshall, et al. J Biol Chem 2004, 279, p14792–802; GenBankTM access.no: AY498550; Y.Han et al. Blood 2004, 104, p2858 66; H.Floyd, et al. GenBankTM access.no: AY426759; C.H.Chen, et al. Blood 2006, 107, p1459 67). Ids: HGNC: 31713; Entrez Gene: 160364; Ensembl: ENSG00000172322; OMIM: 612088; UniProtKB: Q5QGZ9. CLEC12A is an antigen that is expressed on leukemic blast cells and on leukemic stem cells in acute myeloid leukemia (AML), including the CD34 negative or CD34 low expressing leukemic stem cells (side population) (A.B. Bakker et al. Cancer Res 2004, 64, p8443 50; Van Rhenen et al. 2007 Blood 110:2659; Moshaver et al. 2008 Stem Cells 26:3059). Expression of CLEC12A is otherwise thought to be restricted to the hematopoietic lineage, particularly to myeloid cells in peripheral blood and bone marrow, i.e., granulocytes, monocytes and dendritic cell precursors. More importantly, CLEC12A is absent on hematopoietic stem cells. This expression profile makes CLEC12A a particularly favorable target in AML. The full length form of CLEC12A comprises 275 amino acid residues, including an additional intracellular stretch of 10 amino acids which is absent in most other isoforms, and shows the strictly myeloid expression profile (surface expression and mRNA level).

The term 'CLEC12A or functional equivalent thereof' means all (such as

splice and mutation) variants that are referenced above and isoforms thereof that retain the strict myeloid expression profile (both at surface expression level and mRNA level) as described in Bakker et al. Cancer Res 2004, 64, p8443-50 and Marshall 2004 - J Biol Chem 279(15), p14792–802. A CLEC12A binding antibody of the invention binds human CLEC12A. Where herein reference is made to CLEC12A, the reference is to human CLEC12A, unless specifically stated otherwise.

CD3 (cluster of differentiation 3) T-cell co-receptor is a protein complex and is composed of four distinct chains. In mammals, the complex contains a CD3γ chain, a CD3δ chain, and two CD3ε chains. These chains associate with a molecule known as the T-cell receptor (TCR) and the ζ-chain to generate anactivation signal in T lymphocytes. The TCRα, TCRβ, ζ-chain, and CD3 molecules together comprise the TCR complex. CD3 is expressed on T cells. An antibody that binds CD3 can bind a CD3γ chain, a CD3δ chain, a CD3ε chain or a combination of CD3δ/CD3ε or CD3γ/CD3ε. The CD3 binding antibody of the present invention binds the CD3ε chain. CD3ε is known under various aliases some of which are: “CD3e Molecule, Epsilon (CD3-TCR Complex)”; “CD3e Antigen, Epsilon Polypeptide (TiT3 Complex)”; T-Cell Surface Antigen T3/Leu-4 Epsilon Chain; T3E; T-Cell Antigen Receptor Complex, Epsilon Subunit Of T3; CD3e Antigen; CD3-Epsilon 3; IMD18; TCRE. Ids for CD3E Gene are HGNC: 1674; Entrez Gene: 916; Ensembl: ENSG00000198851; OMIM: 186830 and UniProtKB: P07766. Bispecific CD3 binding antibodies targeting the CD3ε chain have been shown to be effective in recruiting T cells to aberrant cells. Hence, an (bispecific) antibody according to the present invention preferably contains one heavy/light chain combination that binds CD3ε. A CD3 binding antibody of the invention binds human CD3. Where herein reference is made to CD3, the reference is to human CD3, unless specifically stated otherwise.

CS-1 is also referred to as Citrate Synthase; EC 2.3.3.1; Citrate Synthase, Mitochondrial; EC 2.3.3. Ids: HGNC: 2422; Entrez Gene: 1431 Ensembl: ENSG00000062485; OMIM: 118950; UniProtKB: O75390.

EGFR is also referred to as Epidermal Growth Factor Receptor; Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog (Avian); ERBB1; PIG61; Proto-Oncogene C-ErbB-1; Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog; Receptor Tyrosine-Protein Kinase ErbB-1; Cell Growth Inhibiting Protein 40; Cell Proliferation-Inducing Protein 61; HER1; mENA; EC 2.7.10.1; EC 2.7.10; Epidermal Growth Factor Receptor (Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog). Ids: HGNC: 3236; Entrez Gene: 1956; Ensembl: ENSG00000146648; OMIM: 131550; UniProtKB: P00533.

EGFRvIII is a common variant of EGFR (Oncogene. 2013 May 23;32(21):2670-81. doi: 10.1038/onc.2012.280. Epub 2012 Jul 16).

Delta like 3 (DLL3) is also referred to as Delta-Like 3); Drosophila Delta Homolog 3; Delta3; Delta (Drosophila)-Like 3; SCDO1. Ids for DLL3 are: HGNC: 2909; Entrez Gene: 10683; Ensembl: ENSG00000090932; OMIM: 602768 and UniProtKB: Q9NYJ7.

LGR5 is Leucine-Rich Repeat Containing G Protein-Coupled Receptor 5 Alternative names for the gene or protein are Leucine-Rich Repeat Containing G Protein-Coupled Receptor 5; Leucine-Rich Repeat-Containing G Protein-Coupled Receptor 5; G-Protein Coupled Receptor HG38; G-Protein Coupled Receptor 49; G-Protein Coupled Receptor 67; GPR67; GPR49; Orphan G Protein-Coupled Receptor HG38; G Protein-Coupled Receptor 49; GPR49; HG38 and FEX. A protein or antibody of the invention that binds LGR5, binds human LGR5. The LGR5 binding protein or antibody of the invention may, due to sequence and tertiary structure similarity between human and other mammalian orthologs, also bind such an ortholog but not necessarily so. Database accession numbers for the human LGR5 protein and the gene encoding it are (NC_000012.12;

NT_029419.13; NC_018923.2; NP_001264155.1; NP_001264156.1; NP_003658.1).

MSLN or mesothelin is also referred to as Mesothelin; Pre-Pro-Megakaryocyte-Potentiating Factor; CAK1 Antigen; MPF; Soluble MPF Mesothelin Related Protein; Megakaryocyte Potentiating Factor and SMRP. Ids for MSLN are: HGNC: 7371; Entrez Gene: 10232; Ensembl: ENSG00000102854; OMIM: 601051; UniProtKB: Q13421.

Folate receptor 1 is also referred to as FOLR1; Folate Receptor 1 Folate Receptor 1; Ovarian Tumor-Associated Antigen MOv18; Adult Folate-Binding Protein; Folate Receptor, Adult; KB Cells FBP; FR-Alpha; FOLR; FBP; Folate Binding Protein; and Folate Receptor 1. Ids for FOLR1 are HGNC: 3791;
Entrez Gene: 2348; Ensembl: ENSG00000110195; OMIM: 136430; UniProtKB: P15328

Folate receptor 3 is also referred to as FOLR3; Folate Receptor 3 (Gamma); FR-Gamma; Folate Receptor 3; Gamma-HFR; and FR-G. Ids for FOLR3 are HGNC: 3795; Entrez Gene: 2352; Ensembl: ENSG00000110203; OMIM: 602469; and UniProtKB: P41439.

EPCAM is also referred to as Epithelial Cell Adhesion Molecule; EGP40; M4S1; ESA; MIC18; KS1/4; Tumor-Associated Calcium Signal Transducer 1; MK-1; TACSTD1; Human Epithelial Glycoprotein-2; TROP1; Membrane Component, Chromosome 4, Surface Marker (35kD Glycoprotein); Adenocarcinoma-Associated Antigen; EGP; Cell Surface Glycoprotein Trop-1; Ep-CAM; Epithelial Glycoprotein 314; GA733-2; Major Gastrointestinal Tumor-Associated Protein GA733-2; M1S2; EGP314; CD326 Antigen; KSA; Epithelial Cell Surface Antigen; DIAR5; Epithelial Glycoprotein; HNPCC8; hEGP314; Antigen Identified By Monoclonal Antibody AUA1; KS 1/4 Antigen; EGP-2; ACSTD1. Ids:
HGNC: 11529; Entrez Gene: 4072; Ensembl: ENSG00000119888; OMIM: 185535; UniProtKB: P16422.

HER2 is also referred to as V-Erb-B2 Avian Erythroblastic Leukemia Viral Oncogene Homolog 2; ERBB2; CD340; NGL; HER-2; HER-2/neu2; NEU2; TKR1; Neuro/Glioblastoma Derived Oncogene Homolog; C-Erb B2/Neu Protein; Metastatic Lymph Node Gene 19 Protein; herstatin; Proto-Oncogene C-ErbB-2; Neuroblastoma/Glioblastoma Derived Oncogene Homolog; Proto-Oncogene Neu; Receptor Tyrosine-Protein Kinase ErbB-2; Tyrosine Kinase-Type Cell Surface Receptor HER2; V-Erb-B2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/Glioblastoma Derived Oncogene Homolog; MLN 19; MLN19; p185erbB2; CD340 Antigen; EC 2.7.10.1; EC 2.7.10; V-Erb-B2 Avian Erythroblastic Leukemia Viral Oncogene Homolog 2 (Neuro/Glioblastoma Derived Oncogene Homolog). Ids: HGNC: 3430; Entrez Gene: 2064; Ensembl: ENSG00000141736; OMIM: 164870; UniProtKB: P04626.

HM1.24 is also referred to as BST2; Bone Marrow Stromal Cell Antigen 2; TETHERIN; BST-2; Bone Marrow Stromal Antigen 2; HM1.24 Antigen; Tetherin; CD317; CD317 Antigen; NPC-A-7. Ids: HGNC: 1119; Entrez Gene: 684; Ensembl: ENSG00000130303; OMIM: 600534; UniProtKB: Q10589.

MCSP is also referred to as Sperm Mitochondria-Associated Cysteine-Rich Protein (SMCP); MCSP; MCS; Mitochondrial Capsule Selenoprotein; HSMCSGEN1; Sperm Mitochondrial-Associated Cysteine-Rich Protein. Ids: HGNC: 6962; Entrez Gene: 4184; Ensembl: ENSG00000163206; OMIM: 601148; UniProtKB: P49901.

PSMA is also referred to as Folate Hydrolase (Prostate-Specific Membrane Antigen) 1; FOLH1; NAALAD1; FOLH; mGCP; Glutamate Carboxypeptidase II; N-Acetylated-Alpha-Linked Acidic Dipeptidase I; PSM; NAALADase I; PSMA; EC 3.4.17.21; Glutamate Carboxylase II; GCP2; Cell Growth-Inhibiting Gene 27 Protein; NAALAdase; Folylpoly-Gamma-Glutamate Carboxypeptidase; Glutamate Carboxypeptidase 2; Membrane

Glutamate Carboxypeptidase; N-Acetylated Alpha-Linked Acidic Dipeptidase 1; Pteroylpoly-Gamma-Glutamate Carboxypeptidase; Prostate Specific Membrane Antigen Variant F; FGCP; Folate Hydrolase 1; GCPII; Prostate-Specific Membrane Antigen. Ids: HGNC: 3788; Entrez Gene: 2346; Ensembl: ENSG00000086205; OMIM: 600934; UniProtKB: Q04609.

PSMA is not to be confused with Proteasome (Prosome, Macropain) Subunit, Alpha Type, 1 which is also known under the alias PSMA1.

Accession numbers are primarily given to provide a further method of identification of a target, the actual sequence of the protein bound may vary, for instance because of a mutation in the encoding gene such as those occurring in some cancers or the like. The antigen binding site binds the antigen and a variety of variants thereof, such as those expressed by some antigen positive immune or tumor cells.

When herein reference is made to a gene, a protein, the reference is preferably to the human form of the gene or protein. When herein reference is made to a gene or protein reference is made to the natural gene or protein and to variant forms of the gene or protein as can be detected in tumours, cancers and the like, preferably as can be detected in human tumours, cancers and the like.

A bispecific antibody of the invention preferably binds to the human BCMA, CD19, CD20, CD30, CD33, CD38, CD44, CD123, CD138, CEA, CLEC12A, CS-1, EGFR, EGFRvIII, EPCAM, DLL3, LGR5, MSLN, FOLR1, FOLR3, HER2, HM1.24, MCSP, PSMA protein or a variant thereof. Needless to say that the antigen binding heavy/light chain combination preferably binds the extracellular part of the antigen. A bispecific antibody according to the invention preferably binds to human CLEC12A or a variant

thereof. A preferred bispecific antibody according to the invention binds to human CD3 and human CLEC12A or a variant thereof.

HGNC stands for the HUGO Gene nomenclature committee. The number following the abbreviation is the accession number with which information on the gene and protein encoded by the gene can be retrieved from the HGNC database. Entrez Gene provides the accession number or gene ID with which information on the gene or protein encoded by the gene can be retrieved from the NCBI (National Center for Biotechnology Information) database. Ensemble provides the accession number with which information on the gene or protein encoded by the gene can be obtained from the Ensemble database. Ensembl is a joint project between EMBL-EBI and the Wellcome Trust Sanger Institute to develop a software system which produces and maintains automatic annotation on selected eukaryotic genomes.

The invention provides an antibody that binds human CD3 which antibody comprises a heavy chain and light chain wherein said heavy chain comprises a variable region that comprises an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably, 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A.

In a preferred embodiment the light chain comprises a light chain variable region comprising the amino acid sequence of an O12 / IgVκ1-39*01 gene segment as depicted in figure 23A with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof. The phrase "O12 light chain" will be used throughout the specification as short for "a light chain comprising a light chain variable region comprising the amino acid sequence of an O12 / IgVκ1-39*01 gene segment as depicted in figure 23A with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof. IgVκ1-39 is short for Immunoglobulin Variable Kappa 1-39 Gene. The gene is also known as Immunoglobulin Kappa Variable 1-39; IGKV139; IGKV1-39; O12a or O12. External Ids for the gene are HGNC: 5740; Entrez Gene: 28930; Ensembl: ENSG00000242371. A preferred amino acid sequence for IgVκ1-39 is given in figure 23A. This lists the sequence of the V-region. The V-region can be combined with one of five J-regions. Figure 23B and 23C describe two preferred sequences for IgVκ1-39 in combination with a J-region. The joined sequences are indicated as IGKV1-39/jk1 and IGKV1-39/jk5; alternative names are IgVκ1-39*01/IGJκ1*01 or IgVκ1-39*01/IGJκ5*01 (nomenclature according to the IMGT database worldwide web at imgt.org).

It is preferred that the O12 / IgVκ1-39*01 comprising light chain variable region is a germline sequence. It is further preferred that the IGJκ1*01 or /IGJκ5*01 comprising light chain variable region is a germline sequence. In a preferred embodiment, the IGKV1-39/jk1 or IGKV1-39/jk5 light chain variable regions are germline sequences.

In a preferred embodiment the light chain variable region comprises a germline O12 / IgVκ1-39*01. In a preferred embodiment the light chain variable region comprises the kappa light chain IgVκ1-39*01/IGJκ1*01 or

IgVκ1-39*01/IGJκ5*01. In a preferred embodiment a IgVκ1-39*01/IGJκ1*01. The light chain variable region preferably comprises a germline kappa light chain IgVκ1-39*01/IGJκ1*01 or germline kappa light chain IgVκ1-39*01/IGJκ5*01, preferably a germline IgVκ1-39*01/IGJκ1*01.

Mature B-cells that produce an antibody with an O12 light chain often produce a light chain that has undergone one or more mutations with respect to the germline sequence, i.e. the normal sequence in non-lymphoid cells of the organism. The process that is responsible for these mutations is often referred to as somatic (hyper)mutation. The resulting light chain is referred to as an affinity matured light chain. Such light chains, when derived from an O12 germline sequence are O12-derived light chains. In this specification, the phrase "O12 light chains" will include O12-derived light chains, The mutations that are introduced by somatic hypermutation can of course also be introduced artificially in the lab. In the lab also other mutations can be introduced without affecting the properties of the light chain in kind, not necessarily in amount. A light chain is at least an O12 light chain if it comprises a sequence as depicted in figure 23A, figure 23B or figure 23C with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof. In a preferred embodiment the O12 light chain is a light chain comprising a sequence as depicted in figure 23A, figure 23B or figure 23C with 0-9, 0-8, 0-7, 0-6, 0-5, 0-4 amino acid insertions, deletions, substitutions, additions or a combination thereof. In a preferred embodiment the O12 light chain is a light chain comprising a sequence as depicted in figure 23A, figure 23B or figure 23C with 0-5, preferably 0-4, more preferably 0-3 amino acid insertions, deletions, substitutions, additions or a combination thereof. In a preferred embodiment the O12 light chain is a light chain comprising a sequence as depicted in figure 23A, figure 23B or figure 23C with 0-2, more preferably 0-1, most preferably 0 amino acid insertions, deletions,

substitutions, additions or a combination thereof. In a preferred embodiment the O12 light chain is a light chain comprising a sequence as depicted in figure 23A or figure 23B with the mentioned amino acid insertions, deletions, substitutions, additions or a combination thereof. In a preferred embodiment the light chain comprises the sequence of figure 23B.

The antibody is preferably a bispecific antibody. The bispecific antibody preferably has one heavy chain variable region/light chain variable region (VH/VL) combination that binds CD3 and a second VH/VL combination that binds an antigen other than an antigen on CD3. In a preferred embodiment the antigen is a tumor antigen. In a preferred embodiment the VL in said first VH/VL combination is similar to the VL in said second VH/VL combination. In a more preferred embodiment, the VLs in the first and second VH/VL combinations are identical. In a preferred embodiment, the bispecific antibody is a full length antibody which has one heavy/light (H/L) chain combination that binds CD3 and one H/L chain combination that binds another antigen, preferably a tumor antigen. In a preferred embodiment the light chain in said first H/L chain combination is similar to the light chain in said second H/L chain combination. In a more preferred embodiment, the light chains in the first and second H/L chain combinations are identical, i.e. a similar or identical human light chain is a so-called 'common light chain', which is a light chain that can combine with different heavy chains to form antibodies with functional antigen binding domains. In a preferred embodiment the light chain in said first H/L chain combination comprises a light chain variable region that is similar to the light chain variable region in said second H/L chain combination. In a more preferred embodiment, the light chain variably regions in the first and second H/L chain combinations are identical, i.e. a similar or identical human light chain variable region is a so-called 'common light chain variable region', which is a light chain variable region that can combine

with different heavy chain variable regions to form antibodies with functional antigen binding domains. The light chain comprising a common light chain variable region is preferably a common light chain. The light chain preferably comprises a light chain variable region comprising the amino acid sequence of an O12 / IgVκ1-39*01 gene segment as depicted in figure 23A with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof as further defined elsewhere herein. Preferably, the common light chain has a germline sequence. A preferred germline sequence is a light chain variable region that is frequently used in the human repertoire and has good thermodynamic stability, yield and solubility. A preferred germline light chain is O12 as indicated herein above. A preferred sequence for O12/IgVκ1-39 is given in figure 23A. This lists the sequence of the V-region. Figures 23B and 23C describe two preferred sequences for IgVκ1-39 in combination with a J-region. The joined sequences are indicated as IGKV1-39/jk1 and IGKV1-39/jk5; alternative names are IgVκ1-39*01/IGJκ1*01 or IgVκ1-39*01/IGJκ5*01.

It is preferred that the O12 / IgVκ1-39*01 light variable region is a germline sequence. It is preferred that the O12 / IgVκ1-39*01 comprising light chain variable region is a germline sequence. It is further preferred that the IGJκ1*01 or /IGJκ5*01 comprising light chain variable region is a germline sequence. In a preferred embodiment, the IGKV1-39/jk1 or IGKV1-39/jk5 light chain variable regions are germline sequences. The O12 light chain of the bispecific antibody is preferably an O12 light chain as indicated herein above.

A tumor antigen is defined by the pattern of its expression. A tumor-specific antigen, is typically present only on cells of a tumor and not on any other cell in the post-natal, preferably adult human body. A tumor-

associated antigen is typically present on cells of a tumor and also some normal cells in the post-natal, preferably adult human body. A tumor antigen as used herein is typically a tumor-specific or a tumor-associated antigen. Tumor antigens may be involved in the oncogenic process or not. The may be different from the "normal" protein in healthy individuals or not. It is noted that various tumor-specific antigens were later shown to be expressed also on some other non-tumorigenic cells. Preferred tumor antigens are tumor-antigens that are expressed on the cell surface and which have an extra-cellular part. The antibody typically binds to an extra-cellular part of the antigen.

The term "antibody" as used herein means a proteinaceous molecule belonging to the immunoglobulin class of proteins, containing one or more domains that bind an epitope on an antigen, where such domains are derived from or share sequence homology with the variable region of an antibody. Antibodies are typically made of basic structural units—each with two heavy chains and two light chains. Antibodies for therapeutic use are preferably as close to natural antibodies of the subject to be treated as possible (for instance human antibodies for human subjects). Antibody binding can be expressed in terms of specificity and affinity. The specificity determines which antigen or epitope thereof is specifically bound by the binding domain. The affinity is a measure for the strength of binding to a particular antigen or epitope. Binding, or "specifically recognizing" is defined as binding with affinities (KD) of at least 1x10e-6 M, 1x10e-7 M, 1x10e-8 M, or at least 1x10e-9 M. Antibodies for therapeutic applications can have affinities of 1x10e-10 M or even higher. Antibodies of the present invention are typically bispecific antibodies and of the human IgG subclass. Preferably, the antibodies of the present invention are of the human IgG1 subclass. Most preferably, antibodies of the present invention are full length IgG molecules. The invention also provides a derivative and/or analogue of

an antibody of the invention. Such a derivative and/or analogue has the VH/VL domains of an antibody of the invention, preferably including the common light chain variable region as defined elsewhere herein. Suitable derivatives are single chain Fv-fragments, monobodies, VHH and Fab-fragments. The derivatives may be fused to the C_H2 and C_H3 domain of a heavy chain of an antibody. The derivative preferably further comprises the C_H1 domain of a heavy an antibody and the C_L domain of a light chain of an antibody. The derivative can also be in a multivalent format, preferably a bispecific format wherein one of the VH/VL domains of an antibody comprises a heavy chain variable region/light chain variable region (VH/VL) combination that binds CD3 of the invention and at least one other VH/VL domain of an antibody that binds an antigen that is not a CD3 antigen. The at least one other VH/VL domain of an antibody preferably binds a tumor antigen, preferably CLEC12A. Multivalent formats are easily produced for instance by producing the derivative as a fusion protein with or without suitable and/or the conventional peptide linker or spacer between the VH/VL domains.

A "bispecific antibody" is an antibody as described herein above comprising one heavy chain variable region/light chain variable region (VH/VL) combination that binds CD3 and a second VH/VL combination that binds an antigen other than CD3, preferably a tumor antigen. In a preferred embodiment the VL in said first VH/VL combination is similar to the VL in said second VH/VL combination. In a more preferred embodiment, the VLs in the first and second VH/VL combinations are identical. In a preferred embodiment, the bispecific antibody is a full length antibody which comprises one heavy/light chain combination that binds CD3 and one heavy/light chain combination that binds another antigen, preferably a tumor antigen.

Binding of the heavy/light chain combination to the antigen is achieved via the antigen binding site in the variable region of the heavy/light chain combination.

The invention also provides alternative bispecific formats, such as those described in Spiess, C., et al., (Alternative molecular formats and therapeutic applications for bispecific antibodies. Mol. Immunol. (2015) http://dx.doi.org/10.1016/j.molimm.2015.01.003). Bispecific antibody formats that are not classical antibodies with two H/L combinations, have at least a variable domain comprising a heavy chain variable region and a light chain variable region of the invention. This variable domain may be linked to a single chain Fv-fragment, monobody, a VHH and a Fab-fragment that provides the second binding activity.

The term bispecific antibody may be replaced by the broader term “a bispecific binding protein comprising an immunoglobulin variable domain that binds CD3 having a heavy chain variable region and a light chain variable region of the invention; and an antigen binding (poly)peptide that binds another antigen. In this embodiment the binding (poly)peptide is preferably a (poly)peptide as specified in Spiess et al (supra).

In a bispecific antibody of the invention the light chain in the CD3-binding H/L chain combination is preferably similar to the light chain in H/L chain combination that can bind an antigen other than CD3, preferably a tumor antigen. In a more preferred embodiment, the light chain in both H/L chain combinations is identical, i.e. said human light chain is a so-called ‘common light chain’, which is a light chain that can combine with different heavy chains to form antibodies with functional antigen binding domains. Preferably, the common light chain has a germline sequence. A preferred germline sequence is a light chain variable region that is frequently used in the human repertoire and has good thermodynamic stability, yield and solubility. A preferred germline light chain is O12, preferably the rearranged germline human kappa light chain IgVκ1-39*01/IGJκ1*01 or a

fragment or a functional equivalent (i.e. same IgVκ1-39 gene segment but different IGJκ gene segment) thereof (nomenclature according to the IMGT database worldwide web at imgt.org).

The term 'common light chain' as used herein refers to the two light chains (or the VL part thereof) in the bispecific antibody. The two light chains (or the VL part thereof) may be identical or have some amino acid sequence differences while the binding specificity of the full length antibody is not affected. It is for instance within the scope of the definition of common light chains as used herein, to prepare or find light chains that are not identical but still functionally equivalent, e.g., by introducing and testing conservative amino acid changes, changes of amino acids in regions that do not or only partly contribute to binding specificity when paired with the heavy chain, and the like. The terms 'common light chain', 'common VL', 'single light chain', 'single VL', with or without the addition of the term 'rearranged' are all used herein interchangeably.

Preferably, the common light chain has a germline sequence. A preferred germline

sequence is a light chain variable region that is frequently used in the human

repertoire. A preferred germline light chain is O12, preferably the rearranged germline human kappa light chain IgVκ1-39*01/IGJκ1*01 or a fragment or a functional equivalent (i.e. same IgVκ1-39 gene segment but different IGJκ gene segment) thereof (nomenclature according to the IMGT database worldwide web at imgt.org). The terms rearranged germline human kappa light chain IgVκ1-39*01/IGJκ1*01, IGKV1-39/IGKJ1, huVκ1-39 light chain or in short huVκ1-39 are used interchangeably throughout the application. Obviously, those of skill in the art will recognize that "common" also refers to functional equivalents of the light chain of which the amino acid sequence is not identical. Many variants of said light chain exist wherein mutations (deletions, substitutions, insertions and/or

additions) are present that do not materially influence the formation of functional binding regions. The light chain of the present invention can also be a light chain as specified herein above, having 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof.

An antibody of the invention is preferably an IgG antibody, preferably an IgG1 antibody. The term 'full length IgG' according to the invention is defined as comprising an essentially complete IgG, which however does not necessarily have all functions of an intact IgG. For the avoidance of doubt, a full length IgG contains two heavy and two light chains. Each chain contains constant (C) and variable (V) regions, which can be broken down into domains designated CH1, CH2, CH3, VH, and CL, VL. An IgG antibody binds to antigen via the variable region domains contained in the Fab portion, and after binding can interact with molecules and cells of the immune system through the constant domains, mostly through the Fc portion. Full length antibodies according to the invention encompass IgG molecules wherein mutations may be present that provide desired characteristics. Full length IgG should not have deletions of substantial portions of any of the regions. However, IgG molecules wherein one or several amino acid residues are deleted, without essentially altering the binding characteristics of the resulting IgG molecule, are embraced within the term "full length IgG". For instance, such IgG molecules can have a deletion of between 1 and 10 amino acid residues, preferably in non-CDR regions, wherein the deleted amino acids are not essential for the binding specificity of the IgG.

Full length IgG antibodies are used because of their favourable half-life and the desire to stay as close to fully autologous (human) molecules for reasons of immunogenicity. IgG1 is favoured based on its long circulatory half-life in man. In order to prevent or avoid immunogenicity in humans it is preferred that the bispecific full length IgG antibody according

to the invention is a human IgG1. The term 'bispecific' means that one heavy and light chain combination (H/L combination) or arm of the antibody binds to a first antigen whereas the other H/L combination or other arm binds to a second antigen, wherein said first and second antigens are not identical. An antigen, is typically a molecule which serves as a target for an antibody. In the present invention it is preferred that an antigen is a protein expressed on the membrane of a cell of an individual. According to the present invention, said first and second antigens are on two different molecules that are preferably located on two different cell types. The term 'one arm [of the antibody]' preferably means the heavy chain/light chain combination comprising one Fab portion of a full length IgG antibody. Bispecific antibodies that mediate cytotoxicity by recruiting and activating endogenous immune cells are an emerging class of next generation antibody therapeutics. This can be achieved by combining antigen binding specificities for target cells (i.e., tumor cells) and effector cells (i.e., T cells, NK cells, and macrophages) in one molecule (Cui et al. JBC 2012 (287) 28206 28214; Kontermann, MABS 2012 (4) 182 197; Chames and Baty, MABS 2009 (1) 539 547; Moore et al. Blood 2011 (117) 4542 4551; Loffler et al. 2000 Blood 95:2098; Zeidler et al. 1999 J. Immunol. 163:1246). According to the invention, bispecific antibodies are provided wherein one heavy/light chain combination binds the CLEC12A antigen on aberrant (tumor) cells whereas the second heavy/light chain combination binds CD3 on immune effector cells.

The invention provides bispecific IgG antibodies wherein one heavy/light chain combination specifically recognizes CLEC12A or a functional equivalent thereof, including those functional CLEC12A equivalents that lack the above mentioned additional intracellular stretch of 10 amino acids. A bispecific IgG antibody wherein one heavy/light chain combination binds the full length form of CLEC12A is preferred. Needless to

say that the tumor antigen binding heavy/light chain combination binds the extracellular part of tumor antigen.

The terms 'variable region domain', 'variable region', 'variable domain', 'VH/VL pair', 'VH/VL', 'VH', 'VL', 'Fab portion', 'Fab arm', 'Fab' or 'arm' are used herein interchangeably.

Antigen binding by an antibody is typically mediated through the complementarity regions of the antibody and the specific three-dimensional structure of both the antigen and the variable domain allowing these two structures to bind together with precision (an interaction similar to a lock and key), as opposed to random, non-specific sticking of antibodies. As an antibody typically recognizes an epitope of an antigen, and as such epitope may be present in other proteins as well, antibodies according to the present invention that bind CD3 or CLEC12A may recognize other proteins as well, if such other proteins contain the same epitope. Hence, the term "binding" does not exclude binding of the antibodies to another protein or protein(s) that contain the same epitope. A heavy/light chain combination that binds CD3 in antibody of the invention does not bind to other proteins on the membrane of cells in a post-natal, preferably adult human. A heavy/light chain combination that binds CLEC12A of the invention does not bind other proteins on the membrane of cells in a post-natal, preferably adult human.

A bispecific antibody according to the present invention that binds CD3 and a tumor antigen binds to CD3 (preferably CD3 on effector cells) with a binding affinity of at least 1x10e-6 M, as outlined in more detail below. In a preferred embodiment the CD3 binding affinity is 1x10e-6 M - 1x10e-10 M, preferably 1x10e-7 M - 1x10e-9 M.

A bispecific antibody according to the present invention that binds CD3 and a tumor antigen binds to the tumor antigen preferably with a binding affinity that is higher than the affinity with which it binds CD3. In a preferred embodiment the affinity of binding of the tumor antigen on tumor cells is at least 2 times, more preferably 4 times more preferably 6 times, or 10 times higher than the affinity of binding to CD3. In a preferred embodiment the tumor antigen binding affinity is 1x10e-6 M - 1x10e-10 M, preferably 1x10e-7 M - 1x10e-10 M, more preferably at least 1x10e-8, preferably at least 1x10e-9. Preferably in combination with a CD3 affinity that is at least 2 times, more preferably 4 times more preferably 6 times, or 10 times lower than the indicated affinity of binding to the tumor antigen. In a preferred embodiment the tumor antigen binding affinity is 1x10e-8-1x10e-10.

The term 'aberrant cells' as used herein includes tumor cells, more specifically tumor cells of hematological origin including also pre-leukemic cells such as cells that cause myelodysplastic syndromes (MDS) and leukemic cells such as acute myeloid leukemia (AML) tumor cells or chronic myelogenous leukemia (CML) cells.

The term 'immune effector cell' or 'effector cell' as used herein refers to a cell within the natural repertoire of cells in the mammalian immune system which can be activated to affect the viability of a target cell. Immune effector cells include cells of the lymphoid lineage such as natural killer (NK) cells, T cells including cytotoxic T cells, or B cells, but also cells of the myeloid lineage can be regarded as immune effector cells, such as monocytes or macrophages, dendritic cells and neutrophilic granulocytes. Hence, said effector cell is preferably an NK cell, a T cell, a B cell, a monocyte, a macrophage, a dendritic cell or a neutrophilic granulocyte. According to the invention, recruitment of effector cells to aberrant cells

means that immune effector cells are brought in close vicinity to the aberrant target cells such that the effector cells can directly kill, or indirectly initiate the killing of the aberrant cells that they are recruited to. It is preferred that a CD3 binding antibody binds CD3 on the surface of effector cells.

An antibody that binds human CD3 of the invention comprises a heavy chain variable region that comprises an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A.

The heavy chain variable region can have 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions with respect to the indicated amino acid sequence, or a combination thereof. Amino acid insertions, deletions, substitutions, additions with respect to the indicated sequence or a combination thereof, are of course only at positions other than the positions indicated by X_1X_2. At the positions indicated by X_1X_2 only the indicated amino acids are allowed. In a preferred embodiment the heavy chain variable region comprises 0-9, 0-8, 0-7, 0-6, 0-5, 0-4, preferably 0-3, preferably 0-2, preferably 0-1 and preferably 0 amino acid insertions,

deletions, substitutions, additions with respect to the indicated amino acid sequence, or a combination thereof at positions other than the positions indicated by X_1X_2. A combination of an insertion, addition, deletion or substitution is a combination as claimed if aligned sequences do not differ at more than 10, preferably no more than 5 positions. A gap in one of the aligned sequences counts for as many amino acids as skipped in the other sequence.

The amino acid insertions, deletions, substitutions, additions or combination thereof are preferably not in the CDR3 region of the heavy chain variable region, preferably not in the CDR1 and/or CDR2 region of the heavy chain variable region. In a preferred embodiment the heavy chain variable region does not comprise a deletion, addition or insertion with respect to the sequence indicated. In this embodiment the heavy chain variable region can have 0-10, preferably 0-5 amino acid substitutions with respect to the indicated amino acid sequence. An amino acid substitution is preferably a conservative amino acid substitution.

An antibody that binds human CD3 of the invention comprising a heavy chain variable region that comprises an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A, is preferably an antibody comprising a heavy chain variable region that comprises an amino acid sequence identified by the numbers 5192; 5193; 5196; 5197; 5351; 5354; 5356; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12, 25 and 28. The heavy chain variable region preferably comprises an amino acid sequence identified by the numbers 5196; 5197; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12 and 25. The heavy chain variable region of the antibody preferably comprises an amino acid sequence identified by the number 5196 as depicted in figures 12.

The invention further provides a bispecific antibody that binds human CD3 of the invention that comprises a heavy chain and a light chain wherein the heavy chain variably region of said heavy chain comprises an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A.

The light chain is preferably a common light chain as defined elsewhere herein. The bispecific antibody further comprises a heavy chain and light chain combination that binds another antigen, preferably a tumor antigen. The light chain of the heavy chain and light chain combination that binds another antigen is preferably a common light chain as defined elsewhere herein. The heavy chain that comprises a heavy chain variable region comprising an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A, is preferably a heavy chain that comprises a heavy chain variable region comprising an amino acid sequence identified by the numbers 5192; 5193; 5196; 5197; 5351; 5354; 5356; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12, 25 and 28. The heavy chain variable region of the bispecific antibody preferably comprises an amino acid sequence identified by the numbers 5196; 5197; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12 and 25. The heavy chain variable region of the bispecific antibody preferably comprises an amino acid sequence identified by the number 5196 as depicted in figures 12.

A bispecific antibody of the invention that comprises a heavy chain variable region that comprises an amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVASG FTFSS YGMHW VRQAP GKGLE WVAAI WYX$_1$X$_2$R KQDYA DSVKG RFTIS RDNSK NTLYL QMNSL RAEDT AVYYC TRGTG YNWFD PWGQG TLVTV SS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A

preferably further comprises a heavy/light chain combination that binds human CLEC12A. In a preferred embodiment the heavy chain of the heavy/light chain combination that binds human CLEC12A comprises a variable region that comprises an amino acid sequence:

QVQLV QSGAE VKKPG ASVKV SCKAS GYTFT SYYMH WVRQA PGQGL EWMGI INPSG GSTSY AQKFQ GRVTM TRDTS TSTVY MELSS LRSED TAVYY CAKGT TGDWF DYWGQ GTLVT VSS;

EVQLV QSGAE VKKPG ASVKV SCKAS GYTFT SYYMH WVRQA PGQGL EWMGI INPSG GSTSY AQKFQ GRVTM TRDTS TSTVY MELSS LRSED TAVYY CARGN YGDEF DYWGQ GTLVT VSS; or

QVQLV QSGAE VKKPG ASVKV SCKAS GYTFT GYYMH WVRQA PGQGL EWMGW INPNS GGTNY AQKFQ GRVTM TRDTS ISTAY MELSR LRSDD TAVYY CARDG YFADA FDYWG QGTLV TVSS;

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof.

The heavy chain variable region of the heavy/light chain combination that binds human CLEC12A can have 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions with respect to the indicated amino acid sequence, or a combination thereof. In a preferred embodiment the heavy chain variable region comprises 0-9, 0-8, 0-7, 0-6, 0-5, 0-4, preferably 0-3, preferably 0-2, preferably 0-1 and preferably 0 amino acid insertions, deletions, substitutions, additions with respect to the indicated amino acid sequence, or a combination thereof. A combination of an insertion, deletion, addition or substitution is a combination as claimed if aligned sequences do not differ at more than 5 positions. A gap in one of the aligned sequences counts for as many amino acid as skipped in the other sequence.

An amino acid insertion, deletion, substitution, addition or combination thereof in a CD3 heavy chain variable region as described herein preferably leaves H35, A61, Y102, N103, and W104 and positions in the CDR3 VH unchanged. If A50 is modified it is preferably substituted by an S, Y, M or a Q. If D59 is modified it is preferably substituted by an Y or an E, However substitution of D59 by L, I, V, F, R, A, N, H, S, T is also possible. If A61 is substituted it is preferably substituted for by N, I, H, Q, L, R, Y, E, S, T, D, K, V. If F105 is modified it is preferably substituted by an Y or an M. For the CD3 VH of the invention H35, Y102, N103, and W104 residues are thought to be relevant for CD3 binding. Other specific substitutions at the A50, D59, A61 and F105 positions are also relevant but do not have to affect CD3 binding. Table 2 lists amino acid substitution introduced in column 2. Those that were also recovered are mentioned in column 3. Amino acid substitutions that were introduced but not recovered

are thought to affect the antibody and are not desired. For instance an A50I mutation is not desired. Tolerated amino acid substitutions can easily be found using the method described in example 5A together with CIEX-HPLC after storage.

An amino acid insertion, deletion, substitution, addition or combination thereof is preferably not done in the binding interphase of the heavy and light chain.

If an amino acid is changed in the interphase of the H/L chain interaction, it is preferred that the corresponding amino acids in the other chain are changed to accommodate the change. An insertion or addition of an amino acid preferably does not entail the insertion or addition of a proline.

An addition of an amino acid can in principle be regarded to be the same as an insertion. Adding an amino acid to one of the ends of a polypeptide chain is sometimes not considered an insertion but as a strict addition (prolongation). For the present invention both an addition within a chain or to one of the ends, are considered to be an insertion.

The amino acid insertions, deletions, substitutions, additions or combination thereof are preferably not in the CDR3 region of the heavy chain variable region, preferably not in the CDR1 or CDR2 region of the heavy chain variable region. In a preferred embodiment the heavy chain variable region does not comprise a deletion, addition or insertion with respect to the sequence indicated. In this embodiment the heavy chain variable region can have 0-5 amino acid substitutions with respect to the indicated amino acid sequence. An amino acid substitution is preferably a conservative amino acid substitution. The CDR1, CDR2 and CDR3 of a CD3

binding VH of the invention preferably comprise respectively the amino acid sequence GFTFSSYG for CDR1 (according to IMGT), IWYNARKQ for CDR2 and GTGYNWFDP for CDR3. The CDR1, CDR2 and CDR3 of a CLEC12A binding VH of the invention preferably comprises respectively the amino acid sequence GYTFTSYY for CDR1, INPSGGST for CDR2, and GTTGDWFDY for CDR3.

The light chain variable region comprises preferably a germline O12 variable region V-segment. In a preferred embodiment the light chain variable region comprises the kappa light chain V-segment IgVκ1-39*01. In a particularly preferred embodiment the light chain variable region comprises the kappa light chain IgVκ1-39*01/IGJκ1*01 or IgVκ1-39*01/IGJκ1*05. In a most preferred embodiment the light chain variable region comprises a germline kappa light chain IgVκ1-39*01/IGJκ1*01 sequence.

In a bispecific antibody of the invention it is preferred that the light chain is the same for both heavy chain/light chain combinations. Such a light chain is also referred to as a "common light chain". The term 'common light chain' according to the invention refers to light chains which may be identical or have some amino acid sequence differences while retaining the binding specificity of the antibody. It is for instance possible within the scope of the definition of common light chains as used herein, to prepare or find light chains that are not identical but still functionally equivalent, e.g., by introducing and testing conservative amino acid changes, changes of amino acids in regions that do not or only partly contribute to binding specificity when paired with the heavy chain, and the like. The terms 'common light chain', 'common VL', 'single light chain', 'single VL', with or without the addition of the term 'rearranged' are all used herein interchangeably. It is an aspect of the present invention to use as

common light chain a human light chain that can combine with different heavy chains to form antibodies with functional antigen binding domains (WO2004/009618, WO2009/157771, Merchant et al. 1998, Nissim et al. 1994). Preferably, the common light chain has a germline sequence. A preferred germline sequence is a light chain variable region that is frequently used in the human repertoire and has superior ability to pair with many different VH regions, and has good thermodynamic stability, yield and solubility.

In a preferred embodiment the common light chain comprises a light chain variable region that comprises a germline O12 / IgVκ1-39*01. In a preferred embodiment the light chain variable region comprises the kappa light chain IgVκ1-39*01/IGJκ1*01 or IgVκ1-39*01/IGJκ5*01. In a preferred embodiment a IgVκ1-39*01/IGJκ1*01. The light chain variable region preferably comprises a germline kappa light chain IgVκ1-39*01/IGJκ1*01 or germline kappa light chain IgVκ1-39*01/IGJκ5*01. In a preferred embodiment a germline IgVκ1-39*01/IGJκ1*01Obviously, those of skill in the art will recognize that “common” also refers to functional equivalents of the light chain of which the amino acid sequence is not identical. Many variants of said light chain exist wherein mutations (deletions, substitutions, additions) are present that do not materially influence the formation of functional binding regions.

In a preferred embodiment the light chain variable region comprises the amino acid sequence DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PTFGQ GTKVE IK or DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PITFG QGTRL EIK with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof. In a preferred embodiment the light chain variable region comprises 0-9, 0-8, 0-7, 0-6, 0-5,

0-4, preferably 0-3, preferably 0-2, preferably 0-1 and preferably 0 amino acid insertions, deletions, substitutions, additions with respect to the indicated amino acid sequence, or a combination thereof. A combination of an insertion, deletion, addition or substitution is a combination as claimed if aligned sequences do not differ at more than 5 positions. A gap in one of the aligned sequences counts for as many amino acid as skipped in the other sequence. In a preferred embodiment the light chain variable region comprises the amino acid sequence DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PTFGQ GTKVE IK or DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PITFG QGTRL EIK. In a preferred embodiment the light chain variable region comprises the amino acid sequence DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PTFGQ GTKVE IK. In another preferred embodiment the light chain variable region comprises the amino acid sequence DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PITFG QGTRL EIK.

The amino acid insertions, deletions, substitutions, additions or combination thereof are preferably not in the CDR3 region of the light chain variable region, preferably not in the CDR1 or CDR2 region of the heavy chain variable region. In a preferred embodiment the heavy chain variable region does not comprise a deletion, addition or insertion with respect to the sequence indicated. In this embodiment the heavy chain variable region can have 0-5 amino acid substitutions with respect to the indicated amino acid sequence. An amino acid substitution is preferably a conservative amino acid substitution. The CDR1, CDR2 and CDR3 of a light chain of an

antibody of the invention preferably comprises respectively the amino acid sequence CDR1 - QSISSY, CDR2 – AAS, CDR3 – QQSYSTP, i.e. the CDRs of IGKV1-39 (according to IMGT).

As mentioned herein above, it is preferred that the antibody of the invention is a bispecific antibody. In a preferred embodiment the bispecific antibody comprises a CD3 binding heavy/light chain combination as indicated herein, and a heavy/light chain combination that binds a tumor antigen. In a preferred embodiment the tumor antigen-binding heavy/light chain combination binds CLEC12A.

The constant region of a (bispecific) antibody of the present invention is preferably a human constant region. The constant region may contain one or more, preferably not more than 10, preferably not more than 5 amino-acid differences with the constant region of a naturally occurring human antibody. Various variable domains of antibodies produced herein are derived from a human antibody variable domain library. As such these variable domains are human. The unique CDR regions may be derived from humans, be synthetic or derived from another organism. An antibody or bispecific antibody of the invention is preferably a human or humanized antibody.

In the art various methods exist to produce antibodies. Antibodies are typically produced by a cell that expresses nucleic acid encoding the antibody. Suitable cells for antibody production are a hybridoma cell, a Chinese hamster ovary (CHO) cell, an NS0 cell or a PER-C6 cell. In a particularly preferred embodiment said cell is a CHO cell.

Various institutions and companies have developed cell lines for the large scale production of antibodies, for instance for clinical use. Non-limiting examples of such cell lines are CHO cells, NS0 cells or PER.C6

cells. These cells are also used for other purposes such as the production of proteins. Cell lines developed for industrial scale production of proteins and antibodies are herein further referred to as industrial cell lines. In a preferred embodiment the invention provides an industrial cell line that produces and an antibody of the invention.

The invention in one embodiment provides a cell comprising an antibody according to the invention and/or a nucleic acid according to the invention. Said cell is preferably an animal cell, more preferably a mammal cell, more preferably a primate cell, most preferably a human cell. For the purposes of the invention a suitable cell is any cell capable of comprising and preferably of producing an antibody according to the invention and/or a nucleic acid according to the invention.

The invention further provides a cell comprising an antibody according to the invention. Preferably said cell (typically an in vitro, isolated or recombinant cell) produces said antibody. In a preferred embodiment said cell is a hybridoma cell, a Chinese hamster ovary (CHO) cell, an NS0 cell or a PER.C6 cell. In a particularly preferred embodiment said cell is a CHO cell. Further provided is a cell culture comprising a cell according to the invention. Various institutions and companies have developed cell lines for the large scale production of antibodies, for instance for clinical use. Non-limiting examples of such cell lines are CHO cells, NS0 cells or PER.C6 cells. These cells are also used for other purposes such as the production of proteins. Cell lines developed for industrial scale production of proteins and antibodies are herein further referred to as industrial cell lines. Thus in a preferred embodiment the invention provides the use of a cell line developed for the large scale production of antibody for the production of an antibody of the invention. The invention further provides a cell for producing an antibody comprising a nucleic acid molecule that codes for a VH, a VL,

and/or a heavy and light chain of an antibody as claimed. Preferably said nucleic acid molecule encodes a VH identified by numeral 5196 of figure 12, a nucleic acid molecule encoding a VH as identified by numeral 4327 of figure 24 or a combination thereof.

The invention further provides a method for producing an antibody comprising culturing a cell of the invention and harvesting said antibody from said culture. Preferably said cell is cultured in a serum free medium. Preferably said cell is adapted for suspension growth. Further provided is an antibody obtainable by a method for producing an antibody according to the invention. The antibody is preferably purified from the medium of the culture. Preferably said antibody is affinity purified.

A cell of the invention is for instance a hybridoma cell line, a CHO cell, a 293F cell, an NS0 cell or another cell type known for its suitability for antibody production for clinical purposes. In a particularly preferred embodiment said cell is a human cell. Preferably a cell that is transformed by an adenovirus E1 region or a functional equivalent thereof. A preferred example of such a cell line is the PER.C6 cell line or equivalent thereof. In a particularly preferred embodiment said cell is a CHO cell or a variant thereof. Preferably a variant that makes use of a Glutamine synthetase (GS) vector system for expression of an antibody.

The invention further provides a method for producing an antibody comprising culturing a cell of the invention and harvesting said antibody from said culture. Preferably said cell is cultured in a serum free medium. Preferably said cell is adapted for suspension growth. Further provided is an antibody obtainable by a method for producing an antibody

according to the invention. The antibody is preferably purified from the medium of the culture. Preferably said antibody is affinity purified.

Bispecific antibodies are typically also produced by cells that express nucleic acid encoding the antibody. In this case the cell expresses the different light and heavy chains that make up the bispecific antibody. To this end the cell expresses two different heavy chains and at least one light chain. As unmodified heavy chains can pair with each other to form dimers such cells typically produce the two monoclonal antibodies (homodimers), in addition to the bispecific antibody (heterodimer). The number of possible heavy/light chain combinations in the produced antibodies increases when the cell expresses two or more light chains. To reduce the number of different antibody species (combinations of different heavy and light chains) produced the afore mentioned "common light chain" is preferred.

An antibody producing cell that expresses a common light chain and equal amounts of the two heavy chains typically produces 50% bispecific antibody and 25% of each of the monospecific antibodies (i.e. having identical heavy light chain combinations). Several methods have been published to favor the production of the bispecific antibody or vice versa, the monospecific antibodies. In the present invention it is preferred that the cell favors the production of the bispecific antibody over the production of the respective monospecific antibodies. Such is typically achieved by modifying the constant region of the heavy chains such that they favor heterodimerization (i.e. dimerization with the heavy chain of the other heavy/light chain combination) over homodimerization. In a preferred embodiment the bispecific antibody of the invention comprises two different immunoglobulin heavy chains with compatible heterodimerization domains. Various compatible heterodimerization domains have been described in the art (see for instance Gunasekaran et al. JBC 2010 (285) 19637-19646). The

compatible heterodimerization domains are preferably compatible immunoglobulin heavy chain CH3 heterodimerization domains. The art describes various ways in which such hetero-dimerization of heavy chains can be achieved. One way is to generate 'knob into hole' bispecific antibodies. See US Patent Application 20030078385 (Arathoon et al. - Genentech).

In US13/866,747 (now issued as US 9,248,181), US14/081,848 (now issued as US 9,358,286) and PCT/NL2013/050294 (published as WO2013/157954); incorporated herein by reference) methods and means are disclosed for producing bispecific antibodies using compatible heterodimerization domains. These means and methods can also be favorably employed in the present invention. Specifically, preferred mutations to produce essentially only bispecific full length IgG molecules are the amino acid substitutions L351K and T366K (numbering according to Kabat) in the first CH3 domain (the 'KK-variant' heavy chain) and the amino acid substitutions L351D and L368E in the second domain (the 'DE-variant' heavy chain), or vice versa. It was previously demonstrated in our US 9,248,181 and US 9,358,286 patents as well as the WO2013/157954 PCT application that the DE-variant and KK-variant preferentially pair to form heterodimers (so-called 'DEKK' bispecific molecules). Homodimerization of DE-variant heavy chains (DEDE homodimers) or KK-variant heavy chains (KKKK homodimers) hardly occurs due to strong repulsion between the charged residues in the CH3-CH3 interface between identical heavy chains. In one embodiment the heavy chain/light chain combination that comprises the variable domain that binds CD3, comprises a KK variant of the heavy chain. In this embodiment the heavy chain/light chain combination that comprises the variable domain that binds an antigen other than CD3 comprises a DE variant of the heavy chain. In a preferred embodiment the antigen other than CD3 is CLEC12A. In a preferred embodiment the VH of

the variable domain that binds CLEC12A is MF4327_VH as depicted in figure 24.

Some antibodies are modified in CH2/lower hinge region, for instance to reduce Fc-receptor interaction or to reduce C1q binding. In some embodiments the antibody of the invention is an IgG antibody with a mutant CH2 and/or lower hinge domain such that interaction of the bispecific IgG antibody to a Fc-gamma receptor is reduced. Such a mutant CH2 and/or lower hinge domain preferably comprise an amino substitution at position 235 and/or 236 (Kabat numbering), preferably an L235G and/or G236R substitution.

The invention further provides a method of treating cancer or a risk of cancer in a subject comprising administering to the subject in need thereof a bispecific antibody that binds human CD3 which antibody comprises a heavy chain and light chain wherein said heavy chain comprises a variable region that comprises the amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVAS GFTFS SYGMH WVRQA PGKGL EWVAA

IWYX$_1$X$_2$ RKQDY ADSVK GRFTI SRDNS KNTLY LQMNS LRAED TAVYY

CTRGT GYNWF DPWGQ GTLVT VSS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A; and

a heavy chain - light chain (H/L) combination that binds a tumor-antigen.

The light chain preferably comprises a common light chain variable region. Said common light chain variable region preferably comprises an O12 / IgVκ1-39light chain variable region. Said light chain variable region is preferably a germline O12 / IgVκ1-39*01 variable region. Said light chain variable region preferably comprises the kappa light chain IgVκ1-39*01/IGJκ1*01 or IgVκ1-39*01/IGJκ5*01. The light chain variable region preferably comprises the germline kappa light chain IgVκ1-39*01/IGJκ1*01 or IgVκ1-39*01/IGJκ5*01. Said light chain variable region preferably comprises the amino acid sequence.
DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PTFGQ GTKVE IK or DIQMT QSPSS LSASV GDRVT ITCRA SQSIS SYLNW YQQKP GKAPK LLIYA ASSLQ SGVPS RFSGS GSGTD FTLTI SSLQP EDFAT YYCQQ SYSTP PITFG QGTRL EIK with 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof. Preferably the heavy chain/light chain (H/L) chain combination that binds a tumor-antigen binds CLEC12A.
The antibody is preferably a human or humanized antibody. Preferably the antibody comprises two different immunoglobulin heavy chains with compatible heterodimerization domains. Said compatible heterodimerization domains are preferably compatible immunoglobulin heavy chain CH3 heterodimerization domains. Said bispecific antibody is preferably an IgG antibody with a mutant CH2 and/or lower hinge domain such that interaction of the bispecific IgG antibody to a Fc-gamma receptor is reduced. The mutant CH2 and/or lower hinge domain preferably comprise an amino substitution at position 235 and/or 236 (Kabat numbering), preferably an L235G and/or G236R substitution. The antibody preferably comprises a common light chain.

Also provided is a bispecific antibody that binds human CD3 which antibody comprises a heavy chain and light chain wherein said heavy chain comprises a variable region that comprises the amino acid sequence:

QVQLV QSGGG VVQPG RSLRL SCVAS GFTFS SYGMH WVRQA PGKGL EWVAA IWYX$_1$X$_2$RKQDY ADSVK GRFTI SRDNS KNTLY LQMNS LRAED TAVYY CTRGT GYNWF DPWGQ GTLVT VSS

with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the position indicated by X_1X_2;

wherein

X_1 = N and X_2 = A;

X_1 = N and X_2 = T;

X_1 = S and X_2 = G;

X_1 = H and X_2 = G;

X_1 = D and X_2 = G; or

X_1 = H and X_2 = A; and

a heavy chain and light chain that binds a tumor antigen.

The invention further provides an antibody of the invention or a derivative thereof or a pharmaceutical composition of the invention, for use in the treatment of a subject in need thereof. For the treatment of a subject that has or is at risk of having a tumor it is preferred that the antibody is a bispecific antibody of the invention. Preferably wherein the CD3 binding antibody comprises a heavy/light chain combination that binds a tumor antigen. The bispecific antibody is preferably a CD3/CLEC12A binding antibody.

Provided are CD3/tumor antigen bispecific antibodies and pharmaceutical compositions comprising such bispecific antibodies for use in the treatment of solid or hematological tumors. Preferred solid tumors are of

epithelial origin; gynecological cancer such as ovarian and endometrial tumors; prostate cancer, brain cancer or any other solid tumor.

Provided is also a CD3/tumor antigen bispecific antibody of the invention or a derivative thereof or pharmaceutical compositions comprising such bispecific antibody or derivative thereof for use in the treatment of various leukemias and pre-leukemic diseases of myeloid origin but also B cell lymphomas. Diseases that can be treated according to the invention include myeloid leukemias or pre-leukemic diseases such as acute myeloid leukemia (AML), myelodysplastic syndrome (MDS) and chronic myelogenous leukemia (CML), and Hodgkin's lymphomas and most non-Hodgkin's lymphomas. Also B-ALL; T-ALL, mantle cell lymphoma are also preferred targets for treatment with antibody of the invention. Thus the invention provides a bispecific full length IgG antibody according to the invention for use as a pharmaceutical in the treatment of myelodysplastic syndrome (MDS), chronic myelogenous leukemia (CML), multiple myeloma (MM) or preferably acute myeloid leukemia (AML). Also provided is a use of a bispecific IgG antibody according to the invention in the preparation of a medicament for the treatment or prevention of MDS, CML, MM or preferably AML. It is preferred that the tumor antigen is CLEC12A.

The amount of antibody according to the invention to be administered to a patient is typically in the therapeutic window, meaning that a sufficient quantity is used for obtaining a therapeutic effect, while the amount does not exceed a threshold value leading to an unacceptable extent of side-effects. The lower the amount of antibody needed for obtaining a desired therapeutic effect, the larger the therapeutic window will typically be. An antibody according to the invention exerting sufficient therapeutic effects at low dosage is, therefore, preferred.

Approximately 30.000 patients are diagnosed each year with AML in Europe and US. The majority of these patients are 60 years of age or older. Older age is a major negative determinant of outcome in AML and long term survival (at 5 years) of intensively treated older AML patients is approximately 10%. In almost all patients that have achieved remission upon induction chemotherapy, disease progression is observed within 3 years. Current post remission treatment has shown limited, if any, value in older patients with AML. Therefore, a significant load of residual resistant leukemia remains, and the surviving subpopulation of drug resistant leukemic cells rapidly generates recurrence. Novel types of drugs with entirely different modes of action are needed to target these chemotherapy non responsive AML tumor cells in efforts to induce and sustain complete remissions. Although complete remission (CR) can be achieved with a number of intensive chemotherapy combinations in more than 50% of elderly AML patients and around 80% in younger patients, advancements of response or survival have remained a major investigational challenge. In a recently published network meta-analysis of 65 randomized clinical trials (15.110 patients) in older patients with AML most of the amended investigational induction regimens have similar or even worse efficacy profiles as compared to the conventional 3+7 induction regimen with daunorubicin and cytarabine. This standard treatment of AML is associated with high morbidity and even mortality. The majority of the patients in CR relapse due to remaining leukemic stem cells after chemotherapy. Further dose intensification is limited due to unacceptable toxicity. An urgent need for new treatment modalities preferably with less toxicity is thus emerging especially in elderly patients with AML.

Treatment of chemotherapy unresponsive AML could be achieved by redirecting T cells from the patient's own immune system to AML tumor cells and subsequent tumor target-specific activation of T cells using a bispecific antibody. This process is also known as a so-called "T-cell

engaging approach". In this manner, the patients' immune system is strengthened and retargeted to attack and eradicate the AML tumor cells. The present invention provides CD3xCLEC12A bispecific IgG antibodies that efficiently redirects T cells towards the AML tumor cells, thereby inducing AML tumor cell lysis. CD3xCLEC12A bispecific antibodies thus are a targeted therapy with fewer side effects, that specifically eradicates AML blasts and leukemic stem cells in order to improve the prognosis of AML patients. Because CLEC12A is expressed on leukemic stem cells (LSC) and not on normal haematopoietic stem cells, therapy directed against this antigen is anticipated to eradicate the LSC while sparing the normal stem cell. These full length IgG bispecific antibodies are clinically evaluated in relapsed and/or refractory AML patients. The clinical efficacy is analyzed using AML blast reduction in the bone marrow as an objective response criterion. An efficacious bispecific IgG for AML provides a novel therapeutic option for a large patient segment for which there is currently no treatment available. In addition to providing a means to achieve durable remissions, this treatment option also has a curative potential for AML when applied during remission. It most probably will have the greatest impact in situations of Minimal Residual Disease (MRD). The expectancy is that relapse percentage will drop due to the eradication of the MRD. So the impact for the AML patient of this new treatment modality would be a less toxic treatment with a lesser percentage of relapse resulting in an improvement of outcome associated with a better quality of life.

The antibodies 15C3 and 3056 described in the art share the same heavy chain variable region but differ in the light chain variable region. Batch to batch variation in the binding potential of the antibody was observed in batches of antibody 3056. This was not noted for antibody 15C3. As the antibodies differ in the light chain the reason for the difference in behavior would be the different light chain. SDS-page revealed that the 3056

antibody was intact also in batches with less active antibody. 3D-modelling of the variable domains of the antibodies did reveal some changes in the folding of the VH/VL domain between the two antibodies. As these changes might explain the different behavior of the antibodies experiments were designed to render the folding of the VH/VL domain of antibody 3056 more akin 15C3. Unfortunately, this did not explain the differences between the antibodies 15C3 and 3056. Iso-electric focusing (IEF) only revealed slight differences between 15C3 (3055) and 3056 linked to the major band at a high iso-electric point of the antibody. Subsequent analysis using CIEX-HPLC, a chromatographic technique that allows the separation of charge variants, revealed, depending on the batch a very complex retention spectrum with a broad elution profile for antibody 3056, this in contrast to the profile observed for 15C3 (3055). Moreover it was found that the 3056 pattern changed significantly over time, suggesting that the 3056 antibody is inherently instable.

Only when variants were designed wherein the 3056_VH chain was changed at one or two specific positions the behavior changed. The behavior varied between unstable, no binding activity at all to binding without significant batch to batch variability.

The 3056 heavy chain contains an NG deamidation motif in its CDR2 region, WYNGRKQ, which could be involved in the observed charge heterogeneity of the 3056 antibody. In silico modeling of the 15C3 and 3056 Fabs did not reveal a significant difference in the folding of the NG deamidation motif in the HCDR2 region. This argued against an involvement of this motif in the observed instability of the 3056 antibody. Surprisingly however, the changes as indicated in the claims significantly reduced the observed batch to batch variation of antibodies of the invention.

The invention further provides an antibody comprising a variable domain that binds CD3 and a variable domain that binds CLEC12A, wherein the variable domain that binds CLEC12A has a VH comprising the amino acid sequence identified by the numbers 4327 of figure 24 with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof, and the variable domain that binds CD3 has a VH comprising the amino acid sequence identified by the numbers 5192, 5193; 5196; 5197; 5351; 5354; 5356; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12, 25 and 28 with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the positions 54 and 55. The light chain preferably comprises a variable domain with amino acid as depicted in figure 23, preferably 23B.

The invention further provides an antibody comprising a variable domain that binds CD3 and a variable domain that binds CLEC12A, wherein the variable domain that binds CLEC12A has a VH comprising the amino acid sequence identified by the numbers 4327 of figure 24 with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof, and the variable domain that binds CD3 has a VH comprising the amino acid sequence identified by the number 5196 as depicted in figure 12 with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the positions 54 and 55.

The heavy chain of the variable domain that binds CD3 preferably has the amino acid sequence identified the by the numbers 5196; 5197; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12 and 25 with 0-10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the positions 54 and 55. The variable domain that binds CD3 preferably has the amino acid sequence identified the by the number 5196 as depicted in figures 12 with 0-

10, preferably 0-5 amino acid insertions, deletions, substitutions, additions or a combination thereof at one or more positions other than the positions 54 and 55;

In a preferred embodiment the heavy chain variable region comprises 0-9, 0-8, 0-7, 0-6, 0-5, 0-4, preferably 0-3, preferably 0-2, preferably 0-1 and preferably 0 amino acid insertions, deletions, substitutions, additions with respect to the indicated amino acid sequence, or a combination thereof. For the CD3 heavy chain the indicated amino acid insertions, deletions, substitutions, additions are at positions other than the positions 54 and 55. A combination of an insertion, addition, deletion or substitution is a combination as claimed if aligned sequences do not differ at more than 10, preferably no more than 5 positions. A gap in one of the aligned sequences counts for as many amino acids as skipped in the other sequence.

The invention further provides an antibody comprising a variable domain that binds CD3 and a variable domain that binds CLEC12A, wherein the variable domain that binds CLEC12A has a VH comprising the amino acid sequence identified by the numbers 4327 of figure 24, and the variable domain that binds CD3 has a VH comprising the amino acid sequence identified by the numbers 5192, 5193; 5196; 5197; 5351; 5354; 5356; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12, 25 and 28. The heavy chain of the variable domain that binds CD3 preferably has the amino acid sequence identified the by the numbers 5196; 5197; 5603; 5616; 5626; 5630; 5648; 5661; or 5694 as depicted in figures 12 and 25. The variable domain that binds CD3 preferably has the amino acid sequence identified by the number 5196 as depicted in figures 12.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. IEF of PG3055 and PG3056

Figure 2. CEX-HPLC analysis of PG3055 and PG3056

Figure 3. Batch to batch variability and stability of PG3055 and PG3056 analyzed by CEX-HPLC analysis. Left 3055 batches over time, right 3056 batches over time, with on top samples stored at -80°C, in bottom samples stored at 2-8°C for > 3 months.

Figure 4. Flow cytometry analysis for binding of PG3055 and PG3056 to CD3 on purified human T cells upon incubation in IMDM+10%FBS medium at 2-8°C or 37°C for 7 days. PG3055 and PG3056: incubated in IMDM+10%FBS medium at 2-8°C for 7 days. PG3055 37°C and PG3056 37°C: PG3055 and PG3056 incubated in IMDM+10%FBS medium at 37°C for 7 days.

Figure 5. Left: Homology model of PG3056 Fab zoomed in on variable domains, VL in light gray, VH in black, HCDR1-3 loops in light gray. Residues Asn54 and Gly55 that form the deamidation motif in HCDR2 are indicated. Right: Overlay of homology models of PG3055 (light gray) and PG3056 (dark gray) Fabs.

Figure 6. Alignment of VH MF3056 (of MF3056_VH) versus the VH3-33 germline sequence

Figure 7. Alignment of VH MF3056 versus VH MF3872, MF3873 and MF3905

Figure 8. Flow cytometry analysis for binding to CD3 on HPB-ALL cells of variants PG3872, PG3873 and PG3905, PG3056 was included as benchmark control

Figure 9. Alignment of VH of MF3056 versus VH of MF3874, MF3878, MF3883, MF3886 and MF3891

Figure 10. Flow cytometry analysis for binding to CD3 on HPB-ALL cells of variants PG3874, PG3878, PG3883, PG3886 and PG3891, PG3056 was included as benchmark control.

Figure 11. CEX-HPLC analysis of PG3891

Figure 12 Alignment of VH of MF3056 versus VH of MF5192-5197 VH

Figure 13. Flow cytometry analysis for binding to CD3 on HPB-ALL cells of variants PG5192-5197, PG3056 was included as benchmark control

Figure 14. IEF analysis of PG5196p06

Figure 15. CEX-HPLC chromatogram of PG5196

Figure 16. Binding of 5196x4327 DM-Fc bsAb to membrane expressed CD3 (HPB-ALL) and CLEC12A (HL-60)

Figure 17. 5196x4327 DM-Fc bsAb retained CLEC12A-specific activation of CD4 and CD8 T cells reflected by upregulation of early activation marker CD69. The bsAb and control IgGs were tested at 1000 ng/mL. T cell activation flow cytometry data are expressed as the percentage of CD69-positive cells within the CD4+ or CD8+ T -cell populations. HD1 and HD2 reflect two different experiments using T cells obtained from different healthy donors

Figure 18. 5196x4327 induced antigen mediated target cell lysis

Figure 19. Sensorgrams showing on- and off-rates of CD3δε-Fc (A) and CLEC12A protein (B) to immobilized 5196x4327 DM-Fc bsAb. Sensorgrams show the response (amount of protein bound to the chip, in artificial units) as a function of the time (in seconds). Both panels show the sensorgrams obtained using a concentration range of antigen (in colour) and the respective curve fittings performed using the BIAevaluation software (in black)

Figure 20. Primary AML patient sample was phenotyped for CLEC12A expression and the fraction of T cells and AML blasts by flow cytometry analysis at start (day = 0) of the co-culture. After days 7 of co-culture with 5196x4327 DM-Fc bsAb or isotype control the fraction and the total number of T cells and AML blasts were quantified by flow cytometry analysis

Figure 21. DSC analysis as described in example 9.

Figure 22. Heavy chain variable sequence (VH) of antibody 15C3 described in WO2005/118635. The patent publication describes two variants of the antibody 15C3. Both variants have the same heavy chain variable domain, but this heavy chain variable domain is combined with two different light chain variable domains. Where reference is made herein to antibody 15C3, reference is made to an antibody having the heavy chain variable domain as depicted in this figure in combination with light chain variable domain L2 as indicated in this figure. The Fab product of the 15C3 VH plus L2 light chain is herein further referred to as MF3055.
The antibody PG3056 has the VH as depicted herein in combination with light chain variable region IGKV1-39 as depicted in this figure. The Fab product of the 15C3 VH plus IGKV1-39 light chain is further referred to as MF3056.

Figure 23. The antibody of the invention preferably has a common light chain. A) The common light chain preferably comprises the amino acid sequence depicted as sequence IGKV1-39 in this figure. B) In a preferred embodiment the common light chain comprises the amino acid sequence depicted as IGKV1-39/jk1 or IGKV1-39/jk5. In a particularly preferred embodiment the common light chain comprises the amino acid sequence of IGKV1-39/jk1 as depicted in this figure.

Figure 24. Amino acid sequence of the VH region of an anti-CLEC12A binding antibody Fab (MF4327) and the amino acid sequence of the VH region of an anti-tetanus toxoid (TT) binding Fab (MF1337). Together with the amino acid sequence of the common light chain depicted in figure 23, these VHs form variable domains of the Fabs MF4327 and MF1337 that bind CLEC12A and tetanus toxoid respectively.

Figure 25. Examples of the CD3 binding variants of MF5196 are MF5603, MF5616, MF5626, MF5630, MF5648, MF5661 and MF5694, all containing the rearranged human IGKVl-39/IGKJl VL region. The amino acid sequence of the VH of the Fabs is indicated.

Figure 26. Binding of antibodies comprising MF5196 VH; MF5603 VH; MF5616 VH; MF5626 VH; MF5630 VH; MF5648 VH; MF5661 VH and MF5694 VH and a common light chain as depicted in figure 23B, to membrane-expressed CD3 on HPB-ALL cells, as analyzed by flow cytometry.

Figure 27. PG5661 CIEX-HPLC chromatogram.

Figure 28 CD3 binding Fabs MF5351, MF5354 and MF5356, composed of the rearranged human IGKV1-39/IGKJ1 VL region have the respective VH as depicted.

Figure 29 PG-format binding to membrane-expressed CD3 on HPB-ALL cells all these examples bound to CD3.

EXAMPLES

As used herein "MFXXXX" wherein X is independently a numeral 0-9, refers to a Fab comprising a variable domain wherein the VH has the amino acid sequence identified by the 4 digits. Unless otherwise indicated the light chain variable region of the variable domain typically has a sequence of figure 23, typically 23B. "MFXXXX VH" refers to the amino acid sequence of the VH identified by the 4 digits. The MF further comprises a constant region of a light chain and a constant region of a heavy chain that normally interacts with a constant region of a light chain. PG refers to a monospecific antibody comprising identical heavy and light chains. PB refers to a bispecific antibody with two different heavy chains. The variable region of the heavy chains differs and typically also the CH3 region, wherein one of the heavy chains has a KK mutation of its CH3 domain and the other has the complementing DE mutation of its CH3 domain (see for reference PCT/NL2013/050294 (published as WO2013/157954).

Example 1: Charge heterogeneity of 3055 and 3056 mAbs

Iso-electric focusing (IEF) was used to determine the pI and charge heterogeneity of PG3056, a full length IgG1 monoclonal antibody comprising the MF3056 VH paired with the IGVK1-39/JK1 common light chain and PG3055, a full length IgG1 monoclonal antibody comprising the same VH paired with the 15C3 VL2 - IGKV1-13 light chain. For this purpose a

Focusgel with pI range 6-11 (Webscientific, cat# 1006-03) was run on a GE Healthcare Multiphor II electrophoresis unit equipped with a cooling plate that was cooled to 10°C. 10 µg of untreated sample was loaded to the sample slot next to a high pI range marker (GE Healthcare, cat# 17047301V). The electrophoresis program consisted of three phases; initial focusing for 10 minutes at 500 V followed by 90 minutes at 1,500 V and finally a focusing phase at 2,000 V for 10 minutes. Consequently the gel was fixed and stained using colloidal coomassie dye (Pierce, cat# 24590).

IEF analysis of PG3056 and PG3055 resulted in the gel shown in Figure 1. For PG3055 a main band is observed at high pI (~ 9) with a satellite band at a somewhat higher pI value. PG3056 displayed a similar IEF pattern, however at subtle higher pI values and with a slightly more diffuse main band.

Both IgGs were analyzed using cation exchange chromatography HPLC (CEX-HPLC) to analyze their charge heterogeneity using an orthogonal method. CEX-HPLC was performed at ambient temperature on a Dionex HPLC system equipped with an SP STAT 7 µm column and an UV/Vis detector. 10 µg of sample was injected; a gradient of 25 mM phosphate buffer pH 6.0 with increasing NaCl concentration was used to separate the antibody charge variants. Data were analyzed using Chromeleon software.

The CEX-HPLC chromatograms of PG3055 and PG3056 are shown in Figure 2. PG3055 shows a main peak at 18.8 minutes flanked by small peaks representing acidic and basic isoforms of the IgG. Surprisingly, the chromatogram of PG3056 contains multiple peaks over a large time interval; two broad main peaks are visible at 18.4 and 20.4 minutes. The chromatograms show considerably increased charge heterogeneity of the IGVK1-39/JK1 common light chain anti-CD3 antibody (PG3056) when compared to the IgG with the 15C3 VL2 - IGKV1-13 light chain (PG3055).

CEX-HPLC was also used to assess the batch to batch variability and stability of the anti-CD3 antibodies. Both antibodies were analyzed after they had been stored at 2-8°C for more than 3 months and after long term storage at -80°C. The overlay of the PG3055 samples (Figure 3, left) shows that a minor difference is observed between the samples; the relative peak areas of the minor peaks at 17.1 minutes and 19.8 minutes change slightly upon storage at 2-8°C for a long period of time. The differences observed between the PG3056 samples (Figure 3 right) are much more substantial. The peak at 20.4 minutes decreases significantly upon storage at 2-8°C whereas the peak at 18.4 minutes increases to the extent of becoming the main peak of the sample. Other early eluting peaks representing other acidic isoforms of the IgG also show a relative increase in peak area, e.g. the peak at 16.4 minutes. The observed changes in the CEX-HPLC chromatograms after long-time storage at 2-8°C indicate that the anti-CD3 antibody containing the IGVK1-39/JK1 common light chain is not stable while being stored under these conditions, while the PG3055 antibody containing the 15C3 VL2 - IGKV1-13 light chain is much more stable.

Example 2: influence of PG3056 antibody batch to batch variation on antigen binding

To assess the stability of the anti-CD3 antibodies in the presence of serum the PG3055 and PG3056 antibodies were diluted to 10 µg/mL in IMDM (Invitrogen, Cat# 21980-065) supplemented 10% FBS (PAA, Cat# A15-101) and subsequently incubated at 37°C for seven days. In this analysis an isotype control IgG (PG1207) was included. After seven days the binding of the IgGs to CD3 was assessed by flow cytometry analysis on healthy donor derived, MACS purified T cells. For comparison PG3055 and PG30566 stored in the same medium for seven days at 2-8°C were included in the flow cytometry analysis. CD3 binding of all antibodies was tested at concentrations 10, 1, 0.1 and 0.01 µg/mL, diluted in IMDM+10%FBS. Bound

antibodies were visualized with a goat-anti-human Fc antibody (Southern Biotech, 2043-02), according to FACS procedure as previously described in WO2014/051433 with the deviation that staining was performed IMDM+10%FBS. The data show (Figure 4) that PG3055 and PG3056 showed similar binding to T cells when incubated at 2-8°C in the presence of serum. Whereas binding of PG3055 was not affected by a seven day incubation at 37°C in IMDM+10%FBS (PG3055 vs PG3055 37°C), the binding of PG3056 to CD3 on T cells was significantly reduced (PG3056 vs PG3056 37°C).

In conclusion PG3056, the anti-CD3 antibody containing the IGVK1-39/JK1 common light chain, showed strongly reduced binding to CD3 after incubation serum at 37°C for 7 days. In contrast the PG3055 antibody retained full CD3 binding under the same conditions.

Example 3: What is the difference between the PG3055 and PG3056 antibodies?

Antibodies PG3055 and PG3056 have identical sequences but for the light chain variable region. Apparently the common light chain does not work well in the context of the other amino acid sequences of the antibody and in particular with the heavy chain variable region with which it is in intimate contact. The most obvious way to try and correct the deficiency of the 3056 antibody would be to see if the common light chain can in any way be altered to make it more similar to the light chain in antibody 3055. In addition, the light chain of antibody PG3056 was not selected to be part of the antigen binding site that binds the CD3 molecule. The heavy chain variable region was selected for that purpose. This is another reason to see if the common light chain can be made more akin the light chain in the parent antibody PG3055.

To find out where the PG3055 and PG3056 variable regions differed as a result of the different light chain their Fab regions were modelled. A homology model of the Fab region of PG3056 and PG3055 were built using MODELLER (Sali *et al*, 1993: J. Mol. Biol. 234, 779-815). A model structure with optimal energy score was selected from the generated ensemble of structures. Side chain optimization and energy minimization algorithms were used to replace the template side chains where these differed from the target sequence. The homology models of the 3055 and 3056 Fabs were visually inspected using Yasara (http://www.yasara.org).The overlay of the models for PG3055 and PG3056 (Figure 5, right picture) shows that the sequence differences in the light chain only cause a few structural changes; the orientation of some parts of the light chain with respect to the heavy chain is changed to some extent between the two IgGs. The changed parts could inherently be less stable and be the root cause for the observed stability differences. Alternatively, the changed parts could be more or less susceptible to different heterogeneity inducing processes. Various processes, known and unknown, can be the cause of the observed features for the PG3056 antibody. Enzymatic and non-enzymatic modifications include the formation of disulfide bonds, glycosylation, N-terminal glutamine cyclization, C-terminal lysine processing, deamidation, oxidation, glycation, and peptide bond cleavage are among the processes that can cause heterogeneity (Liu et al. Journal of Pharmaceutical Sciences, Vol. 97, 2426–2447 (2008)). Depending on the type of modification, the heterogeneity of monoclonal antibodies can be introduced by intracellular processes, extracellular processes for instance taking place in serum, ascites, and/or cell culture medium. Heterogeneity can also be introduced by incubation with buffers, during the purification process, storage, under different stressed conditions such as elevated temperature or exposure to intense light.

The modelling did not pinpoint to a particular amino acid or region to focus the mutation efforts of the variable region of PG3056 on. The observed differences between the homology models of PG3055 and PG3056 where minor.

In the present invention it was found that there is no need to change the amino acid sequence of the light chain of the PG3056 antibody. Adaptation of the heavy chain can produce an antibody with good binding properties, good stability and good uniformity even when the heavy chain is present in a variable region with the common light chain. As will be exemplified in more detail herein below it was surprisingly found that specific changes in the CDR2 region of the heavy chain are tolerated with respect to binding and provide the antibody with the desired stability and uniformity.

The changes result in a change in an NG deamination motif in the CDR2 region of the heavy chain. The HCDR2 region of both PG3055 and PG3056 contain Asn54 and Gly55 residues. The residues are surface exposed in both antibodies as is shown in Figure 5. The structural position and surface exposure are very similar in both molecules, with a slightly different orientation for the asparagine side chain. Considering that the motif is surface exposed in both antibodies and thus easily accessible to the environment and that there appears to be no significant difference in the folding of the HCDR2 NG motif in PG3055 versus P3056, it would be considered unlikely that enhanced deamidation of Asn54 in PG3056 would be the root cause for the observed binding variation of the different PG3056 batches.

Example 4: Generation and characterization of PG3056 variants

Analytical characterization of PG3056 by CIEX-HPLC showed that the lgG is highly heterogeneous. As this heterogeneity could obstruct CIEX-

HPLC based purification of the CD3xCLEC12A bispecific lgG we aimed to improve the CIEX-HPLC profile of the MF3056 Fab. The heavy chain variable region of MF3056 contains several residues and/or motifs that might contribute to the PG3056 heterogeneity. These are the C-terminal lysine residue, an NG asparagine deamidation motif in the HCDR2 and an acid labile DP motif in the HCDR3 (see Figure 6 for an alignment of the MF3056_VH versus the VH 3-33 germline sequence).

Although the in silico modeling did not pinpoint at all to the HCDR2 NG motif as probable cause for the observed heterogeneity, it was attempted to identify variants of the VH of MF3056 that lack this post-translational modification motif, and which in parallel might display an improved CIEX-HPLC retention profile as well as improved stability. To this end the following variants of the VH of MF3056 were generated and tested: MF3872, MF3873 and MF3905 (Figure 7).

These Fabs containing these VH variants and the common light chain (MF3872, MF3873 and MF3905) were expressed as full length monoclonal IgG (PG3872, PG3873 and PG3905) and tested for binding to membrane-expressed CD3 on HPB-ALL cells by flow cytometry (according to the FACS procedure as previously described in WO2014/051433). The following results were obtained (Figure 8):

These results show that the variants PG3873 and PG3905 completely lost CD3 binding, whereas very low binding to CD3 was retained for variant PG3872.

As an alternative approach to obtain improved variants with reduced heterogeneity and reduced immunogenicity, the VH of MF3056 was germlined towards the VH3-33 sequence at several residues by making

individual or combined amino acid substitutions. The following variants of the MF3056_VH were generated: MF3874_VH, MF3878_VH, MF3883_VH, MF3886_VH and MF3891_VH (Figure 9).

Again, Fabs containing these VH variants and the common light chain (MF3874_VH, MF3878_VH, MF3883_VH, MF3886_VH and MF3891_VH) were expressed as full length monoclonal IgG (PG3874, PG3878, PG3883, PG3886 and PG3891) and tested for CD3 binding as described above. The following results were obtained (Figure 10):

As shown in Figure 10, all individual (PG3874 (Q6E), PG3878(V23A), PG3883 (A50V), PG3886 (T97A)) and combined (PG3891 (Q6E/V23A/T97A)) germlined variants retained full CD3 binding capacity. Subsequently, PG3891 was analyzed by CIEX-HPLC (as described in example 1) to assess whether the germlining had resulted in reduced heterogeneity.

As shown in Figure 11, the CIEX-HPLC profile of PG3891 still displayed significant charge heterogeneity. Similar CIEX-HPLC profiles were obtained for the individual germlining variants (data not shown).

In a next attempt to reduce the charge heterogeneity of PG3056, MF3056_VH variants lacking the HCDR2 NG motif were generated (Figure 12).

Fabs containing these VH variants and the common light chain (MF5192-5197_VH) were generated and expressed as full length monoclonal IgG (PG numbers) and tested for binding to membrane-expressed CD3 on HPB-ALL cells by flow cytometry as described above. This analysis (Figure 13) showed that PG5196 ($N_{54}G_{55}$ into $N_{54}A_{55}$ substitution) retained CD3 binding comparable to PG3056, whereas all other tested MF3056 variants showed

significantly reduced (PG5192, PG5193 or PG5197) or no CD3 binding (PG5194 and PG5195).

To assess the charge heterogeneity of the PG5196 mAb, isoelectric focusing was performed as described in example 1. After staining of the gel, a narrow band at high pI is observed for PG5196 with a minor satellite band at a somewhat higher pI value (see Figure 14).
To assess the charge heterogeneity of PG5196 in further detail, CIEX-HPLC was performed according to the procedure described in example 1, the resulting chromatogram is shown in Figure 15. The chromatogram shows a main peak with a retention time of 19 minutes, preceded by a small peak at 16.9 minutes. Surprisingly, these data demonstrate that PG5196 displays a significantly improved charge heterogeneity profile when compared to PG3056.

Example 5: Generation of additional variants of PG5196 using phage display selections

Based on the MF5196 VH, phage display libraries were designed with the aim to obtain additional CD3 binding Fabs with similarly reduced charge heterogeneity. Phage display libraries were generated which contained the rearranged human IGKV1-39/IGKJ1 VL region (De Kruif et al. Biotechnol Bioeng. 2010 (106)741-50), and a collection of MF5196-based VH regions incorporating amino acid substitutions that potentially could improve the VH/VL interface. The specific substitutions and the allowed alternative amino acids per position are indicated in Table 1. Per mutated position all the indicated substitutions as well as the original amino acid were introduced in an equal ratio.

Table 1

Amino-acid and position in MF5196_VH	**Region**	**Substitutions introduced per position**
H35	FR2	FYASN
A50	FR2	ILFYNRQSK
N54	HCDR2	H
A55	HCDR2	GTN
D59	HCDR2	LIVFYRANEHST
A61	FR3	FNIHQLRYE STDKV
Y102	HCDR3	ARNDCEQGHILKMFPSTWV
N103	HCDR3	ARDCEQGHILKMFPSTWYV
W104	HCDR3	MFYHLIV
F105	HCDR3	WMYHLIV

Bacteriophages from these phage display libraries were selected in one or two rounds using HBP-ALL cells and/or recombinant human CD3δε-Fc protein using procedures known to a person skilled in the art. Binding phages were chemically eluted, and used to re-infect bacteria. After picking a number of surviving bacterial colonies, phages were rescued and were screened for binding to cell surface expressed CD3/TCR complexes by flow cytometry. Colony PCR for was performed for all phages that showed CD3 binding to amplify and sequence the VH regions.

Analysis of the VH genes revealed which substitution variants retained CD3 binding. The selected MF5196_VH variants had the following substitutions: A50 into QSYL, D59 into LIVFRANEHST, A61 into NIHQLRYESTDKV and/or F105 into MY (Table 2). In contrast, the in Table 1 listed substitutions at H35, Y102, N103, and W104 were not allowed as all selected CD3 binding variants retained the original amino acid at positions 35, 102, 103 and 104. This shows that the H35, Y102, N103, and W104 residues are critical amino acids for CD3 binding.

Examples of the CD3 binding variants of MF5196_VH are MF5603_VH, MF5616_VH, MF5626_VH, MF5630_VH, MF5648_VH, MF5661_VH and MF5694_VH, all in combination with the rearranged human IGKVl-39/IGKJl VL region. The VH sequences of these MFs are listed in Figure 25. Testing of these MF variants in monospecific IgG format for binding to membrane-expressed CD3 on HPB-ALL cells, by flow cytometry as described above, showed that all these examples bound to CD3 (Figure 26). As an example of their inherent stability, PG5661 was analyzed by CIEX-HPLC was performed according to the procedure described in example 1, the resulting chromatogram is shown in Figure 27. The chromatogram shows a main peak with a retention time of ~20 minutes, similar to the profile as shown for PG5196.

Table 2

Amino-acid and position in MF5196_VH	**Substitutions introduced in MF5196**	**CD3 binding MF5196 variants found with substitutions**
A50	ILFYNRQSK	QSYL
D59	LIVFYRANEHST	LIVFRANEHST
A61	FNIHQLRYESTDKV	NIHQLRYESTDKV
F105	WMYHLIV	MY

Example 5B

Based on the MF5196 VH, phage display libraries were designed with the aim to obtain additional stable CD3 binding Fabs. Phage display libraries were generated which contained the rearranged human IGKVl-39/IGKJl VL region (De Kruif et al. Biotechnol Bioeng. 2010 (106)741-50),

and a collection of VH3-33 variants to which the heavy chain CDR3 region of MF5196 was fused.

Bacteriophages from these phage display libraries were selected in one or two rounds using HBP-ALL cells and/or recombinant human CD3δε-Fc protein using procedures known to a person skilled in the art. Binding phages were chemically eluted, and used to re-infect bacteria. After picking a number of surviving bacterial colonies, phages were rescued and were screened for binding to cell surface expressed CD3/TCR complexes by flow cytometry. Colony PCR for was performed for all phages that showed CD3 binding to amplify and sequence the VH regions.

Examples of the resulting additional CD3 binding variants of MF5196_VH are MF5351_VH, MF5354_VH and MF5356_VH (listed in Figure 28), all in combination with the rearranged human IGKV1-39/IGKJ1 VL region.

Testing of these MF variants in monospecific IgG format for binding to membrane-expressed CD3 on HPB-ALL cells, by flow cytometry as described above, showed that all these examples bound to CD3 (Figure 29).

Example 6 Functional characterization of the MF5196 Fab in the CD3xCLEC12A bispecific IgG format

To examine the functional activity of the MF5196 Fab, this CD3 Fab and the MF3056 CD3 Fab were expressed together with the CLEC12A Fab MF4327 as the fixed arm. The CD3xCLEC12A bispecific IgGs were expressed in the full length bispecific IgG format as described in WO2014/051433, including the lower hinge / CH2 engineering at positions 235-236 (referred to as DM-Fc, CH2 double mutation in Fc region). Like MF3056 and MF5196, the MF4327 Fab uses the human IGKV1-39/IGKJ1 light chain. The MF4327 Fab sequence is given in patent application WO2014/051433. First, binding of the 5196x4327 DM-Fc bsAb to CD3 and CLEC12A was demonstrated by flow cytometry using CD3+ HPB-ALL cells

and CLEC12A+ HL-60 cells (according to procedures as previously described in WO2014/051433). The 3056x4327 DM-Fc bsAb was included as reference and an irrelevant IgG1 isotype control, PG1337, was included as control (Figure 16). Both CD3xCLEC12A DM-Fc bsAbs bound membrane expressed CD3 and HPB-ALL with slightly improved binding for 5196x4327 DM-Fc bsAb.

Next, the functional activity of 5196x4327 CD3xCLEC12A DM-Fc bsAb was tested. First, the T-cell stimulatory capacity was investigated with healthy donor resting T-cells. Purified resting T cells were obtained according the procedure described in patent WO2014/051433. Purified resting T-cells were subsequently incubated with cells from the leukemia-derived HL-60 cell line in 10% human serum (HS) at an effector: target cell ratio of 5 : 1 for two days as described in WO2014/051433. The 3056x4327 DM-Fc bsAb was included as reference. As negative control benchmark IgGs an isotype control IgG (control IgG) and the 5196x1337 DM-Fc bsAb were included. The 5196x1337 DM-Fc bsAb binds CD3 with one arm (MF5196) and binds tetanus toxoid (TT) with second arm (MF1337) and is included to examine potential off-target induced activity by MF5196. The bsAb and control IgGs were tested at 1,000 ng/mL. T cell activation data are expressed as the percentage of CD69-positive cells within the CD4-positive or CD8-positive T -cell population (Figure 17). The 5196x4327 DM-Fc bsAb induced activation of CD4 and CD8 T cells as reflected by the upregulation of CD69 early activation marker. Also the 3056x4327 DM-Fc bsAb induced upregulation of CD69 on CD4 and CD8 T cells, however to a less extent compared to the 5196x4327 DM-Fc bsAb. The observed upregulation of CD69 on both T cell subsets was CLEC12A antigen specific as the 5196x1337 DM-Fc bsAb did not induce upregulation of CD69.

This analysis showed that the 5196x4327 DM-Fc bsAb had the capacity to induce antigen specific activation of CD4 and CD8 T cells,

slightly better than 3056x4327 DM-Fc bsAb (Figure 17). The 5196x4327 DM-Fc bsAb induced T cell activation was CLEC12A specific as the control 5196x1337 DM-Fc bsAb induced no T cell activation. Taken together, this shows that the HCDR2 N into A amino acid substitution, resulting in CD3 binding MF5196 Fab, fully retained CLEC12A-specific T cell activation.

To investigate whether the extent of T-cell activation by the 5196x4327 versus 3056x4327 CD3xCLEC12A DM-Fc bsAb was sufficient to induce target cell lysis, the HL-60 cells were labeled with carboxyfluorescein diacetate succimidyl ester (CFSE) and co-cultured with T -cells from healthy donor at effector:target cell ratio of 5:1 in presence of 10%HS. The 5196x1337 CD3xTT DM-Fc bsAb was included to examine potential off-target lysis. The bispecific IgGs were tested in a 4-fold dilution range starting at 1,000 ng/ml. After two days, the surviving CFSE-positive HL-60 cells were quantified by flow cytometry. Results were expressed as the percentage of specific lysis related to the PBS control condition (Figure 18).

This analysis showed that the 5196x4327 DM-Fc bsAb had fully retained the capacity to induce CLEC12A antigen specific target cell lysis. Surprisingly, the potency of 5196x4327 DM-Fc was significantly better than 3056x4327 DM-Fc bsAb.

In conclusion, this example showed that MF5196 Fab is functional as the 5196x4327 CD3xCLEC12A DM-Fc bsAb efficiently induced CLEC12A antigen specific T cell activation and lysis of CLEC12A+ HL-60 cells. Moreover this example showed that the 5196x4327 DM-Fc bsAb has an improved potency when compared to the 3056x4327 DM-Fc bsAb.

Example 7

Affinity of the anti-CD3 and anti-CLEC12A arms of 5196x4327 DM-Fc bsAb

The affinities of the MF5196 CD3 and MF4327 CLEC12A Fabs for their targets were measured by surface plasmon resonance (SPR) technology using a BIAcore T100. An anti-human IgG mouse monoclonal antibody (Becton and Dickinson, cat. Nr. 555784) was coupled the surfaces of a CM5 sensor chip using free amine chemistry (NHS/EDC). Then the 5196x4327 DM-Fc bsAb was captured onto this sensor surface. Subsequently the recombinant purified antigens human CLEC12A (Sino Biological Inc, cat. Nr. 11896-H07H) and human CD3δε-Fc protein were run over the sensor surface in a concentration range to measure on- and off-rates. After each cycle, the sensor surface was regenerated by a pulse of HCl and 5196x4327 DM-Fc bsAb was captured again. From the obtained sensorgrams, on- and off-rates were determined using the BIAevaluation software.

These data (Figure 19) showed that 5196x4327 DM-Fc bsAb had an affinity for 3 nM for human CLEC12A and an affinity of 177 nM for CD3. This showed that affinity of the CLEC12A arm was ~60 fold higher than the affinity of the human CD3 binding arm in the 5196x4327 DM-Fc bsAb.

Table 3: on- and off-rates and affinity values for binding to human CD3 and human CLEC12A. The value is the average of three measurements. KD: affinity (equilibrium dissociation) constant.

Antigen	**KD (M)**
CLEC12A	3×10^{-9}
CD3δε-Fc	177×10^{-9}

Example 8 Efficacy of 5196x4327 DM-Fc bsAb to induce AML blast lysis in primary AML patient samples

It was shown in example 6 that the 5196x4327 DM-Fc bsAb potently induces HL-60 target cell lysis by healthy donor derived T cells. In patent WO2014/051433 the inventors showed that a CD3xCLEC12A DM-Fc bsAb had the capacity to induce lysis of AML blast by autologous AML patient derived T cells at effector to target ratio 5:1. Here, the efficacy of a CD3xCLEC12A DM-Fc bsAb, more specific of 5196x4327 CD3xCLEC12A DM-Fc bsAb, to induce lysis of AML blasts in primary AML samples with low effector to target, T cell to AML blast, ratios was examined.

AML patient samples taken at diagnosis (from AML FAB classifications M1, M2, M4, M4/M5, Table 4) were thawed and characterized for the fraction of T cells and AML blasts by flow cytometric analysis for CD4, CD8, CD14, CD33, CD34, CD45 and 7AAD. AML samples analysed had an effector to target ratio ranging from 1:7-1:40.

Subsequently, the primary AML patient bone marrow samples were cultured in IMDM medium supplemented with 10% normal HS plus 20 ng/mL IL-15 (Miltenyi, #130-095-766), 2.5 ng/mL GM-CSF (Immunotools, #11343125), 12.5 ng/mL G-CSF (described in Norde et al., 2009), 6.25 ng/mL IL-3 (Immunotools, #11340035), 3.0 ng/mL SCF (Immunotools, #11343325) and 2.5 ng/mL Flt3L (Immunotools, #311340035). The conditions tested included PBS, isotype control Ab WT-Fc, 5196x4327 DM-Fc bsAb, 5196x1337 DM-Fc bsAb and positive control CD3 WT-Fc Ab (all antibodies at 1,000 ng/mL). After seven days of culture T cell expansion and AML blast killing was determined by flow cytometric analysis using the same markers as used on day 0. Results were expressed as fold T cell expansion or frequency of AML blast lysis relative to PBS condition.

These data demonstrated (Table 4 and Figure 20) that 5196x4327 DM-Fc bsAb efficiently induced T cell expansion (5-30-fold T cell expansion) after 7 days. More importantly, these data showed that the 5196x4327 DM-Fc bsAb efficiently induced lysis (26-88%) of patient's AML tumor cells in 5/5 tested primary AML patient samples, even in AML samples with very low effector to target ratios.

Table 4

Patient#	E:T ratio at day 0	AML FAB classification	% Blast killing (after 7 days)	Fold T cell expansion (after 7 days)
#1	1:21	M4/M5	26%	30
#2	1:10	M4	44%	8
#3	1:7	M2	88%	4
#4	1:39	M4/M5	65%	6
#5	1:40	M1	83%	6

The efficacy of the 5196x4327 DM-Fc bsAb to induce T cell proliferation and AML blast lysis was analyzed in additional AML patient samples taken at diagnosis.

AML patient samples taken at diagnosis (from AML FAB classifications M1, M2, M4, M4/M5, Table 5) were thawed and characterized for the fraction of T cells and AML blasts by flow cytometric analysis for CD4, CD8, CD14, CD33, CD34, CD45 and 7AAD. AML samples analysed had an effector to target ratio ranging from 1:3-1:97. Subsequently, the primary AML patient samples were cultured as described above in example 8. The conditions tested included PBS, isotype control Ab WT-Fc, 5196x4327 DM-Fc bsAb, 5196x1337 DM-Fc bsAb and positive control CD3 WT-Fc Ab (all antibodies at 200 ng/mL). After seven and ten days of culture T cell expansion and AML blast killing was determined by flow cytometric analysis using the same markers as used on day 0. Results were expressed as fold T cell expansion or frequency of AML blast lysis relative to PBS condition.

These data demonstrated (Table 5) that 5196x4327 DM-Fc bsAb efficiently induced T cell expansion (7-226-fold T cell expansion) after 10 days. More importantly, these data showed that the 5196x4327 DM-Fc bsAb efficiently induced lysis (38-99%) of patient's AML tumor cells in 6/8 tested primary AML patient samples, even in AML samples with very low effector to target ratios of 1:45-1:97.

Table 5

Patient #	E:T ratio at day 0	AML FAB classification	AML risk classification	% Blast killing (after 10 days)	Fold T cell expansion (after 10 days)
#6	1:45	M1	Good	95%	20
#7	1:3	M2	Good	99%	39
#8	1:17	M2	Poor	87%	226
#9	1:94	M4	Poor	0%	7
#10	1:46	M4/M5	Poor	38%	23
#11	1:97	M4/M5	Poor	39%	55
#12	1:31	M4/M5	Intermediate	0%	9
#13	1:15	M4/M5	Intermediate	67%	130

Example 9

Differential scanning calorimetry (DSC) was used to measure the thermo stability of the domains of the IgGs described here. DSC experiments were performed on a MicroCal VP-DSC using Origin v7.0 (VPViewer and VPAnalyzer) software. The antibodies were first dialyzed against a 10 mM phosphate, 150 mM NaCl buffer at pH 6.5. IgG samples were analyzed at a protein concentration of 0.25 mg/mL as determined by UV absorption, the dialysis buffer was used as reference sample. Scans ran from 50˚C - 95˚C with a scan rate of 1 ˚C/min and were analyzed using GraphPad Prism 5 and Microsoft Excel 2010 software.

DSC analysis of wildtype (WT) IgG1 resulted in two peaks as shown in Figure 21 (indicated as WT | WT for CH2 | CH3). Tm1 at 70.9 ˚C corresponds to the melting of the CH2 domain, while the peak at 85.0˚C (Tm2) represents the melting of the Fabs and CH3 domain. The DSC graph of an IgG1 with identical Fabs comprising two mutations (L235G,G236R) in the CH2 domain (DM | WT) shows a very similar Tm2 peak at 85.0˚C. The

Tm1 peak however has shifted to 73.5°C, indicating that these mutations increase the stability of the CH2 domain significantly. Since the CH2 domain is not only the most fragile domain of a WT IgG1, but also of a CH3-engineered bispecific IgG1, it can be concluded that the L235G,G236R engineered CH2 domain also confers additional stability to the CD3xCLEC12A bispecific IgG antibodies carrying these CH2 mutations.