HUMANIZED ANTI-HUMAN CD19 ANTIBODIES AND METHODS OF USE

FIELD OF THE INVENTION

The present invention relates to humanized antibodies against human CD19 (anti-human CD19 antibody), methods for their production, pharmaceutical compositions containing these antibodies, and uses thereof.

BACKGROUND

Human CD19 is a 95 kDa transmembrane protein (B-cell co-receptor) exclusively expressed on B-cells and on follicular dendritic cells. CD 19 is found in association with CD21 and CD81. CD19 and CD21 are required for normal B-cell differentiation (Carter, R.H., et al., Immunol. Res. 26 (2002) 45-54). Antibodies against CD19 have been used in several clinical trials (see e. g. Hekman, A., et al., Cancer Immunol. Immunother. 32 (191) 364-372; Vlasfeld, L.T., et al., Cancer Immunol. Immunother. 40 (1995) 37-47; Conry, R.M., et al., J. Immunother. Emphasis Tumor Immunol. 18 (1995) 231-241; Manzke, O., et al., Int. J. Cancer 91 (2001) 516-522).

Antibodies against CD19 are e.g. mentioned in WO 2004/106381, WO 2005/012493, WO 2006/089133, WO 2007/002223, WO 2006/133450, WO 2006/121852, WO 2003/048209, US 7,109,304, US 2006/0233791, US 2006/0280738, US 2006/0263357, US 2006/0257398, EP 1648512, EP 1629012, US 2008/0138336, WO 2008/022152 and in Bruenke, J., et al., Br. J. Hematol. 130 (2005) 218-228; Vallera, D.A., et al., Cancer Biother. Radiopharm. 19 (2004) 11-23; Ghetie, M.A., et al., Blood 104 (2004) 178-183; Lang, P., et al., Blood 103 (2004) 3982-3985; Loeffler, A., et al., Blood 95 (2000) 2098-2103; Le Gall, F., et al., FEBS Lett. 453 (1999) 164-168; Li, Q., et al., Cancer Immunol. Immunother. 47 (1998) 121-130; Eberl, G., et al., Clin. Exp. Immunol. 114 (1998) 173-178; Pietersz, G.A., et al., Cancer Immunol. Immunother. 41 (1995) 53-60; Myers, D.E., et al., Leuk. Lymphoma. 18 (1995) 93-102; Bejcek, B.E., et al., Cancer Res. 55 (1995) 2346-2351; Hagen, I.A., et al, Blood 85 (1995) 3208-3212; Vlasfeld, L.T., et al., Cancer Immunol. Immunother. 40 (1995) 37-47; Rhodes, E.G. et al., Bone Marrow Transplant. 10 (1992) 485-489; Zola, H., et al., Immunol. Cell Biol. 69 (1991) 411-422; Watanabe, M., et al., Cancer Res. 50 (1990) 3245-3248; Uckun, F.M., et al., Blood 71 (1988) 13-29; Pezzutto, A., et al.; J Immunol. 138 (1987)

2793-2799. Monoclonal antibody SJ25-C1 is commercially available (Product No. 4737, Sigma-Aldrich Co. USA, SEQ ID NO: 21 to 24). Antibodies with increased affinity to the FcγRIIIA are mentioned in WO 2008/022152.

Antibody against CD19 can have inhibitory or stimulating effects on B-cell activation. Binding of CD19 antibodies to mitogen-stimulated B-cells inhibits the subsequent rise in Ca2+ and the resulting activation and proliferation of these cells and B-cell proliferation and differentiation can either be inhibited or enhanced by CD19 antibody depending on the mitogenic stimulus used and the degree of crosslinking by the antibody.

In WO 2004/106381 pharmaceutical compositions comprising bispecific anti-CD3, anti-CD19 antibody constructs for the treatment of B-cell related disorders are reported. Anti-CD19 antibodies are reported in WO 2005/012493. In WO 2006/089133 anti-CD19 antibodies and uses in oncology are reported. Anti-CD19 antibodies and their uses are reported in WO 2007/002223. In WO 2006/133450 anti-CD19 antibody therapy for the transplantation is reported.

In WO 2011/147834 antibodies against CD19 and uses thereof are reported.

SUMMARY

Herein are provided antibodies against (human) CD19 which are useful as a therapeutic agent for treatment of an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease or for tumor treatment.

The invention is based, in part, on the finding that for removing multiple deamidation hotspots in a humanized anti-human CD19 antibody a single mutation is sufficient.

The antibodies as reported herein have properties causing a benefit for a patient suffering from a disease associated with pathologic increase of B-cells.

One aspect as reported herein is an antibody that specifically binds to human CD19, wherein the antibody comprises

(a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03,
(b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11,
(c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05,
(d) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20 or 28,

(e) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and
(f) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In one embodiment the antibody is a monoclonal antibody.

In one embodiment the antibody is a human, humanized or chimeric antibody.

In one embodiment the antibody is an antibody fragment that specifically binds to human CD19.

In one embodiment the antibody comprises
(a) a VH sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 09 and a VL sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 19, or
(b) a VH sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 09 and a VL sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 27,or
(c) a VH sequence and a VL sequence as in (a) or (b).

In one embodiment the antibody is a bispecific antibody that specifically binds to human CD19 and a second different antigen.

One aspect as reported herein is a pharmaceutical formulation comprising the antibody as reported herein and a pharmaceutically acceptable carrier.

One aspect as reported herein is the antibody as reported herein for the treatment of B-cell malignancies. In one embodiment the B-cell malignancy is selected from the group consisting of CLL, NHL and DLBCL.

One aspect as reported herein is the antibody as reported herein for use as a medicament.

In one embodiment the medicament is for the treatment of a B-cell cancer, an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease. In one embodiment the medicament is for the depletion of B-cells.

One aspect as reported herein is the antibody as reported herein for use in treating a B-cell cancer, an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease.

One aspect as reported herein is the antibody as reported herein for use in depleting B-cells.

One aspect as reported herein is the use of the antibody as reported herein in the manufacture of a medicament. In one embodiment the medicament is for the treatment of a B-cell cancer, an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease. In one embodiment the medicament is for the depletion of B-cells.

One aspect as reported herein is a method of treating an individual having a B-cell cancer comprising administering to the individual an effective amount of the antibody as reported herein.

One aspect as reported herein is a method of depleting B-cells in an individual comprising administering to the individual an effective amount of the antibody as reported herein.

One aspect as reported herein is a method for the manufacture of a medicament for the treatment of a disease comprising an antibody as reported herein. In one embodiment the disease is a B-cell cancer, an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease.

One aspect as reported herein is an isolated nucleic acid encoding the antibody as reported herein.

One aspect as reported herein is a host cell comprising the nucleic acid as reported herein.

One aspect as reported herein is a method of producing an antibody comprising culturing the host cell comprising the nucleic acid encoding the antibody so that the antibody is produced, recovering the antibody from the cell or the cultivation medium and purifying the antibody.

One aspect as reported herein is an immunoconjugate comprising the antibody as reported herein and a cytotoxic agent.

DETAILED DESCRIPTION OF EMBODIMENTS OF THE INVENTION

I. DEFINITIONS

An "acceptor human framework" for the purposes herein is a framework comprising the amino acid sequence of a light chain variable domain (VL) framework or a heavy chain variable domain (VH) framework derived from a human immunoglobulin framework or a human consensus framework, as defined below. An acceptor human framework "derived from" a human immunoglobulin framework or a human consensus framework may comprise the same amino acid sequence thereof, or it may contain amino acid sequence changes. In some embodiments, the number of amino acid changes are 10 or less, 9 or less, 8 or less, 7 or less, 6 or less, 5 or less, 4 or less, 3 or less, or 2 or less. In some embodiments, the VL acceptor human framework is identical in sequence to the VL human immunoglobulin framework sequence or human consensus framework sequence.

"Affinity" refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (k_d). Affinity can be measured by common methods known in the art, including those described herein.

An "affinity matured" antibody refers to an antibody with one or more alterations in one or more hypervariable regions (HVRs), compared to a parent antibody which does not possess such alterations, such alterations resulting in an improvement in the affinity of the antibody for antigen.

The terms "anti-human CD19 antibody" and "an antibody that specifically binds to human CD19" refer to an antibody that is capable of binding human CD19 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting human CD19. In one embodiment, the extent of binding of an anti-human CD19 antibody to an unrelated, non-CD19 protein is less than about 10 % of the binding of the antibody to human CD19 as measured, by Surface Plasmon Resonance. In certain embodiments, an antibody that specifically binds to human CD19 has a dissociation constant (K_D) of 10^{-8} M or less.

The term "antibody" herein is used in the broadest sense and encompasses various antibody structures, including but not limited to monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments so long as they exhibit the desired antigen-binding activity.

The term "antibody-dependent cellular cytotoxicity (ADCC)" is a function mediated by Fc receptor binding and refers to lysis of target cells by an antibody as reported herein in the presence of effector cells. ADCC is measured in one embodiment by the treatment of a preparation of CD19 expressing erythroid cells (e.g. K562 cells expressing recombinant human CD19) with an antibody as reported herein in the presence of effector cells such as freshly isolated PBMC (peripheral blood mononuclear cells) or purified effector cells from buffy coats, like monocytes or NK (natural killer) cells. Target cells are labeled with ^{51}Cr and subsequently incubated with the antibody. The labeled cells are incubated with effector cells and the supernatant is analyzed for released ^{51}Cr. Controls include the incubation of the target endothelial cells with effector cells but without the antibody. The capacity of the antibody to induce the initial steps mediating ADCC is investigated by measuring their binding to Fcγ receptors expressing cells, such as cells, recombinantly expressing FcγRI and/or FcγRIIA or NK cells (expressing essentially FcγRIIIA). In one preferred embodiment binding to FcγR on NK cells is measured.

An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds. Examples of antibody fragments include but are not limited to Fv, Fab, Fab', Fab'-SH, $F(ab')_2$; diabodies; linear antibodies; single-chain antibody molecules (e.g. scFv); and multispecific antibodies formed from antibody fragments.

The term "chimeric" antibody refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

The “class” of an antibody refers to the type of constant domain or constant region possessed by its heavy chain. There are five major classes of antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG_1, IgG_2, IgG_3, IgG_4, IgA_1, and IgA_2. The heavy chain constant

domains that correspond to the different classes of immunoglobulins are called α, δ, ε, γ, and μ, respectively.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents a cellular function and/or causes cell death or destruction. Cytotoxic agents include, but are not limited to, radioactive isotopes (e.g., At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32}, Pb^{212} and radioactive isotopes of Lu); chemotherapeutic agents or drugs (e.g., methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents); growth inhibitory agents; enzymes and fragments thereof such as nucleolytic enzymes; antibiotics; toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof; and the various antitumor or anticancer agents disclosed below.

The term "complement-dependent cytotoxicity (CDC)" refers to lysis of cells induced by the antibody as reported herein in the presence of complement. CDC is measured in one embodiment by the treatment of CD19 expressing human endothelial cells with an antibody as reported herein in the presence of complement. The cells are in one embodiment labeled with calcein. CDC is found if the antibody induces lysis of 20 % or more of the target cells at a concentration of 30 μg/ml. Binding to the complement factor C1q can be measured in an ELISA. In such an assay in principle an ELISA plate is coated with concentration ranges of the antibody, to which purified human C1q or human serum is added. C1q binding is detected by an antibody directed against C1q followed by a peroxidase-labeled conjugate. Detection of binding (maximal binding B_{max}) is measured as optical density at 405 nm (OD405) for peroxidase substrate ABTS® (2,2'-azino-di-[3-ethylbenzthiazoline-6-sulfonate (6)]).

“Effector functions” refer to those biological activities attributable to the Fc region of an antibody, which vary with the antibody class. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g. B cell receptor); and B cell activation.

Fc receptor binding dependent effector functions can be mediated by the interaction of the Fc-region of an antibody with Fc receptors (FcRs), which are specialized cell

surface receptors on hematopoietic cells. Fc receptors belong to the immunoglobulin superfamily, and have been shown to mediate both the removal of antibody-coated pathogens by phagocytosis of immune complexes, and the lysis of erythrocytes and various other cellular targets (e.g. tumor cells) coated with the corresponding antibody, via antibody dependent cell mediated cytotoxicity (ADCC) (see e.g. Van de Winkel, J.G. and Anderson, C.L., J. Leukoc. Biol. 49 (1991) 511-524). FcRs are defined by their specificity for immunoglobulin isotypes: Fc receptors for IgG antibodies are referred to as FcγR. Fc receptor binding is described e.g. in Ravetch, J.V. and Kinet, J.P., Annu. Rev. Immunol. 9 (1991) 457-492; Capel, P.J., et al., Immunomethods 4 (1994) 25-34; de Haas, M., et al., J. Lab. Clin. Med. 126 (1995) 330-341; and Gessner, J.E., et al., Ann. Hematol. 76 (1998) 231-248.

Cross-linking of receptors for the Fc-region of IgG antibodies (FcγR) triggers a wide variety of effector functions including phagocytosis, antibody-dependent cellular cytotoxicity, and release of inflammatory mediators, as well as immune complex clearance and regulation of antibody production. In humans, three classes of FcγR have been characterized, which are:

- FcγRI (CD64) binds monomeric IgG with high affinity and is expressed on macrophages, monocytes, neutrophils and eosinophils. Modification in the Fc-region IgG at least at one of the amino acid residues E233-G236, P238, D265, N297, A327 and P329 (numbering according to EU index of Kabat) reduce binding to FcγRI. IgG2 residues at positions 233–236, substituted into IgG1 and IgG4, reduced binding to FcγRI by 10^3-fold and eliminated the human monocyte response to antibody-sensitized red blood cells (Armour, K.L., et al., Eur. J. Immunol. 29 (1999) 2613–2624).

- FcγRII (CD32) binds complexed IgG with medium to low affinity and is widely expressed. This receptor can be divided into two sub-types, FcγRIIA and FcγRIIB. FcγRIIA is found on many cells involved in killing (e.g. macrophages, monocytes, neutrophils) and seems able to activate the killing process. FcγRIIB seems to play a role in inhibitory processes and is found on B-cells, macrophages and on mast cells and eosinophils. On B-cells it seems to function to suppress further immunoglobulin production and isotype switching to, for example, the IgE class. On macrophages, FcγRIIB acts to inhibit phagocytosis as mediated through FcγRIIA. On eosinophils and mast cells the B-form may help to suppress activation of these cells through IgE binding to its

separate receptor. Reduced binding for FcγRIIA is found e.g. for antibodies comprising an IgG Fc-region with mutations at least at one of the amino acid residues E233-G236, P238, D265, N297, A327, P329, D270, Q295, A327, R292, and K414 (numbering according to EU index of Kabat).

- FcγRIII (CD16) binds IgG with medium to low affinity and exists as two types. FcγRIIIA is found on NK cells, macrophages, eosinophils and some monocytes and T cells and mediates ADCC. FcγRIIIB is highly expressed on neutrophils. Reduced binding to FcγRIIIA is found e.g. for antibodies comprising an IgG Fc-region with mutation at least at one of the amino acid residues E233-G236, P238, D265, N297, A327, P329, D270, Q295, A327, S239, E269, E293, Y296, V303, A327, K338 and D376 (numbering according to EU index of Kabat).

Mapping of the binding sites on human IgG1 for Fc receptors, the above mentioned mutation sites and methods for measuring binding to FcγRI and FcγRIIA are described in Shields, R.L., et al. J. Biol. Chem. 276 (2001) 6591-6604.

An "effective amount" of an agent, e.g., a pharmaceutical formulation, refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

The term “Fc receptor” as used herein refers to activation receptors characterized by the presence of a cytoplasmatic ITAM sequence associated with the receptor (see e.g. Ravetch, J.V. and Bolland, S., Annu. Rev. Immunol. 19 (2001) 275-290). Such receptors are FcγRI, FcγRIIA and FcγRIIIA. The term “no binding of FcγR” denotes that at an antibody concentration of 10 µg/ml the binding of an antibody as reported herein to NK cells is 10 % or less of the binding found for anti-OX40L antibody LC.001 as reported in WO 2006/029879.

While IgG4 shows reduced FcR binding, antibodies of other IgG subclasses show strong binding. However Pro238, Asp265, Asp270, Asn297 (loss of Fc carbohydrate), Pro329 and 234, 235, 236 and 237 Ile253, Ser254, Lys288 , Thr307, Gln311, Asn434, and His435 are residues which provide if altered also reduce FcR binding (Shields, R.L., et al. J. Biol. Chem. 276 (2001) 6591-6604; Lund, J., et al., FASEB J. 9 (1995) 115-119; Morgan, A., et al., Immunology 86 (1995) 319-324; and EP 0 307 434). In one embodiment the antibody as reported herein is of IgG1 or IgG2 subclass and comprises the mutation PVA236, GLPSS331, and/or L234A/L235A. In one embodiment the antibody as reported herein is of IgG4

subclass and comprises the mutation L235E. In one embodiment the antibody further comprises the mutation S228P.

The term "Fc region" herein is used to define a C-terminal region of an immunoglobulin heavy chain that contains at least a portion of the constant region. The term includes native sequence Fc regions and variant Fc regions. In one embodiment, a human IgG heavy chain Fc region extends from Cys226, or from Pro230, to the carboxyl-terminus of the heavy chain. However, the C-terminal lysine (Lys447) of the Fc region may or may not be present. Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat, E.A. et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991), NIH Publication 91-3242.

The antibodies as reported herein comprise as Fc-region, in one embodiment an Fc-region derived from human origin. In one embodiment the Fc-region comprises all parts of the human constant region. The Fc-region of an antibody is directly involved in complement activation, C1q binding, C3 activation and Fc receptor binding. While the influence of an antibody on the complement system is dependent on certain conditions, binding to C1q is caused by defined binding sites in the Fc-region. Such binding sites are known in the state of the art and described e.g. by Lukas, T.J., et al., J. Immunol. 127 (1981) 2555-2560; Brunhouse, R., and Cebra, J. J., Mol. Immunol. 16 (1979) 907-917; Burton, D.R., et al., Nature 288 (1980) 338-344; Thommesen, J.E., et al., Mol. Immunol. 37 (2000) 995-1004; Idusogie, E.E., et al., J. Immunol. 164 (2000) 4178-4184; Hezareh, M., et al., J. Virol. 75 (2001) 12161-12168; Morgan, A., et al., Immunology 86 (1995) 319-324; and EP 0 307 434. Such binding sites are e.g. L234, L235, D270, N297, E318, K320, K322, P331 and P329 (numbering according to EU index of Kabat; Unless otherwise specified herein, numbering of amino acid residues in the Fc-region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat, E.A. et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991), NIH Publication 91-3242). Antibodies of subclass IgG1, IgG2 and IgG3 usually show complement activation, C1q binding and C3 activation, whereas IgG4 do not activate the complement system, do not bind C1q and do not activate C3. An "Fc-region of an antibody" is a term well known to the skilled artisan and defined on

the basis of papain cleavage of antibodies. In one embodiment the Fc-region is a human Fc-region. In one embodiment the Fc-region is of the human IgG4 subclass comprising the mutations S228P and/or L235E (numbering according to EU index of Kabat). In one embodiment the Fc-region is of the human IgG1 subclass comprising the mutations L234A and L235A (numbering according to EU index of Kabat).

"Framework" or "FR" refers to variable domain residues other than hypervariable region (HVR) residues. The FR of a variable domain generally consists of four FR domains: FR1, FR2, FR3, and FR4. Accordingly, the HVR and FR sequences generally appear in the following sequence in VH (or VL): FR1-H1(L1)-FR2-H2(L2)-FR3-H3(L3)-FR4.

The terms “full length antibody”, “intact antibody,” and “whole antibody” are used herein interchangeably to refer to an antibody having a structure substantially similar to a native antibody structure or having heavy chains that contain an Fc region as defined herein.

The terms "host cell", "host cell line", and "host cell culture" are used interchangeably and refer to cells into which exogenous nucleic acid has been introduced, including the progeny of such cells. Host cells include "transformants" and "transformed cells," which include the primary transformed cell and progeny derived therefrom without regard to the number of passages. Progeny may not be completely identical in nucleic acid content to a parent cell, but may contain mutations. Mutant progeny that have the same function or biological activity as screened or selected for in the originally transformed cell are included herein.

A “human consensus framework” is a framework which represents the most commonly occurring amino acid residues in a selection of human immunoglobulin VL or VH framework sequences. Generally, the selection of human immunoglobulin VL or VH sequences is from a subgroup of variable domain sequences. Generally, the subgroup of sequences is a subgroup as in Kabat, E.A. et al., Sequences of Proteins of Immunological Interest, 5th ed., Bethesda MD (1991), NIH Publication 91-3242, Vols. 1-3. In one embodiment, for the VL, the subgroup is subgroup kappa I as in Kabat et al., *supra.* In one embodiment, for the VH, the subgroup is subgroup III as in Kabat et al., *supra*.

A "humanized" antibody refers to a chimeric antibody comprising amino acid residues from non-human HVRs and amino acid residues from human FRs. In certain embodiments, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the HVRs (e.g., CDRs) correspond to those of a non-human antibody, and all or substantially all of the FRs correspond to those of a human antibody. A humanized antibody optionally may comprise at least a portion of an antibody constant region derived from a human antibody. A "humanized form" of an antibody, e.g., a non-human antibody, refers to an antibody that has undergone humanization.

The term "hypervariable region" or "HVR", as used herein, refers to each of the regions of an antibody variable domain comprising the amino acid residue stretches which are hypervariable in sequence ("complementarity determining regions" or "CDRs") and/or form structurally defined loops ("hypervariable loops"), and/or contain the antigen-contacting residues ("antigen contacts"). Generally, antibodies comprise six HVRs; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3).

HVRs include

(a) hypervariable loops occurring at amino acid residues 26-32 (L1), 50-52 (L2), 91-96 (L3), 26-32 (H1), 53-55 (H2), and 96-101 (H3) (Chothia, C. and Lesk, A.M., J. Mol. Biol. 196 (1987) 901-917);

(b) CDRs occurring at amino acid residues 24-34 (L1), 50-56 (L2), 89-97 (L3), 31-35b (H1), 50-65 (H2), and 95-102 (H3) (Kabat, E.A. et al., Sequences of Proteins of Immunological Interest, 5th ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991), NIH Publication 91-3242.);

(c) antigen contacts occurring at amino acid residues 27c-36 (L1), 46-55 (L2), 89-96 (L3), 30-35b (H1), 47-58 (H2), and 93-101 (H3) (MacCallum et al. J. Mol. Biol. 262: 732-745 (1996)); and

(d) combinations of (a), (b), and/or (c), including amino acid residues 46-56 (L2), 47-56 (L2), 48-56 (L2), 49-56 (L2), 26-35 (H1), 26-35b (H1), 49-65 (H2), 93-102 (H3), and 94-102 (H3).

Unless otherwise indicated, HVR residues and other residues in the variable domain (e.g., FR residues) are numbered herein according to Kabat et al., *supra*.

An “immunoconjugate” is an antibody conjugated to one or more heterologous molecule(s), including but not limited to a cytotoxic agent.

An “individual” or “subject” is a mammal. Mammals include, but are not limited to, domesticated animals (e.g. cows, sheep, cats, dogs, and horses), primates (e.g., humans and non-human primates such as monkeys), rabbits, and rodents (e.g., mice and rats). In certain embodiments, the individual or subject is a human.

An "isolated" antibody is one which has been separated from a component of its natural environment. In some embodiments, an antibody is purified to greater than 95% or 99% purity as determined by, for example, electrophoretic (e.g., SDS-PAGE, isoelectric focusing (IEF), capillary electrophoresis) or chromatographic (e.g., ion exchange or reverse phase HPLC). For review of methods for assessment of antibody purity, see, e.g., Flatman, S. et al., J. Chromatogr. B 848 (2007) 79-87.

An "isolated" nucleic acid refers to a nucleic acid molecule that has been separated from a component of its natural environment. An isolated nucleic acid includes a nucleic acid molecule contained in cells that ordinarily contain the nucleic acid molecule, but the nucleic acid molecule is present extrachromosomally or at a chromosomal location that is different from its natural chromosomal location.

“Isolated nucleic acid encoding an anti-human CD19 antibody” refers to one or more nucleic acid molecules encoding antibody heavy and light chains (or fragments thereof), including such nucleic acid molecule(s) in a single vector or separate vectors, and such nucleic acid molecule(s) present at one or more locations in a host cell.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical and/or bind the same epitope, except for possible variant antibodies, e.g., containing naturally occurring mutations or arising during production of a monoclonal antibody preparation, such variants generally being present in minor amounts. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. Thus, the modifier “monoclonal” indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be

construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by a variety of techniques, including but not limited to the hybridoma method, recombinant DNA methods, phage-display methods, and methods utilizing transgenic animals containing all or part of the human immunoglobulin loci, such methods and other exemplary methods for making monoclonal antibodies being described herein.

A “naked antibody” refers to an antibody that is not conjugated to a heterologous moiety (e.g., a cytotoxic moiety) or radiolabel. The naked antibody may be present in a pharmaceutical formulation.

"Native antibodies" refer to naturally occurring immunoglobulin molecules with varying structures. For example, native IgG antibodies are heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light chains and two identical heavy chains that are disulfide-bonded. From N- to C-terminus, each heavy chain has a variable region (VH), also called a variable heavy domain or a heavy chain variable domain, followed by three constant domains (CH1, CH2, and CH3), whereby between the first and the second constant domain a hinge region is located. Similarly, from N- to C-terminus, each light chain has a variable region (VL), also called a variable light domain or a light chain variable domain, followed by a constant light (CL) domain. The light chain of an antibody may be assigned to one of two types, called kappa (κ) and lambda (λ), based on the amino acid sequence of its constant domain.

The term “package insert” is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, combination therapy, contraindications and/or warnings concerning the use of such therapeutic products.

“Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly

available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc., and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available from Genentech, Inc., South San Francisco, California, or may be compiled from the source code. The ALIGN-2 program should be compiled for use on a UNIX operating system, including digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

The term "pharmaceutical formulation" refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered.

A "pharmaceutically acceptable carrier" refers to an ingredient in a pharmaceutical formulation, other than an active ingredient, which is nontoxic to a subject., A pharmaceutically acceptable carrier includes, but is not limited to, a buffer, excipient, stabilizer, or preservative.

The term "CD19", as used herein, refers to human B-lymphocyte antigen CD19 (alternative name(s) are: Differentiation antigen CD19, B-lymphocyte surface antigen B4, T-cell surface antigen Leu-12; UniProtKB P15391-1 (isoform 1; SEQ ID NO: 33) and P15391-2 (isoform 2; SEQ ID NO: 34)). The term encompasses "full-length" unprocessed human CD19 as well as any form of human CD19 that results from processing in the cell as long as the antibody as reported herein binds thereto.

As used herein, "treatment" (and grammatical variations thereof such as "treat" or "treating") refers to clinical intervention in an attempt to alter the natural course of the individual being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include, but are not limited to, preventing occurrence or recurrence of a disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies as reported herein are used to delay development of a disease or to slow the progression of a disease.

The term "variable region" or "variable domain" refers to the domain of an antibody heavy or light chain that is involved in binding the antibody to antigen. The variable domains of the heavy chain and light chain (VH and VL, respectively) of a native antibody generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three hypervariable regions (HVRs). (see, e.g., Kindt, T.J., et al. Kuby Immunology, 6th ed., W.H. Freeman and Co., N.Y. (2007), page 91) A single VH or VL domain may be sufficient to confer antigen-binding specificity. Furthermore, antibodies that bind a particular antigen may be isolated using a VH or VL domain from an antibody that binds the antigen to screen a library of complementary VL or VH domains, respectively. See, e.g., Portolano, S. et al., J. Immunol. 150 (1993) 880-887; Clackson, T. et al., Nature 352 (1991) 624-628).

The term "vector", as used herein, refers to a nucleic acid molecule capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Certain vectors are capable of directing the expression of nucleic acids to which they are operatively linked. Such vectors are referred to herein as "expression vectors".

II. COMPOSITIONS AND METHODS

In one aspect, the invention is based, in part, on the finding that for removing multiple deamidation hotspots in a humanized anti-human CD19 antibody a single mutation is sufficient. In certain embodiments, antibodies that bind to human CD19 are provided. Antibodies as reported herein are useful, e.g., for diagnosis or treatment.

A. Exemplary Anti-human CD19 Antibodies

It has been found that the wild-type humanized anti-human CD19 antibody has three deamidation hotspots in the HVR-L1: **N**S**N**G**N**T (SEQ ID NO: 36). Additionally it has been found that in the HVR-H2 a further deamidation hotspot is present: KF**N**G (SEQ ID NO: 37).

In one aspect, herein is provided an isolated humanized antibody that specifically bind to human CD19 and that has improved stability, especially deamidation stability in the heavy and light chain HVRs HVR-H2 and HVR-L1, compared to other humanized variants. In this improved humanized anti-human CD19 antibody the human/cynomolgus cross-reactivity of the parental murine antibody is retained.

To address the deamidation hotspot in the HVR-H2 an N (Asn) to Q (Gln) point mutation at position 64 (numbering according to Kabat) has been introduced. Thus, the antibody as reported herein has a HVR-H2 comprising the amino acid sequence TEKFQG (SEQ ID NO: 38). In one preferred embodiment the humanized anti-human CD19 antibody comprises a HVR-H2 that has the amino acid sequence YINPYNDGSK YTEKFQG (SEQ ID NO: 11).

To address the deamidation hotspots in the light chain and to obtain a humanized anti-human CD19 antibody with improved deamidation stability individual mutations at Kabat position 27d, 27e, 28 and 29 and a double mutation at positions 27e and 28 (numbering according to Kabat) were introduced. In total 9 variants

(var.1 to var.9; SEQ ID NO: 60 to 68 and 70) of the wild-type humanized antibody (var.0; SEQ ID NO: 59 and 69) have been generated.

	Kabat position	2222 7789	Kabat position	6 4
	LC:	de	HC:	
	var.0:wt	QSLENSNGNTYL		TEKFNGKATL
	var.1:N27dH	QSLE**H**SNGNTYL		TEKF**Q**GRVTM
	var.2:N27dQ	QSLE**Q**SNGNTYL		TEKF**Q**GRVTM
	var.3:S27eA	QSLEN**A**NGNTYL		TEKF**Q**GRVTM
	var.4:S27eV	QSLEN**V**NGNTYL		TEKF**Q**GRVTM
	var.5:S27eP	QSLEN**P**NGNTYL		TEKF**Q**GRVTM
	var.6:N28Q	QSLENS**Q**GNTYL		TEKF**Q**GRVTM
	var.7:G29A	QSLENSN**A**NTYL		TEKF**Q**GRVTM
	var.8:G29V	QSLENSN**V**NTYL		TEKF**Q**GRVTM
	var.9:S27eP/N28S	QSLEN**PS**GNTYL		TEKF**Q**GRVTM

variant → **↓parameter**	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
K_D (BIAcore) [nM]	5	250	136	2	1	6	54	4	16	45
$t_{1/2}$ [min]	-	0.1	1.1	105.2	191.5	43.6	4.4	51.5	17.6	4
human CD19 binding after pH 7.4 incubation [%]	46	0	75	84	85	95	91	72	83	83
human CD19 binding after pH 6.0 incubation [%]	90	0	95	95	97	99	97	86	91	87
SEC main peak after incubation [%]	> 95	> 95	> 95	> 95	> 95	> 95	> 95	> 95	> 95	-

It has been found that with a single mutation at position 27e according to Kabat from S (serine) to P (proline) all deamidation hotspots in the HVR-L1 can be

addressed. This is a mutation not of the deamidation prone N (asparagine) residue but of a neighboring residue.

Thus, the antibody as reported herein has a HVR-L1 comprising the amino acid sequence LENPNGNT (SEQ ID NO: 39). In one embodiment the humanized anti-human CD19 antibody comprises a HVR-L1 that has the amino acid sequence LENPSGNT (SEQ ID NO: 40). In one preferred embodiment the humanized anti-human CD19 antibody comprises a HVR-L1 that has the amino acid sequence RSSQSLENPN GNTYLN (SEQ ID NO: 20). In one preferred embodiment the humanized anti-human CD19 antibody comprises a HVR-L1 that has the amino acid sequence RSSQSLENPS GNTYLN (SEQ ID NO: 28).

Additionally these antibodies maintain the cross-reactivity to cynomolgus CD19 as shown in the following Table.

EC50 [µg/ml]	**var.0**	**var.5**	**var.9**
huCD19 ECD	0.087	0.084	0.089
cyCD19 ECD	0.313	0.255	0.435

Thus, in one embodiment the anti-human CD19 antibody specifically binds to human CD19 and cynomolgus CD 19.

The wild-type humanized anti-human CD19 antibody (var.0) shows after purification approx. 7.5 % deamidation. After storage for two weeks at pH 7.4 the amount of deamidated antibody is increased to approx. 18.5 %. The variant antibody with an S27eP mutation (var.5) shows approx. 2% deamidation and 2% succinimide formation after purification. During storage at pH 7.4 for two weeks only approx. 7.5 % deamidated antibody is present.

In one aspect, herein is provided an isolated humanized antibody that specifically binds to human CD19 and cynomolgus CD19 comprising a HVR-H2 of SEQ ID NO: 11 and HVR-L1 of SEQ ID NO: 20 or 28.

In one aspect, herein is provided an anti-human CD19 antibody comprising at least one, two, three, four, five, or six HVRs selected from (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05, (d) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20, (e) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (f) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In one aspect, herein is provided an anti-human CD19 antibody comprising at least one, two, three, four, five, or six HVRs selected from (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05, (d) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 28, (e) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (f) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In one aspect, herein is provided an anti-human CD19 antibody comprising at least one, at least two, or all three VH HVR sequences selected from (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, and (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05. In one embodiment, the antibody comprises HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05. In another embodiment, the antibody comprises HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05 and HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08. In a further embodiment, the antibody comprises HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05, HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08, and HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11. In a further embodiment, the antibody comprises (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, and (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05.

In another aspect, herein is provided an antibody comprising at least one, at least two, or all three VL HVR sequences selected from (a) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20, (b) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08. In one embodiment, the antibody comprises (a) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20, (b) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In another aspect, herein is provided an antibody comprising at least one, at least two, or all three VL HVR sequences selected from (a) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 28, (b) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08. In one embodiment, the antibody comprises (a) HVR-L1

comprising the amino acid sequence of SEQ ID NO: 28, (b) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In another aspect, an antibody as reported herein comprises (a) a VH domain comprising at least one, at least two, or all three VH HVR sequences selected from (i) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (ii) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11 and (iii) HVR-H3 comprising an amino acid sequence selected from SEQ ID NO: 05, and (b) a VL domain comprising at least one, at least two, or all three VL HVR sequences selected from (i) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20, (ii) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In another aspect, an antibody as reported herein comprises (a) a VH domain comprising at least one, at least two, or all three VH HVR sequences selected from (i) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (ii) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11 and (iii) HVR-H3 comprising an amino acid sequence selected from SEQ ID NO: 05, and (b) a VL domain comprising at least one, at least two, or all three VL HVR sequences selected from (i) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 28, (ii) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In another aspect, herein is provided an antibody comprising (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05, (d) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20, (e) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (f) HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:08.

In another aspect, herein is provided an antibody comprising (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05, (d) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 28, (e) HVR-L2 comprising the amino acid sequence of

SEQ ID NO: 07, and (f) HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:08.

The anti-human CD19 antibody as reported herein is a humanized antibody. In one embodiment, the humanized anti-human CD19 antibody comprises HVRs as in any of the above embodiments, and further comprises an acceptor human framework, e.g. a human immunoglobulin (germline) framework or a human consensus framework.

In another aspect, an anti-human CD19 antibody comprises a heavy chain variable domain (VH) sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID NO: 09. In certain embodiments, a VH sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity contains substitutions (e.g., conservative substitutions), insertions, or deletions relative to the reference sequence, but an anti- human CD19 antibody comprising that sequence retains the ability to bind to human CD19. In certain embodiments, a total of 1 to 10 amino acids have been substituted, inserted and/or deleted in SEQ ID NO: 09. In certain embodiments, substitutions, insertions, or deletions occur in regions outside the HVRs (i.e., in the FRs). Optionally, the anti- human CD19 antibody comprises the VH sequence in SEQ ID NO: 09, including post-translational modifications of that sequence. In a particular embodiment, the VH comprises one, two or three HVRs selected from: (a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03, (b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11, and (c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05.

In another aspect, an anti- human CD19 antibody is provided, wherein the antibody comprises a light chain variable domain (VL) having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of SEQ ID NO: 19 or SEQ ID NO: 27 (SEQ ID NO: 19 and SEQ ID NO: 27 differ at a single amino acid position). In certain embodiments, a VL sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity contains substitutions (e.g., conservative substitutions), insertions, or deletions relative to the reference sequence, but an anti-human CD19 antibody comprising that sequence retains the ability to bind to human CD19. In certain embodiments, a total of 1 to 10 amino acids have been substituted, inserted and/or deleted in SEQ ID NO: 19 or SEQ ID NO: 27. In certain embodiments, the substitutions, insertions, or deletions occur in regions outside the HVRs (i.e., in the

FRs). Optionally, the anti-human CD19 antibody comprises the VL sequence in SEQ ID NO: 19, including post-translational modifications of that sequence. Optionally, the anti-human CD19 antibody comprises the VL sequence in SEQ ID NO: 27, including post-translational modifications of that sequence. In a particular embodiment, the VL comprises one, two or three HVRs selected from (a) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20, (b) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08. In a particular embodiment, the VL comprises one, two or three HVRs selected from (a) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 28, (b) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and (c) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

In another aspect, an anti-human CD19 antibody is provided, wherein the antibody comprises a VH as in any of the embodiments provided above, and a VL as in any of the embodiments provided above. In one embodiment, the antibody comprises the VH and VL sequences in SEQ ID NO: 09 and SEQ ID NO: 19 or 27, respectively, including post-translational modifications of those sequences.

In a further aspect, herein is provided an antibody that binds to the same epitope as an anti-human CD19 antibody as reported herein. For example, in certain embodiments, an antibody is provided that binds to the same epitope as an anti-human CD19 antibody comprising a VH sequence of SEQ ID NO: 09 and a VL sequence of SEQ ID NO: 19.

In one embodiment, an anti-human CD19 antibody according to any of the above embodiments is a monoclonal antibody. In one embodiment, an anti-human CD19 antibody is an antibody fragment, e.g., an Fv, Fab, Fab', scFv, diabody, or $F(ab')_2$ fragment. In another embodiment, the antibody is a full length antibody, e.g., an intact IgG1 or IgG 4 antibody or other antibody class or isotype as defined herein.

In one embodiment of all aspects the antibody comprises (all positions according to EU index of Kabat)

i) a homodimeric Fc-region of the human IgG1 subclass optionally with the mutations P329G, L234A and L235A, or

ii) a homodimeric Fc-region of the human IgG4 subclass optionally with the mutations P329G, S228P and L235E, or

iii) a homodimeric Fc-region of the human IgG1 subclass with the mutations (P329G, L234A, L235A) I253A, H310A, and H435A, or with the mutations (P329G, L234A, L235A) H310A, H433A, and Y436A, or

iv) a heterodimeric Fc-region whereof

a) one Fc-region polypeptide comprises the mutation T366W, and the other Fc-region polypeptide comprises the mutations T366S, L368A and Y407V, or

b) one Fc-region polypeptide comprises the mutations T366W and Y349C, and the other Fc-region polypeptide comprises the mutations T366S, L368A, Y407V, and S354C, or

c) one Fc-region polypeptide comprises the mutations T366W and S354C, and the other Fc-region polypeptide comprises the mutations T366S, L368A, Y407V and Y349C,

or

v) a heterodimeric Fc-region of the human IgG1 subclass whereof both Fc-region polypeptides comprise the mutations P329G, L234A and L235A and

a) one Fc-region polypeptide comprises the mutation T366W, and the other Fc-region polypeptide comprises the mutations T366S, L368A and Y407V, or

b) one Fc-region polypeptide comprises the mutations T366W and Y349C, and the other Fc-region polypeptide comprises the mutations T366S, L368A, Y407V, and S354C, or

c) one Fc-region polypeptide comprises the mutations T366W and S354C, and the other Fc-region polypeptide comprises the mutations T366S, L368A, Y407V and Y349C,

or

vi) a heterodimeric Fc-region of the human IgG4 subclass whereof both Fc-region polypeptides comprise the mutations P329G, S228P and L235E and

a) one Fc-region polypeptide comprises the mutation T366W, and the other Fc-region polypeptide comprises the mutations T366S, L368A and Y407V, or

b) one Fc-region polypeptide comprises the mutations T366W and Y349C, and the other Fc-region polypeptide comprises the mutations T366S, L368A, Y407V, and S354C, or

c) one Fc-region polypeptide comprises the mutations T366W and S354C, and the other Fc-region polypeptide comprises the mutations T366S, L368A, Y407V and Y349C,

or

vii) a combination of one of iii) with one of vi), v) and vi).

One aspect as reported herein is a bivalent, bispecific antibody comprising

a) a first light chain and a first heavy chain of an antibody specifically binding to a first antigen, and

b) a second light chain and a second heavy chain of an antibody specifically binding to a second antigen, wherein the variable domains VL and VH of the second light chain and the second heavy chain are replaced by each other,

wherein the first antigen or the second antigen is human CD19.

The antibody under a) does not contain a modification as reported under b) and the heavy chain and the light chain under a) are isolated chains.

In the antibody under b)

within the light chain

the variable light chain domain VL is replaced by the variable heavy chain domain VH of said antibody,

and

within the heavy chain

the variable heavy chain domain VH is replaced by the variable light chain domain VL of said antibody.

In one embodiment

i) in the constant domain CL of the first light chain under a) the amino acid at position 124 (numbering according to Kabat) is substituted by a positively charged amino acid, and wherein in the constant domain CH1 of the first heavy chain under a) the amino acid at position 147 or

the amino acid at position 213 (numbering according to Kabat EU index) is substituted by a negatively charged amino acid,

or

ii) in the constant domain CL of the second light chain under b) the amino acid at position 124 (numbering according to Kabat) is substituted by a positively charged amino acid, and wherein in the constant domain CH1 of the second heavy chain under b) the amino acid at position 147 or the amino acid at position 213 (numbering according to Kabat EU index) is substituted by a negatively charged amino acid.

In one preferred embodiment

i) in the constant domain CL of the first light chain under a) the amino acid at position 124 is substituted independently by lysine (K), arginine (R) or histidine (H) (numbering according to Kabat) (in one preferred embodiment independently by lysine (K) or arginine (R)), and wherein in the constant domain CH1 of the first heavy chain under a) the amino acid at position 147 or the amino acid at position 213 is substituted independently by glutamic acid (E) or aspartic acid (D) (numbering according to Kabat EU index),

or

ii) in the constant domain CL of the second light chain under b) the amino acid at position 124 is substituted independently by lysine (K), arginine (R) or histidine (H) (numbering according to Kabat) (in one preferred embodiment independently by lysine (K) or arginine (R)), and wherein in the constant domain CH1 of the second heavy chain under b) the amino acid at position 147 or the amino acid at position 213 is substituted independently by glutamic acid (E) or aspartic acid (D) (numbering according to Kabat EU index).

In one embodiment in the constant domain CL of the second heavy chain the amino acids at position 124 and 123 are substituted by K (numbering according to Kabat EU index).

In one embodiment in the constant domain CH1 of the second light chain the amino acids at position 147 and 213 are substituted by E (numbering according to EU index of Kabat).

In one preferred embodiment in the constant domain CL of the first light chain the amino acids at position 124 and 123 are substituted by R and K, respectively, and in the constant domain CH1 of the first heavy chain the amino acids at position 147 and 213 are substituted by E (numbering according to Kabat EU index).

In one embodiment in the constant domain CL of the second heavy chain the amino acids at position 124 and 123 are substituted by K, and wherein in the constant domain CH1 of the second light chain the amino acids at position 147 and 213 are substituted by E, and in the variable domain VL of the first light chain the amino acid at position 38 is substituted by K, in the variable domain VH of the first heavy chain the amino acid at position 39 is substituted by E, in the variable domain VL of the second heavy chain the amino acid at position 38 is substituted by K, and in the variable domain VH of the second light chain the amino acid at position 39 is substituted by E (numbering according to Kabat EU index).

One aspect as reported herein is a bivalent, bispecific antibody comprising

a) a first light chain and a first heavy chain of an antibody specifically binding to a first antigen, and

b) a second light chain and a second heavy chain of an antibody specifically binding to a second antigen, wherein the variable domains VL and VH of the second light chain and the second heavy chain are replaced by each other, and wherein the constant domains CL and CH1 of the second light chain and the second heavy chain are replaced by each other,

wherein the first antigen or the second antigen is human CD19.

The antibody under a) does not contain a modification as reported under b) and the heavy chain and the light chain und a) are isolated chains.

In the antibody under b)

within the light chain

the variable light chain domain VL is replaced by the variable heavy chain domain VH of said antibody, and the constant light chain domain CL is replaced by the constant heavy chain domain CH1of said antibody;

and

within the heavy chain

the variable heavy chain domain VH is replaced by the variable light chain domain VL of said antibody, and the constant heavy chain domain CH1 is replaced by the constant light chain domain CL of said antibody.

One aspect as reported herein is a bivalent, bispecific antibody comprising

a) a first light chain and a first heavy chain of an antibody specifically binding to a first antigen, and

b) a second light chain and a second heavy chain of an antibody specifically binding to a second antigen, wherein the constant domains CL and CH1 of the second light chain and the second heavy chain are replaced by each other,

wherein the first antigen or the second antigen is human CD19.

The antibody under a) does not contain a modification as reported under b) and the heavy chain and the light chain under a) are isolated chains.

In the antibody under b)

within the light chain

the constant light chain domain CL is replaced by the constant heavy chain domain CH1of said antibody;

and within the heavy chain

the constant heavy chain domain CH1 is replaced by the constant light chain domain CL of said antibody.

One aspect as reported herein is a multispecific antibody comprising

a) a full length antibody specifically binding to a first antigen and consisting of two antibody heavy chains and two antibody light chains, and

b) one, two, three or four single chain Fab fragments specifically binding to one to four further antigens (i.e. a second and/or third and/or fourth and/or fifth antigen, preferably specifically binding to one further antigen, i.e. a second antigen),

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

wherein the first antigen or one of the further antigens is human CD19.

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

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

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

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

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

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

One aspect as reported herein is a trivalent, bispecific antibody comprising

a) a full length antibody specifically binding to a first antigen and consisting of two antibody heavy chains and two antibody light chains,

b) a first polypeptide consisting of
   ba) an antibody heavy chain variable domain (VH),
   or
   bb) an antibody heavy chain variable domain (VH) and an antibody constant domain 1 (CH1),
   wherein said first polypeptide is fused with the N-terminus of its VH domain via a peptidic linker to the C-terminus of one of the two heavy chains of said full length antibody,

c) a second polypeptide consisting of
   ca) an antibody light chain variable domain (VL),
   or
   cb) an antibody light chain variable domain (VL) and an antibody light chain constant domain (CL),
   wherein said second polypeptide is fused with the N-terminus of the VL domain via a peptidic linker to the C-terminus of the other of the two heavy chains of said full length antibody,

and

wherein the antibody heavy chain variable domain (VH) of the first polypeptide and the antibody light chain variable domain (VL) of the second polypeptide together form an antigen-binding site specifically binding to a second antigen,

and

wherein the first antigen or the second antigen is human CD19.

In one embodiment the antibody heavy chain variable domain (VH) of the polypeptide under b) and the antibody light chain variable domain (VL) of the polypeptide under c) are linked and stabilized via an interchain disulfide bridge by introduction of a disulfide bond between the following positions:

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

Techniques to introduce unnatural disulfide bridges for stabilization are described e.g. in WO 94/029350, Rajagopal, V., et al., Prot. Eng. (1997) 1453-59; Kobayashi, H., et al., Nuclear Medicine & Biology, Vol. 25, (1998) 387-393; or Schmidt, M., et al., Oncogene (1999) 18 1711-1721. In one embodiment the optional disulfide bond between the variable domains of the polypeptides under b) and c) is between heavy chain variable domain position 44 and light chain variable domain position 100. In one embodiment the optional disulfide bond between the variable domains of the polypeptides under b) and c) is between heavy chain variable domain position 105 and light chain variable domain position 43 (numbering always according to Kabat). In one embodiment a trivalent, bispecific antibody without said optional disulfide stabilization between the variable domains VH and VL of the single chain Fab fragments is preferred.

One aspect as reported herein is a trispecific or tetraspecific antibody, comprising

a) a first light chain and a first heavy chain of a full length antibody which specifically binds to a first antigen, and

b) a second (modified) light chain and a second (modified) heavy chain of a full length antibody which specifically binds to a second antigen, wherein the variable domains VL and VH are replaced by each other, and/or wherein the constant domains CL and CH1 are replaced by each other, and

c) wherein one to four antigen binding peptides which specifically bind to one or two further antigens (i.e. to a third and/or fourth antigen) are fused via a peptidic linker to the C- or N-terminus of the light chains or heavy chains of a) and/or b),

wherein the first antigen or the second antigen or one of the further antigens is human CD19.

The antibody under a) does not contain a modification as reported under b) and the heavy chain and the light chain und a) are isolated chains.

In one embodiment the trispecific or tetraspecific antibody comprises under c) one or two antigen binding peptides which specifically bind to one or two further antigens.

In one embodiment the antigen binding peptides are selected from the group of a scFv fragment and a scFab fragment.

In one embodiment the antigen binding peptides are scFv fragments.

In one embodiment the antigen binding peptides are scFab fragments.

In one embodiment the antigen binding peptides are fused to the C-terminus of the heavy chains of a) and/or b).

In one embodiment the trispecific or tetraspecific antibody comprises under c) one or two antigen binding peptides which specifically bind to one further antigen.

In one embodiment the trispecific or tetraspecific antibody comprises under c) two identical antigen binding peptides which specifically bind to a third antigen. In one preferred embodiment such two identical antigen binding peptides are fused both via the same peptidic linker to the C-terminus of the heavy chains of a) and b). In one preferred embodiment the two identical antigen binding peptides are either a scFv fragment or a scFab fragment.

In one embodiment the trispecific or tetraspecific antibody comprises under c) two antigen binding peptides which specifically bind to a third and a fourth antigen. In one embodiment said two antigen binding peptides are fused both via the same peptide connector to the C-terminus of the heavy chains of a) and b). In one preferred embodiment said two antigen binding peptides are either a scFv fragment or a scFab fragment.

One aspect as reported herein is a bispecific, tetravalent antibody comprising

a) two light chains and two heavy chains of an antibody, which specifically bind to a first antigen (and comprise two Fab fragments),

b) two additional Fab fragments of an antibody, which specifically bind to a second antigen, wherein said additional Fab fragments are fused both via a peptidic linker either to the C- or N-termini of the heavy chains of a),

and

wherein in the Fab fragments the following modifications were performed

i) in both Fab fragments of a), or in both Fab fragments of b), the variable domains VL and VH are replaced by each other, and/or the constant domains CL and CH1 are replaced by each other,

or

ii) in both Fab fragments of a) the variable domains VL and VH are replaced by each other, and the constant domains CL and CH1 are replaced by each other,

and

in both Fab fragments of b) the variable domains VL and VH are replaced by each other, or the constant domains CL and CH1 are replaced by each other,

or

iii) in both Fab fragments of a) the variable domains VL and VH are replaced by each other, or the constant domains CL and CH1 are replaced by each other,

and

in both Fab fragments of b) the variable domains VL and VH are replaced by each other, and the constant domains CL and CH1 are replaced by each other,

or

iv) in both Fab fragments of a) the variable domains VL and VH are replaced by each other, and in both Fab fragments of b) the constant domains CL and CH1 are replaced by each other,

or

v) in both Fab fragments of a) the constant domains CL and CH1 are replaced by each other, and in both Fab fragments of b) the variable domains VL and VH are replaced by each other,

wherein the first antigen or the second antigen is human CD19.

In one embodiment said additional Fab fragments are fused both via a peptidic linker either to the C-termini of the heavy chains of a), or to the N-termini of the heavy chains of a).

In one embodiment said additional Fab fragments are fused both via a peptidic linker either to the C-termini of the heavy chains of a).

In one embodiment said additional Fab fragments are fused both via a peptide connector to the N-termini of the heavy chains of a).

In one embodiment in the Fab fragments the following modifications are performed:

i) in both Fab fragments of a), or in both Fab fragments of b), the variable domains VL and VH are replaced by each other,
and/or
the constant domains CL and CH1 are replaced by each other.

In one embodiment in the Fab fragments the following modifications are performed:

i) in both Fab fragments of a) the variable domains VL and VH are replaced by each other,
and/or
the constant domains CL and CH1 are replaced by each other.

In one embodiment in the Fab fragments the following modifications are performed:

i) in both Fab fragments of a) the constant domains CL and CH1 are replaced by each other.

In one embodiment in the Fab fragments the following modifications are performed:

i) in both Fab fragments of b) the variable domains VL and VH are replaced by each other,
and/or
the constant domains CL and CH1 are replaced by each other.

In one embodiment in the Fab fragments the following modifications are performed:

i) in both Fab fragments of b) the constant domains CL and CH1 are replaced by each other.

One aspect as reported herein is a bispecific, tetravalent antibody comprising:

a) a (modified) heavy chain of a first antibody, which specifically binds to a first antigen and comprises a first VH-CH1 domain pair, wherein to the C-terminus of said heavy chain the N-terminus of a second VH-CH1 domain pair of said first antibody is fused via a peptidic linker,

b) two light chains of said first antibody of a),

c) a (modified) heavy chain of a second antibody, which specifically binds to a second antigen and comprises a first VH-CL domain pair, wherein to the C-terminus of said heavy chain the N-terminus of a second VH-CL domain pair of said second antibody is fused via a peptidic linker, and

d) two (modified) light chains of said second antibody of c), each comprising a CL-CH1 domain pair,

wherein the first antigen or the second antigen is human CD19.

One aspect as reported herein is a bispecific antibody comprising

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

b) the heavy chain and the light chain of a second full length antibody that specifically binds to a second antigen, wherein the N-terminus of the

heavy chain is connected to the C-terminus of the light chain via a peptidic linker,

wherein the first antigen or the second antigen is human CD19.

The antibody under a) does not contain a modification as reported under b) and the heavy chain and the light chain are isolated chains.

One aspect as reported herein is a bispecific antibody comprising

a) a full length antibody specifically binding to a first antigen and consisting of two antibody heavy chains and two antibody light chains, and

b) an Fv fragment specifically binding to a second antigen comprising a VH^2 domain and a VL^2 domain, wherein both domains are connected to each other via a disulfide bridge,

wherein only either the VH^2 domain or the VL^2 domain is fused via a peptidic linker to the heavy or light chain of the full length antibody specifically binding to a first antigen,

wherein the first antigen or the second antigen is human CD19.

In the bispecific the heavy chains and the light chains under a) are isolated chains.

In one embodiment the other of the VH^2 domain or the VL^2 domain is not fused via a peptide linker to the heavy or light chain of the full length antibody specifically binding to a first antigen.

In all aspects as reported herein the first light chain comprises a VL domain and a CL domain and the first heavy chain comprises a VH domain, a CH1 domain, a hinge region, a CH2 domain and a CH3 domain.

One aspect as reported herein is a bispecific trivalent antibody comprising

a) two Fab fragments that specifically binds to a first antigen,

b) one CrossFab fragment that specifically binds to a second antigen in which the CH1 and the CL domain are exchanged for each other,

c) one Fc-region comprising a first Fc-region heavy chain and a second Fc-region heavy chain,

wherein the C-terminus of CH1 domains of the two Fab fragments are connected to the N-terminus of the heavy chain Fc-region polypeptides, and

wherein the C-terminus of the CL domain of the CrossFab fragment is connected to the N-terminus of the VH domain of one of the Fab fragments, and

wherein the first antigen or the second antigen is human CD19.

One aspect as reported herein is a bispecific trivalent antibody comprising

a) a first and a second Fab fragment that each specifically bind to a first antigen,

b) one CrossFab fragment that specifically binds to a second antigen in which the CH1 and the CL domain are exchanged for each other,

c) one Fc-region comprising a first Fc-region heavy chain and a second Fc-region heavy chain,

wherein the C-terminus of CH1 domain of the first Fab fragment is connected to the N-terminus of one of the heavy chain Fc-region polypeptides and the C-terminus of the CL-domain of the CrossFab fragment is connected to the N-terminus of the other heavy chain Fc-region polypeptide, and

wherein the C-terminus of the CH1 domain of the second Fab fragment is connected to the N-terminus of the VH domain of the first Fab fragment or to the N-terminus of the VH domain of the CrossFab fragment, and

wherein the first antigen or the second antigen is human CD19.

One aspect as reported herein is a bispecific trivalent antibody comprising

a) a first and a second Fab fragment that each specifically bind to a first antigen,

b) one CrossFab fragment that specifically binds to a second antigen in which the VH and the VL domain are exchanged for each other,

c) one Fc-region comprising a first Fc-region heavy chain and a second Fc-region heavy chain,

wherein the C-terminus of CH1 domain of the first Fab fragment is connected to the N-terminus of one of the heavy chain Fc-region polypeptides and the C-terminus of the CH1-domain of the CrossFab fragment is connected to the N-terminus of the other heavy chain Fc-region polypeptide, and

wherein the C-terminus of the CH1 domain of the second Fab fragment is connected to the N-terminus of the VH domain of the first Fab fragment or to the N-terminus of the VL domain of the CrossFab fragment, and

wherein the first antigen or the second antigen is human CD19.

One aspect as reported herein is a bispecific antibody comprising

a) a full length antibody specifically binding to a first antigen and consisting of two antibody heavy chains and two antibody light chains, and

b) a Fab fragment specifically binding to a second antigen comprising a VH^2 domain and a VL^2 domain comprising a heavy chain fragment and a light chain fragment, wherein

within the light chain fragment

the variable light chain domain VL^2 is replaced by the variable heavy chain domain VH^2 of said antibody,

and

within the heavy chain fragment

the variable heavy chain domain VH^2 is replaced by the variable light chain domain VL^2 of said antibody

wherein the heavy chain Fab fragment is inserted between the CH1 domain of one of the heavy chains of the full length antibody and the respective Fc-region of the full length antibody, and the N-terminus of the light chain Fab fragment is conjugated to the C-terminus of the light chain of the full length antibody that is paired with the heavy chain of the full length antibody into which the heavy chain Fab fragment has been inserted, and

wherein the first antigen or the second antigen is human CD19.

One aspect as reported herein is a bispecific antibody comprising

a) a full length antibody specifically binding to a first antigen and consisting of two antibody heavy chains and two antibody light chains, and

b) a Fab fragment specifically binding to a second antigen comprising a VH^2 domain and a VL^2 domain comprising a heavy chain fragment and a light chain fragment, wherein

within the light chain fragment

the variable light chain domain VL^2 is replaced by the variable heavy chain domain VH^2 of said antibody,

and

within the heavy chain fragment

the variable heavy chain domain VH^2 is replaced by the variable light chain domain VL^2 of said antibody

wherein the C-terminus of the heavy chain fragment of the Fab fragment is conjugated to the N-terminus of one of the heavy chains of the full length antibody and the C-terminus of the light chain fragment of the Fab fragment is conjugated to the N-terminus of the light chain of the full length antibody that pairs with the heavy chain of the full length antibody to which the heavy chain fragment of the Fab fragment is conjugated, and

wherein the first antigen or the second antigen is human CD19.

In one embodiment of all aspects the antibody as reported herein is a multispecific antibody, which requires heterodimerization of at least two heavy chain polypeptides, and wherein the antibody specifically binds to human transferrin receptor and a second non-human transferrin receptor antigen.

Several approaches for CH3-modifications in order to support heterodimerization have been described, for example in WO 96/27011, WO 98/050431, EP 1870459, WO 2007/110205, WO 2007/147901, WO 2009/089004, WO 2010/129304, WO 2011/90754, WO 2011/143545, WO 2012/058768, WO 2013/157954,

WO 2013/096291, which are herein included by reference. Typically, in the approaches known in the art, the CH3 domain of the first heavy chain and the CH3 domain of the second heavy chain are both engineered in a complementary manner so that the heavy chain comprising one engineered CH3 domain can no longer homodimerize with another heavy chain of the same structure (e.g. a CH3-engineered first heavy chain can no longer homodimerize with another CH3-engineered first heavy chain; and a CH3-engineered second heavy chain can no longer homodimerize with another CH3-engineered second heavy chain). Thereby the heavy chain comprising one engineered CH3 domain is forced to heterodimerize with another heavy chain comprising the CH3 domain, which is engineered in a complementary manner. For this embodiment, the CH3 domain of the first heavy chain and the CH3 domain of the second heavy chain are engineered in a complementary manner by amino acid substitutions, such that the first heavy chain and the second heavy chain are forced to heterodimerize, whereas the first heavy chain and the second heavy chain can no longer homodimerize (e.g. for steric reasons).

The different approaches for supporting heavy chain heterodimerization known in the art, that were cited and included above, are contemplated as different alternatives used in providing a multispecific antibody as reported herein, which comprises a "non-crossed Fab region" derived from a first antibody, which specifically binds to a first antigen, and a "crossed Fab region" derived from a second antibody, which specifically binds to a second antigen, in combination with the particular amino acid substitutions described above.

The CH3 domains of the multispecific antibody as reported herein can be altered by the "knob-into-holes" technology which is described in detail with several examples in e.g. WO 96/027011, Ridgway, J.B., et al., Protein Eng. 9 (1996) 617-621; and Merchant, A.M., et al., Nat. Biotechnol. 16 (1998) 677-681. In this method the interaction surfaces of the two CH3 domains are altered to increase the heterodimerization of both heavy chains containing these two CH3 domains. Each of the two CH3 domains (of the two heavy chains) can be the "knob", while the other is the "hole". The introduction of a disulfide bridge further stabilizes the heterodimers (Merchant, A.M., et al., Nature Biotech. 16 (1998) 677-681; Atwell, S., et al., J. Mol. Biol. 270 (1997) 26-35) and increases the yield.

In one preferred embodiment the multispecific antibody as reported herein comprises a T366W mutation in the CH3 domain of the "knobs chain" and T366S,

L368A, Y407V mutations in the CH3 domain of the "hole-chain" (numbering according to Kabat EU index). An additional interchain disulfide bridge between the CH3 domains can also be used (Merchant, A.M., et al., Nature Biotech. 16 (1998) 677-681) e.g. by introducing a Y349C mutation into the CH3 domain of the "knobs chain" and a E356C mutation or a S354C mutation into the CH3 domain of the "hole chain". Thus in a another preferred embodiment, the multispecific antibody as reported herein comprises the Y349C and T366W mutations in one of the two CH3 domains and the E356C, T366S, L368A and Y407V mutations in the other of the two CH3 domains or the multispecific antibody as reported herein comprises the Y349C and T366W mutations in one of the two CH3 domains and the S354C, T366S, L368A and Y407V mutations in the other of the two CH3 domains (the additional Y349C mutation in one CH3 domain and the additional E356C or S354C mutation in the other CH3 domain forming a interchain disulfide bridge) (numbering according to Kabat EU index).

But also other knobs-in-holes technologies as described by EP 1 870 459A1, can be used alternatively or additionally. In one embodiment the multispecific antibody as reported herein comprises the R409D and K370E mutations in the CH3 domain of the "knobs chain" and the D399K and E357K mutations in the CH3 domain of the "hole-chain" (numbering according to Kabat EU index).

In one embodiment the multispecific antibody as reported herein comprises a T366W mutation in the CH3 domain of the "knobs chain" and the T366S, L368A and Y407V mutations in the CH3 domain of the "hole chain" and additionally the R409D and K370E mutations in the CH3 domain of the "knobs chain" and the D399K and E357K mutations in the CH3 domain of the "hole chain" (numbering according to the Kabat EU index).

In one embodiment the multispecific antibody as reported herein comprises the Y349C and T366W mutations in one of the two CH3 domains and the S354C, T366S, L368A and Y407V mutations in the other of the two CH3 domains, or the multispecific antibody as reported herein comprises the Y349C and T366W mutations in one of the two CH3 domains and the S354C, T366S, L368A and Y407V mutations in the other of the two CH3 domains and additionally the R409D and K370E mutations in the CH3 domain of the "knobs chain" and the D399K and E357K mutations in the CH3 domain of the "hole chain" (numbering according to the Kabat EU index).

Apart from the "knob-into-hole technology" other techniques for modifying the CH3 domains of the heavy chains of a multispecific antibody to enforce heterodimerization are known in the art. These technologies, especially the ones described in WO 96/27011, WO 98/050431, EP 1870459, WO 2007/110205, WO 2007/147901, WO 2009/089004, WO 2010/129304, WO 2011/90754, WO 2011/143545, WO 2012/058768, WO 2013/157954 and WO 2013/096291 are contemplated herein as alternatives to the "knob-into-hole technology" in combination with a multispecific antibody as reported herein.

In one embodiment of a multispecific antibody as reported herein the approach described in EP 1870459 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. This approach is based on the introduction of charged amino acids with opposite charges at specific amino acid positions in the CH3/CH3-domain-interface between both, the first and the second heavy chain.

Accordingly, this embodiment relates to a multispecific antibody as reported herein, wherein in the tertiary structure of the antibody the CH3 domain of the first heavy chain and the CH3 domain of the second heavy chain form an interface that is located between the respective antibody CH3 domains, wherein the respective amino acid sequences of the CH3 domain of the first heavy chain and the CH3 domain of the second heavy chain each comprise a set of amino acids that is located within said interface in the tertiary structure of the antibody, wherein from the set of amino acids that is located in the interface in the CH3 domain of one heavy chain a first amino acid is substituted by a positively charged amino acid and from the set of amino acids that is located in the interface in the CH3 domain of the other heavy chain a second amino acid is substituted by a negatively charged amino acid. The multispecific antibody according to this embodiment is herein also referred to as "CH3(+/-)-engineered multispecific antibody" (wherein the abbreviation "+/-" stands for the oppositely charged amino acids that were introduced in the respective CH3 domains).

In one embodiment of said CH3(+/-)-engineered multispecific antibody as reported herein the positively charged amino acid is selected from K, R and H, and the negatively charged amino acid is selected from E or D.

In one embodiment of said CH3(+/-)-engineered multispecific antibody as reported herein the positively charged amino acid is selected from K and R, and the negatively charged amino acid is selected from E or D.

In one embodiment of said CH3(+/-)-engineered multispecific antibody as reported herein the positively charged amino acid is K, and the negatively charged amino acid is E.

In one embodiment of said CH3(+/-)-engineered multispecific antibody as reported herein in the CH3 domain of one heavy chain the amino acid R at position 409 is substituted by D and the amino acid K at position is substituted by E, and in the CH3 domain of the other heavy chain the amino acid D at position 399 is substituted by K and the amino acid E at position 357 is substituted by K (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein the approach described in WO 2013/157953 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. In one embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid T at position 366 is substituted by K, and in the CH3 domain of the other heavy chain the amino acid L at position 351 is substituted by D (numbering according to Kabat EU index). In another embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid T at position 366 is substituted by K and the amino acid L at position 351 is substituted by K, and in the CH3 domain of the other heavy chain the amino acid L at position 351 is substituted by D (numbering according to Kabat EU index).

In another embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid T at position 366 is substituted by K and the amino acid L at position 351 is substituted by K, and in the CH3 domain of the other heavy chain the amino acid L at position 351 is substituted by D (numbering according to Kabat EU index). Additionally at least one of the following substitutions is comprised in the CH3 domain of the other heavy chain: the amino acid Y at position 349 is substituted by E, the amino acid Y at position 349 is substituted by D and the amino acid L at position 368 is substituted by E (numbering according to Kabat EU index). In one embodiment the amino acid L at position 368 is substituted by E (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein the approach described in WO 2012/058768 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. In one embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid L at position 351 is substituted by Y and the amino acid Y at position 407 is substituted by A, and in the CH3 domain of the other heavy chain the amino acid T at position 366 is substituted by A and the amino acid K at position 409 is substituted by F (numbering according to Kabat EU index). In another embodiment, in addition to the aforementioned substitutions, in the CH3 domain of the other heavy chain at least one of the amino acids at positions 411 (originally T), 399 (originally D), 400 (originally S), 405 (originally F), 390 (originally N) and 392 (originally K) is substituted (numbering according to Kabat EU index). Preferred substitutions are:

- substituting the amino acid T at position 411 by an amino acid selected from N, R, Q, K, D, E and W (numbering according to Kabat EU index),
- substituting the amino acid D at position 399 by an amino acid selected from R, W, Y, and K (numbering according to Kabat EU index),
- substituting the amino acid S at position 400 by an amino acid selected from E, D, R and K (numbering according to Kabat EU index),
- substituting the amino acid F at position 405 by an amino acid selected from I, M, T, S, V and W (numbering according to Kabat EU index;
- substituting the amino acid N at position 390 by an amino acid selected from R, K and D (numbering according to Kabat EU index; and
- substituting the amino acid K at position 392 by an amino acid selected from V, M, R, L, F and E (numbering according to Kabat EU index).

In another embodiment of said multispecific antibody as reported herein (engineered according to WO 2012/058768), in the CH3 domain of one heavy chain the amino acid L at position 351 is substituted by Y and the amino acid Y at position 407 is substituted by A, and in the CH3 domain of the other heavy chain the amino acid T at position 366 is substituted by V and the amino acid K at position 409 is substituted by F (numbering according to Kabat EU index). In another embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid Y at position 407 is substituted by A, and in the CH3 domain of the other heavy chain the amino acid T at position 366 is substituted by A and the amino acid K at position 409 is substituted by F (numbering according to Kabat EU index). In said last aforementioned embodiment,

in the CH3 domain of said other heavy chain the amino acid K at position 392 is substituted by E, the amino acid T at position 411 is substituted by E, the amino acid D at position 399 is substituted by R and the amino acid S at position 400 is substituted by R (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein the approach described in WO 2011/143545 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. In one embodiment of said multispecific antibody as reported herein, amino acid modifications in the CH3 domains of both heavy chains are introduced at positions 368 and/or 409 (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein the approach described in WO 2011/090762 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. WO 2011/090762 relates to amino acid modifications according to the "knob-into-hole" technology. In one embodiment of said CH3(KiH)-engineered multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid T at position 366 is substituted by W, and in the CH3 domain of the other heavy chain the amino acid Y at position 407 is substituted by A (numbering according to Kabat EU index). In another embodiment of said CH3(KiH)-engineered multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid T at position 366 is substituted by Y, and in the CH3 domain of the other heavy chain the amino acid Y at position 407 is substituted by T (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein, which is of IgG2 isotype, the approach described in WO 2011/090762 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody.

In one embodiment of a multispecific antibody as reported herein, the approach described in WO 2009/089004 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. In one embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid K or N at position 392 is substituted by a negatively charged amino acid (in one preferred embodiment by E or D, in one preferred embodiment by D), and in the CH3 domain of the other heavy chain the

amino acid D at position 399 the amino acid E or D at position 356 or the amino acid E at position 357 is substituted by a positively charged amino acid (in one preferred embodiment K or R, in one preferred embodiment by K, in one preferred embodiment the amino acids at positions 399 or 356 are substituted by K) (numbering according to Kabat EU index). In one further embodiment, in addition to the aforementioned substitutions, in the CH3 domain of the one heavy chain the amino acid K or R at position 409 is substituted by a negatively charged amino acid (in one preferred embodiment by E or D, in one preferred embodiment by D) (numbering according to Kabat EU index). In one even further embodiment, in addition to or alternatively to the aforementioned substitutions, in the CH3 domain of the one heavy chain the amino acid K at position 439 and/or the amino acid K at position 370 is substituted independently from each other by a negatively charged amino acid (in one preferred embodiment by E or D, in one preferred embodiment by D) (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein, the approach described in WO 2007/147901 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody. In one embodiment of said multispecific antibody as reported herein, in the CH3 domain of one heavy chain the amino acid K at position 253 is substituted by E, the amino acid D at position 282 is substituted by K and the amino acid K at position 322 is substituted by D, and in the CH3 domain of the other heavy chain the amino acid D at position 239 is substituted by K, the amino acid E at position 240 is substituted by K and the amino acid K at position 292 is substituted by D (numbering according to Kabat EU index).

In one embodiment of a multispecific antibody as reported herein, the approach described in WO 2007/110205 is used to support heterodimerization of the first heavy chain and the second heavy chain of the multispecific antibody

In one embodiment of all aspects and embodiments as reported herein the multispecific antibody is a bispecific antibody or a trispecific antibody. In one preferred embodiment the multispecific antibody is a bispecific antibody.

In one embodiment of all aspects as reported herein, the antibody is a bivalent or trivalent antibody. In one embodiment the antibody is a bivalent antibody.

In one embodiment of all aspects as reported herein, the multispecific antibody has a constant domain structure of an IgG type antibody. In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG1, or of human subclass IgG1 with the mutations L234A and L235A. In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG2. In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG3. In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG4 or, of human subclass IgG4 with the additional mutation S228P. In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG1 or human subclass IgG4. In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG1 with the mutations L234A and L235A (numbering according to Kabat EU index). In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG1 with the mutations L234A, L235A and P329G (numbering according to Kabat EU index). In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG4 with the mutations S228P and L235E (numbering according to Kabat EU index). In one further embodiment of all aspects as reported herein, the multispecific antibody is characterized in that said multispecific antibody is of human subclass IgG4 with the mutations S228P, L235E and P329G (numbering according to Kabat EU index).

In one embodiment of all aspects as reported herein, an antibody comprising a heavy chain including a CH3 domain as specified herein, comprises an additional C-terminal glycine-lysine dipeptide (G446 and K447, numbering according to Kabat EU index). In one embodiment of all aspects as reported herein, an antibody comprising a heavy chain including a CH3 domain, as specified herein, comprises an additional C-terminal glycine residue (G446, numbering according to Kabat EU index).

The antibody as reported herein is in one embodiment characterized by being of human subclass IgG1 with mutations PVA236, L234A/L235A, and/or GLPSS331 (numbering according to EU index of Kabat), or of subclass IgG4. In a further embodiment, the antibody is characterized by being of any IgG class, in one embodiment being IgG1 or IgG4, containing at least one mutation in E233, L234, L235, G236, D270, N297, E318, K320, K322, A327, A330, P331 and/or P329 (numbering according to EU index of Kabat). It is further in one embodiment that the antibody of IgG4 subclass contains the mutation S228P, or the mutations S228P and L235E (Angal, S., et al., Mol. Immunol. 30 (1993) 105-108) (numbering according to EU index of Kabat).

The C-terminus of the heavy chain of the antibody as reported herein can be a complete C-terminus ending with the amino acid residues PGK. The C-terminus of the heavy chain can be a shortened C-terminus in which one or two of the C-terminal amino acid residues have been removed. In one preferred embodiment the C-terminus of the heavy chain is a shortened C-terminus ending PG.

In certain embodiments, an antibody provided herein may be further modified to contain one or more blood-brain-barrier shuttle modules that are known in the art and readily available.

The blood-brain-barrier shuttle module is characterized by having a binding specificity for a blood-brain-barrier receptor. This binding specificity can be obtained either by fusing a blood-brain-barrier shuttle module to the anti-human CD19 antibody as reported herein or it can be obtained by introducing the binding specificity to the blood-brain-barrier receptor as one of the binding specificities of a multispecific antibody that specifically binds to human CD19 and, thus, comprises the binding specificity of the anti-human CD19 antibody as reported herein and the binding specificity to the blood-brain-barrier receptor.

One or more blood-brain-barrier shuttle modules can be fused to any terminus of the light or heavy chain of the anti-human CD19 antibody as reported herein. In one preferred embodiment the blood-brain-barrier shuttle module is fused to the C-terminus of the heavy chain.

The one or more blood-brain-barrier shuttle modules can be fused to the respective antibody chain either directly or via linker peptide. In one preferred embodiment

the linker peptide has the amino acid sequence GGSGGGGSGGGGSGGGGS (SEQ ID NO: 41).

The blood-brain-barrier shuttle module can be an antibody scFv fragment. In one embodiment the blood-brain-barrier shuttle module is a scFv comprising in N- to C-terminal order a light chain variable domain-a light chain constant domain-a linker peptide-a heavy chain variable domain-the heavy chain constant domain1.

In one preferred embodiment the blood-brain-barrier shuttle module is the scFv fragment of the anti-transferrin receptor-antibody 8D3 with a $(G4S)_6$ linker peptide or a humanized variant thereof

The term humanized variant thereof denotes a molecule that has been obtained by grafting the CDRs of the murine 8D3 antibody on a human framework with the optional introduction of one to three mutations independently of each other in each of the framework regions (FRs) and/or the hypervariable regions (HVRs).

In one aspect, herein is provided an anti-human CD19 antibody fusion polypeptide comprising an anti-human CD19 antibody, two peptide linker and two monovalent binding entities which bind to a blood-brain-barrier receptor, wherein the linker couples the anti-human CD19 antibody to the monovalent binding entities which bind to the blood-brain-barrier receptor.

In one aspect, herein is provided an anti-human CD19 antibody fusion polypeptide comprising an anti-human CD19 antibody, a peptide linker and one monovalent binding entity which binds to a blood-brain-barrier receptor, wherein the linker couples the anti-human CD19 antibody to the monovalent binding entity which bind to the blood-brain-barrier receptor.

In one embodiment, the monovalent binding entity which binds to the blood-brain-barrier receptor is selected from the group consisting of proteins, polypeptides and peptides.

In one embodiment, the monovalent binding entity which binds to the blood-brain-barrier receptor comprises a molecule selected from the group consisting of a blood-brain-barrier receptor ligand, a scFv, an Fv, a scFab, a VHH, in one preferred embodiment a scFv or a scFab.

In one embodiment, the blood-brain-barrier receptor is selected from the group consisting of transferrin receptor, insulin receptor, insulin-like growth factor receptor, low density lipoprotein receptor-related protein 8, low density lipoprotein receptor-related protein 1 and heparin-binding epidermal growth factor-like growth factor. In one preferred embodiment the blood-brain-barrier receptor is the transferrin receptor.

In one embodiment, the monovalent binding entity which binds to the blood-brain-barrier receptor comprises one scFab or one scFv directed to the transferrin receptor, more particular a scFab or scFv recognizing an epitope in the transferrin receptor comprised within the amino acid sequence of SEQ ID NO: 42, 43 and 44.

In one embodiment, the monovalent binding entity which binds to the blood-brain-barrier receptor is coupled to the C-terminal end of the heavy chain of the anti-human CD19 antibody by the linker.

In one embodiment, the peptide linker is an amino acid sequence with a length of at least 15 amino acids, more preferably with a length of 18 to 25 amino acids.

In one embodiment, the anti-human CD19 antibody is a full length antibody, in one preferred embodiment a full length IgG. The term full length antibody denotes an antibody consisting of two antibody light chain polypeptides and two antibody heavy chain polypeptides wherein in the two antibody heavy chain polypeptides the C-terminal lysine residue (K) can be present or not.

In one preferred embodiment, the anti-human CD19 antibody fusion polypeptide comprises a full length IgG anti-human CD19 antibody as brain effector entity, a linker of the sequence GGSGGGGSGGGGSGGGGS (SEQ ID NO: 41) and one scFab as monovalent binding entity which binds to the human transferrin receptor as blood brain receptor, wherein the scFab is coupled by the linker to the C-terminal end (of the Fc part) of one of the heavy chains of the full length anti-human CD19 antibody, and wherein the scFab recognizes an epitope in the human transferrin receptor comprised within the amino acid sequence of SEQ ID NO: 52, 53 and 54.

In one preferred embodiment, the anti-human CD19 antibody fusion polypeptide comprises a full length IgG anti-human CD19 antibody as brain effector entity, a linker of the sequence GGSGGGGSGGGGSGGGGS (SEQ ID NO: 41) and one scFv as monovalent binding entity which binds to the human transferrin receptor as

blood brain receptor, wherein the scFab is coupled by the linker to the C-terminal end (of the Fc part) of one of the heavy chains of the full length anti-human CD19 antibody, and wherein the scFab recognizes an epitope in the human transferrin receptor comprised within the amino acid sequence of SEQ ID NO: 42, 43 and 44.

In one embodiment, the first heavy chain of the anti-human CD19 antibody comprises a first dimerization module and the second heavy chain of the antibody comprises a second dimerization module allowing heterodimerization of the two heavy chains.

In one embodiment, the first dimerization module of the first heavy chain of the anti-human CD19 antibody is a knob heavy chain and the dimerization module of the second heavy chain of the anti-human CD19 antibody is a hole heavy chain (according to the knobs-into-holes strategy).

The anti-human CD19 antibody fusion polypeptide as reported herein can be used to transport the anti-human CD19 antibody across the blood brain barrier.

In one embodiment, the heavy chain of the anti-human CD19 antibody that is coupled at its C-terminal end of the Fc-region to the scFab as monovalent binding entity which binds to the human transferrin receptor has the following structure in N- to C-terminal direction:

- IgG heavy chain,
- peptidic linker coupling the C-terminal end of the Fc-region of the IgG heavy chain to the N-terminal end of the VL domain of the scFab, in one preferred embodiment the peptidic linker has the amino acid sequence GGSGGGGSGGGGSGGGGS (SEQ ID NO: 41),
- variable light chain domain (VL) and C-kappa light chain domain of the scFab,
- peptidic linker coupling the C-terminal end of the C-kappa light chain domain of the scFab to the N-terminal end of the VH domain of the scFab, in one preferred embodiment the peptidic linker has the amino acid sequence $(G_4S)_6GG$ (SEQ ID NO: 45),
- variable heavy chain domain (VH) of the scFab antibody and IgG CH1 heavy chain domain.

In one embodiment, the heavy chain of the anti-human CD19 antibody that is coupled at its C-terminal end of the Fc-region to the scFv as monovalent binding

entity which binds to the human transferrin receptor has the following structure in N- to C-terminal direction:

- IgG heavy chain,
- peptidic linker coupling the C-terminal end of the Fc part of the IgG heavy chain to the N-terminal end of the VL domain of the scFv antibody fragment, in one preferred embodiment the peptidic linker is a peptide with the amino acid sequence GGSGGGGSGGGGSGGGGS (SEQ ID NO: 41),
- variable light chain domain (VL),
- peptidic linker coupling the C-terminal end of the variable light chain domain to the N-terminal end of the VH domain of the scFv, in one preferred embodiment the peptidic linker is a peptide with the amino acid sequence $(G_4S)_6GG$ (SEQ ID NO: 45),
- variable heavy chain domain (VH) of the scFv antibody fragment.

In one embodiment the blood-brain-barrier shuttle module/the scFab or scFv directed to a blood-brain-barrier receptor is derived from a humanized anti-transferrin receptor antibody 8D3 (see e.g. Boado, R.J., et al., Biotechnol. Bioeng. 102 (2009) 1251-1258).The murine heavy chain variable domain has the amino acid sequence of

EVQLVESGGG LVQPGNSLTL SCVASGFTFS NYGMHWIRQA PKKGLEWIAM IYYDSSKMNY ADTVKGRFTI SRDNSKNTLY LEMNSLRSED TAMYYCAVPT SHYVVDVWGQ GVSVTVSS

(SEQ ID NO: 46).

The murine light chain variable domain (variant 1) has the amino acid sequence of

DIQMTQSPAS LSASLEEIVT ITCQASQDIG NWLAWYQQKP GKSPQLLIYG ATSLADGVPS RFSGSRSGTQ FSLKISRVQV EDIGIYYCLQ AYNTPWTFGG GTKLELK

(SEQ ID NO: 47), and

the murine light chain variable domain (variant 2) has the amino acid sequence of

DIQMTQSPAS LSASLEEIVT ITCQASQDIG NWLAWYQQKP GKSPQLLIYG ATSLADGVPS RFSGSRSGTQ FSLKISRVQV EDIGIYYCLQ AYNTPWTFGG GTKVEIK

(SEQ ID NO: 48).

In one embodiment the anti-transferrin receptor antibody or transferrin receptor binding specificity comprises (a) a HVR-H1 comprising the amino acid sequence of SEQ ID NO: 51; (b) a HVR-H2 comprising the amino acid sequence of SEQ ID NO: 52; (c) a HVR-H3 comprising the amino acid sequence of SEQ ID NO: 53, 54 or 55; (d) a HVR-L1 comprising the amino acid sequence of SEQ ID NO: 56; (e) a HVR-L2 comprising the amino acid sequence of SEQ ID NO: 57; and (f) a HVR-L3 comprising the amino acid sequence of SEQ ID NO: 58.

In one embodiment the anti-transferrin receptor antibody comprises at least one pair of the heavy chain variable domain of SEQ ID NO: 49 and the light chain variable domain of SEQ ID NO: 50 forming a binding site for the transferrin receptor.

<u>One blood-brain-barrier shuttle module</u>

In one aspect the anti-human CD19 antibody or anti-human CD19 antibody fusion polypeptide comprises exactly one blood-brain-barrier binding specificity or shuttle module, thus is at least bispecific, wherein the blood-brain-barrier binding specificity or shuttle module comprises the humanized variable domains of the anti-human transferrin receptor antibody 8D3 or the pair of the heavy chain variable domain of SEQ ID NO: 49 and the light chain variable domain of SEQ ID NO: 50, whereby the blood-brain-barrier binding specificity or shuttle module transports the anti-human CD19 antibody across the blood-brain-barrier

<u>One or two blood-brain-barrier shuttle modules</u>

In one aspect the anti-human CD19 antibody or anti-human CD19 antibody fusion polypeptide comprises one or two blood-brain-barrier binding specificities or shuttle module(s), thus is at least bispecific, wherein the blood-brain-barrier shuttle binding site or module is/are derived from an antibody which binds with low affinity to a blood-brain-barrier receptor (BBB-R, BBB-R binding specificity), whereby the blood-brain-barrier binding specificity or shuttle module derived from

an antibody which binds with low affinity to a blood-brain-barrier receptor transports the anti-human CD19 antibody across the blood-brain-barrier.

In one embodiment, the BBB-R is selected from the group consisting of transferrin receptor (TfR), insulin receptor, insulin-like growth factor receptor (IGF receptor), low density lipoprotein receptor-related protein 8 (LRP8), low density lipoprotein receptor-related protein 1 (LRP1), and heparin-binding epidermal growth factor-like growth factor (HB-EGF). In another such aspect, the BBB-R is a human BBB-R. In one such aspect, the BBB-R is TfR. In another such aspect, the BBB-R is TfR and the antibody does not inhibit TfR activity. In another such aspect, the BBB-R is TfR and the antibody does not inhibit the binding of TfR to transferrin.

In one embodiment, the antibody does not impair the binding of the BBB-R to one or more of its native ligands. In one such embodiment, the antibody specifically binds to human transferrin receptor (hTfR) in such a manner that it does not inhibit binding of the hTfR to human transferrin.

In one embodiment, the BBB-R binding specificity has an IC_{50} for the BBB-R from about 1 nM to about 100 μM. In one embodiment, the IC_{50} is from about 5 nM to about 100 μM. In one embodiment, the IC_{50} is from about 50 nM to about 100 μM. In one embodiment, the IC_{50} is from about 100 nM to about 100 μM. In one embodiment, the BBB-R binding specificity has an affinity for the BBB-R from about 5 nM to about 10 μM. In one embodiment, the BBB-R binding specificity, when conjugated to or comprised in the anti-human CD19, has an affinity for the BBB-R from about 30 nM to about 1 μM. In one embodiment, the BBB-R binding specificity, when conjugated to or comprised in the anti-human CD19 antibody, has an affinity for the BBB-R from about 50 nM to about 1 μM. In one embodiment, the affinity of the BBB-R binding specificity or the anti-human CD19 antibody fusion polypeptide for the BBB-R is measured using scatchard analysis. In one embodiment, the affinity of the BBB-R binding specificity or the anti-human CD19 antibody fusion polypeptide for the BBB-R is measured using BIACORE analysis. In one embodiment, the affinity of the BBB-R binding specificity or the anti-human CD19 antibody fusion polypeptide for the BBB-R is measured using a competition ELISA.

Use of the blood-brain-barrier shuttle containing antibody fusion polypeptides

In another embodiment, herein is provided a method of increasing exposure of the CNS to an anti-human CD19 antibody, wherein the anti-human CD19 antibody is coupled to an antibody or antibody fragment which binds with low affinity to a BBB-R, thereby increasing the exposure of the CNS to the anti-human CD19 antibody. The term "coupled" includes cases wherein the anti-BBB-R antibody binding specificity is introduced as second binding specificity in an at least bispecific anti-human CD19/BBB-R antibody. In one embodiment, the increase in CNS exposure to the anti-human CD19 antibody is measured relative to the CNS exposure of an anti-human CD19 antibody coupled with a typical antibody not having lowered affinity for the BBB-R. In one embodiment, the increase in CNS exposure to the anti-human CD19 antibody is measured as a ratio of the amount of the anti-human CD19 antibody found in the CNS relative to the amount found in the serum after administration. In one embodiment, the increase in CNS exposure results in a ratio of greater than 0.1%. In one embodiment, the increase in CNS exposure to the anti-human CD19 antibody is measured relative to the CNS exposure of the anti-human CD19 antibody in the absence of a coupled anti-BBB-R antibody. In one embodiment, the increase in CNS exposure to the anti-human CD19 antibody is measured by imaging. In one embodiment, the increase in CNS exposure to the anti-human CD19 antibody is measured by an indirect readout such as a modification of one or more physiological symptoms.

A method of increasing retention in the CNS of an anti-human CD19 antibody administered to a subject, wherein the anti-human CD19 antibody is coupled to an antibody or antibody fragment, which binds with low affinity to a BBB-R, such that the retention in the CNS of the anti-human CD19 antibody is increased.

In another embodiment, herein is provided a method of optimizing the pharmacokinetics and/or pharmacodynamics of an anti-human CD19 antibody to be efficacious in the CNS of a subject, wherein the anti-human CD19 antibody is coupled to an antibody or antibody fragment, which binds with low affinity to a BBB-R, whereby the antibody or antibody fragment is selected such that its affinity for the BBB-R after coupling to the anti-human CD19 antibody results in an amount of transport of the antibody or antibody fragment conjugated to the anti-human CD19 antibody across the BBB that optimizes the pharmacokinetics and/or pharmacodynamics of the anti-human CD19 antibody in the CNS.

In another embodiment herein is provided a method of treating a neurological disorder in a mammal comprising treating the mammal with an antibody or antibody fragment, which binds a BBB-R and which is coupled to an anti-human CD19 antibody, wherein the antibody has been selected to have a low affinity for the BBB-R and thereby improves CNS uptake of the antibody and coupled anti-human CD19 antibody. In one embodiment, the treating results in lessening or elimination of disorder symptoms. In another aspect, the treating results in amelioration of the neurological disorder.

In one embodiment of all previous aspects, the anti-BBB-R antibody has an IC_{50} for the BBB-R from about 1 nM to about 100 μM. In another such embodiment, the IC_{50} is from about 5 nM to about 100 μM. In another such embodiment, the IC_{50} is from about 50 nM to about 100 μM. In another such embodiment, the IC_{50} is from about 100 nM to about 100 μM. In another embodiment, the antibody has an affinity for the BBB-R from about 5 nM to about 10 μM. In another embodiment, the antibody, when coupled to the anti-human CD19 antibody, has an affinity for the BBB-R from about 30 nM to about 1 μM. In another embodiment, the antibody, when coupled to the anti-human CD19 antibody, has an affinity for the BBB-R from about 50 nM to about 1 μM. In one embodiment, the affinity of the anti-BBB-R antibody or the anti-human CD19 antibody fusion polypeptide for the BBB-R is measured using scatchard analysis. In another embodiment, the affinity of the anti-BBB-R antibody or the anti-human CD19 antibody fusion polypeptide for the BBB-R is measured using BIACORE analysis. In another embodiment, the affinity of the anti-BBB-R antibody or the anti-human CD19 antibody fusion polypeptide for the BBB-R is measured using a competition ELISA.

In another embodiment, the anti-human CD19 antibody fusion polypeptide is labeled. In another embodiment, the anti-BBB-R antibody or fragment does not impair the binding of the BBB-R to one or more of its native ligands. In another embodiment, the anti-BBB-R antibody specifically binds to hTfR in such a manner that it does not inhibit binding of the hTfR to human transferrin. In another embodiment, the anti-human CD19 antibody fusion polypeptide is administered to a mammal. In another embodiment, the mammal is a human. In another embodiment, the mammal has a neurological disorder. In another embodiment, the neurological disorder is selected from the group consisting of Alzheimer's disease (AD), stroke, dementia, muscular dystrophy (MD), multiple sclerosis (MS), amyotrophic lateral sclerosis (ALS), cystic fibrosis, Angelman's syndrome, Liddle

syndrome, Parkinson's disease, Pick's disease, Paget's disease, cancer, and traumatic brain injury.

Non-covalent complexes as blood-brain barrier shuttles

One part of the non-covalent complex is a blood brain barrier-shuttle module (BBB-shuttle module) that is a bispecific antibody with a first binding specificity for a hapten and a second binding specificity for a blood-brain-barrier receptor (BBBR). Such a BBB-shuttle module recognizes a transcytoseable cell surface target on the blood brain barrier (such as TfR, LRPs or other targets, BBB-R) and simultaneously binds to a haptenylated anti-human CD19 antibody.

In more detail, the antibody that specifically binds to human CD19 is conjugated with a hapten and complexed by the hapten-binding site of the blood brain barrier shuttle. This complex is defined and stable and specifically delivers the haptenylated antibody that specifically binds to human CD19 over the blood brain barrier. Since the haptenylated antibody that specifically binds to human CD19 is complexed in a non-covalent manner by the blood-brain-barrier shuttle, the haptenylated antibody that specifically binds to human CD19 is on the one hand bound to its delivery vehicle (=blood-brain-barrier shuttle = bispecific antibody) during its time in the circulation but can also on the other hand be efficiently released after transcytosis. The conjugation with the hapten can be effected without interfering with the activity of the antibody that specifically binds to human CD19. The blood-brain-barrier shuttle does not contain an unusual covalent addition and therefore obviates any risk of immunogenicity. Complexes of haptenylated antibody that specifically binds to human CD19 with the bispecific antibody containing the hapten-specific binding sites confer benign biophysical behavior to the antibody that specifically binds to human CD19. Furthermore, such complexes are capable to target the load to cells or tissues which display the antigen that is recognized by the bispecific antibody's second binding specificity.

The antibody that specifically binds to human CD19 retains its functionality despite being haptenylated, as well as while being complexed by the blood-brain-barrier shuttle (=bispecific antibody). In addition, the blood-brain-barrier receptor binding site of the bispecific antibody retains its binding specificity and affinity in the presence of complexed haptenylated antibody that specifically binds to human CD19. The complexes of haptenylated antibody that specifically binds to human CD19 with the bispecific antibody as reported herein can be used to target the

antibody that specifically binds to human CD19 specifically to cells that express the blood-brain-barrier receptor. Since the haptenylated antibody that specifically binds to human CD19 is coupled in a non-covalent manner to the bispecific antibody the antibody that specifically binds to human CD19 can be released after internalization or transcytosis.

In a further aspect, an anti-human CD19 antibody according to any of the above embodiments may incorporate any of the features, singly or in combination, as described in Sections 1-5 below:

1. Antibody Affinity

In certain embodiments, an antibody provided herein has a K_D value of ≤ 1 μM, ≤ 100 nM, or ≤ 10 nM (e.g. 10^{-8} M or less, e.g. from 10^{-7} M to 10^{-8} M).

For example, K_D can be measured using a BIACORE® surface plasmon resonance assay. An assay using a BIACORE®-2000 or a BIACORE ®-3000 (BIAcore, Inc., Piscataway, NJ) is performed at 25°C with immobilized antigen CM5 chips at ~10 response units (RU). The carboxymethylated dextran biosensor chips (CM5, BIACORE, Inc.) are activated with *N*-ethyl-*N'*-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and *N*-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, to 5 μg/ml (~0.2 μM) before injection at a flow rate of 5 μl/minute to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% polysorbate 20 (TWEEN-20™) surfactant (PBST) at 25°C at a flow rate of approximately 25 μl/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIACORE ® Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (K_D) is calculated as the ratio k_{off}/k_{on} (see, e.g., Chen, Y. et al., J. Mol. Biol. 293 (1999) 865-881).

2. Antibody Fragments

In certain embodiments, an antibody provided herein is an antibody fragment. Antibody fragments include, but are not limited to, Fab, Fab', Fab'-SH, F(ab')$_2$, Fv, and scFv fragments, and other fragments described below. For a review of certain

antibody fragments, see Hudson, P.J. et al., Nat. Med. 9 (2003) 129-134. For a review of scFv fragments, see, e.g., Plueckthun, A., In; The Pharmacology of Monoclonal Antibodies, Vol. 113, Rosenburg and Moore (eds.), Springer-Verlag, New York (1994), pp. 269-315; see also WO 93/16185; US 5,571,894 and US 5,587,458. For discussion of Fab and $F(ab')_2$ fragments comprising salvage receptor binding epitope residues and having increased in vivo half-life, see US 5,869,046.

Diabodies are antibody fragments with two antigen-binding sites that may be bivalent or bispecific. See, for example, EP 0 404 097; WO 1993/01161; Hudson, P.J. et al., Nat. Med. 9 (2003) 129-134; and Holliger, P. et al., Proc. Natl. Acad. Sci. USA 90 (1993) 6444-6448. Triabodies and tetrabodies are also described in Hudson, P.J. et al., Nat. Med. 9 (20039 129-134).

Single-domain antibodies are antibody fragments comprising all or a portion of the heavy chain variable domain or all or a portion of the light chain variable domain of an antibody. In certain embodiments, a single-domain antibody is a human single-domain antibody (Domantis, Inc., Waltham, MA; see, e.g., US 6,248,516).

Antibody fragments can be made by various techniques, including but not limited to proteolytic digestion of an intact antibody as well as production by recombinant host cells (e.g. E. coli or phage), as described herein.

3. Chimeric and Humanized Antibodies

An antibody provided herein is a chimeric antibody. Certain chimeric antibodies are described, e.g., in US 4,816,567; and Morrison, S.L. et al., Proc. Natl. Acad. Sci. USA 81 (1984) 6851-6855). In one example, a chimeric antibody comprises a non-human variable region (e.g., a variable region derived from a mouse, rat, hamster, rabbit, or non-human primate, such as a monkey) and a human constant region. In a further example, a chimeric antibody is a "class switched" antibody in which the class or subclass has been changed from that of the parent antibody. Chimeric antibodies include antigen-binding fragments thereof.

A humanized antibody is a chimeric antibody is. Typically, a non-human antibody is humanized to reduce immunogenicity to humans, while retaining the specificity and affinity of the parental non-human antibody. Generally, a humanized antibody comprises one or more variable domains in which HVRs, e.g., CDRs, (or portions thereof) are derived from a non-human antibody, and FRs (or portions thereof) are

derived from human antibody sequences. A humanized antibody optionally will also comprise at least a portion of a human constant region. In some embodiments, some FR residues in a humanized antibody are substituted with corresponding residues from a non-human antibody (e.g., the antibody from which the HVR residues are derived), e.g., to restore or improve antibody specificity or affinity.

Humanized antibodies and methods of making them are reviewed, e.g., in Almagro, J.C. and Fransson, J., Front. Biosci. 13 (2008) 1619-1633, and are further described, e.g., in Riechmann, I. et al., Nature 332 (1988) 323-329; Queen, C. et al., Proc. Natl. Acad. Sci. USA 86 (1989) 10029-10033; US 5, 821,337, US 7,527,791, US 6,982,321, and US 7,087,409; Kashmiri, S.V. et al., Methods 36 (2005) 25-34 (describing specificity determining region (SDR) grafting); Padlan, E.A., Mol. Immunol. 28 (1991) 489-498 (describing "resurfacing"); Dall'Acqua, W.F. et al., Methods 36 (2005) 43-60 (describing "FR shuffling"); and Osbourn, J. et al., Methods 36 (2005) 61-68 and Klimka, A. et al., Br. J. Cancer 83 (2000) 252-260 (describing the "guided selection" approach to FR shuffling).

Human framework regions that may be used for humanization include but are not limited to: framework regions selected using the "best-fit" method (see, e.g., Sims, M.J. et al., J. Immunol. 151 (1993) 2296-2308; framework regions derived from the consensus sequence of human antibodies of a particular subgroup of light or heavy chain variable regions (see, e.g., Carter, P. et al., Proc. Natl. Acad. Sci. USA 89 (1992) 4285-4289; and Presta, L.G. et al., J. Immunol. 151 (1993) 2623-2632); human mature (somatically mutated) framework regions or human germline framework regions (see, e.g., Almagro, J.C. and Fransson, J., Front. Biosci. 13 (2008) 1619-1633); and framework regions derived from screening FR libraries (see, e.g., Baca, M. et al., J. Biol. Chem. 272 (1997) 10678-10684 and Rosok, M.J. et al., J. Biol. Chem. 271 (19969 22611-22618).

4. Multispecific Antibodies

In certain embodiments, an antibody provided herein is a multispecific antibody, e.g. a bispecific antibody. Multispecific antibodies are monoclonal antibodies that have binding specificities for at least two different sites. In certain embodiments, one of the binding specificities is for human CD19 and the other is for any other antigen. In certain embodiments, bispecific antibodies may bind to two different epitopes of human CD19. Bispecific antibodies may also be used to localize

cytotoxic agents to cells which express human CD19. Bispecific antibodies can be prepared as full length antibodies or antibody fragments.

Techniques for making multispecific antibodies include, but are not limited to, recombinant co-expression of two immunoglobulin heavy chain-light chain pairs having different specificities (see Milstein, C. and Cuello, A.C., Nature 305 (1983) 537-540, WO 93/08829, and Traunecker, A. et al., EMBO J. 10 (1991) 3655-3659), and "knob-in-hole" engineering (see, e.g., US 5,731,168). Multi-specific antibodies may also be made by engineering electrostatic steering effects for making antibody Fc-heterodimeric molecules (WO 2009/089004); cross-linking two or more antibodies or fragments (see, e.g., US 4,676,980, and Brennan, M. et al., Science 229 (1985) 81-83); using leucine zippers to produce bi-specific antibodies (see, e.g., Kostelny, S.A. et al., J. Immunol. 148 (1992) 1547-1553; using "diabody" technology for making bispecific antibody fragments (see, e.g., Holliger, P. et al., Proc. Natl. Acad. Sci. USA 90 (1993) 6444-6448); and using single-chain Fv (sFv) dimers (see, e.g. Gruber, M et al., J. Immunol. 152 (1994) 5368-5374); and preparing trispecific antibodies as described, e.g., in Tutt, A. et al., J. Immunol. 147 (1991) 60-69).

Engineered antibodies with three or more functional antigen binding sites, including "Octopus antibodies," are also included herein (see, e.g. US 2006/0025576).

The antibody or fragment herein also includes a "Dual Acting Fab" or "DAF" comprising an antigen binding site that binds to human CD19 as well as another, different antigen (see, US 2008/0069820, for example).

The antibody or fragment herein also includes multispecific antibodies described in WO 2009/080251, WO 2009/080252, WO 2009/080253, WO 2009/080254, WO 2010/112193, WO 2010/115589, WO 2010/136172, WO 2010/145792, and WO 2010/145793.

5. Antibody Variants

In certain embodiments, amino acid sequence variants of the antibodies provided herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of an antibody may be prepared by introducing appropriate modifications

into the nucleotide sequence encoding the antibody, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution can be made to arrive at the final construct, provided that the final construct possesses the desired characteristics, e.g., antigen-binding.

a) Substitution, Insertion, and Deletion Variants

In certain embodiments, antibody variants having one or more amino acid substitutions are provided. Sites of interest for substitutional mutagenesis include the HVRs and FRs. Conservative substitutions are shown in the Table below under the heading of "preferred substitutions". More substantial changes are provided in Table 1 under the heading of "exemplary substitutions," and as further described below in reference to amino acid side chain classes. Amino acid substitutions may be introduced into an antibody of interest and the products screened for a desired activity, e.g., retained/improved antigen binding, decreased immunogenicity, or improved ADCC or CDC.

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Asp, Lys; Arg	Gln
Asp (D)	Glu; Asn	Glu
Cys (C)	Ser; Ala	Ser
Gln (Q)	Asn; Glu	Asn
Glu (E)	Asp; Gln	Asp
Gly (G)	Ala	Ala
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe; Norleucine	Leu
Leu (L)	Norleucine; Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Trp; Leu; Val; Ile; Ala; Tyr	Tyr

Original Residue	Exemplary Substitutions	Preferred Substitutions
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Val; Ser	Ser
Trp (W)	Tyr; Phe	Tyr
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala; Norleucine	Leu

Amino acids may be grouped according to common side-chain properties:

(1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile;

(2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;

(3) acidic: Asp, Glu;

(4) basic: His, Lys, Arg;

(5) residues that influence chain orientation: Gly, Pro;

(6) aromatic: Trp, Tyr, Phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class.

One type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (*e.g.* a humanized or human antibody). Generally, the resulting variant(s) selected for further study will have modifications (e.g., improvements) in certain biological properties (e.g., increased affinity, reduced immunogenicity) relative to the parent antibody and/or will have substantially retained certain biological properties of the parent antibody. An exemplary substitutional variant is an affinity matured antibody, which may be conveniently generated, e.g., using phage display-based affinity maturation techniques such as those described herein. Briefly, one or more HVR residues are mutated and the variant antibodies displayed on phage and screened for a particular biological activity (e.g. binding affinity).

Alterations (e.g., substitutions) may be made in HVRs, e.g., to improve antibody affinity. Such alterations may be made in HVR "hotspots," i.e., residues encoded by codons that undergo mutation at high frequency during the somatic maturation process (see, e.g., Chowdhury, P.S., Methods Mol. Biol. 207 (2008) 179-196),

and/or residues that contact antigen, with the resulting variant VH or VL being tested for binding affinity. Affinity maturation by constructing and reselecting from secondary libraries has been described, e.g., in Hoogenboom, H.R. et al. in Methods in Molecular Biology 178 (2002) 1-37. In some embodiments of affinity maturation, diversity is introduced into the variable genes chosen for maturation by any of a variety of methods (e.g., error-prone PCR, chain shuffling, or oligonucleotide-directed mutagenesis). A secondary library is then created. The library is then screened to identify any antibody variants with the desired affinity. Another method to introduce diversity involves HVR-directed approaches, in which several HVR residues (e.g., 4-6 residues at a time) are randomized. HVR residues involved in antigen binding may be specifically identified, e.g., using alanine scanning mutagenesis or modeling. CDR-H3 and CDR-L3 in particular are often targeted.

In certain embodiments, substitutions, insertions, or deletions may occur within one or more HVRs so long as such alterations do not substantially reduce the ability of the antibody to bind antigen. For example, conservative alterations (e.g., conservative substitutions as provided herein) that do not substantially reduce binding affinity may be made in HVRs. Such alterations may, for example, be outside of antigen contacting residues in the HVRs. In certain embodiments of the variant VH and VL sequences provided above, each HVR either is unaltered, or contains no more than one, two or three amino acid substitutions.

A useful method for identification of residues or regions of an antibody that may be targeted for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham, B.C. and Wells, J.A., Science 244 (1989) 1081-1085. In this method, a residue or group of target residues (e.g., charged residues such as arg, asp, his, lys, and glu) are identified and replaced by a neutral or negatively charged amino acid (e.g., alanine or polyalanine) to determine whether the interaction of the antibody with antigen is affected. Further substitutions may be introduced at the amino acid locations demonstrating functional sensitivity to the initial substitutions. Alternatively, or additionally, a crystal structure of an antigen-antibody complex to identify contact points between the antibody and antigen. Such contact residues and neighboring residues may be targeted or eliminated as candidates for substitution. Variants may be screened to determine whether they contain the desired properties.

Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include an antibody with an N-terminal methionyl residue. Other insertional variants of the antibody molecule include the fusion to the N- or C-terminus of the antibody to an enzyme (e.g. for ADEPT) or a polypeptide which increases the serum half-life of the antibody.

b) Glycosylation variants

In certain embodiments, an antibody provided herein is altered to increase or decrease the extent to which the antibody is glycosylated. Addition or deletion of glycosylation sites to an antibody may be conveniently accomplished by altering the amino acid sequence such that one or more glycosylation sites is created or removed.

Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. Native antibodies produced by mammalian cells typically comprise a branched, biantennary oligosaccharide that is generally attached by an N-linkage to Asn297 of the CH2 domain of the Fc region. See, e.g., Wright, A. and Morrison, S.L., TIBTECH 15 (1997) 26-32. The oligosaccharide may include various carbohydrates, e.g., mannose, N-acetyl glucosamine (GlcNAc), galactose, and sialic acid, as well as a fucose attached to a GlcNAc in the "stem" of the biantennary oligosaccharide structure. In some embodiments, modifications of the oligosaccharide in an antibody as reported herein may be made in order to create antibody variants with certain improved properties.

In one embodiment, antibody variants are provided having a carbohydrate structure that lacks fucose attached (directly or indirectly) to an Fc region. For example, the amount of fucose in such antibody may be from 1% to 80%, from 1% to 65%, from 5% to 65% or from 20% to 40%. The amount of fucose is determined by calculating the average amount of fucose within the sugar chain at Asn297, relative to the sum of all glycostructures attached to Asn 297 (e. g. complex, hybrid and high mannose structures) as measured by MALDI-TOF mass spectrometry, as described in WO 2008/077546, for example. Asn297 refers to the asparagine residue located at about position 297 in the Fc region (EU numbering of Fc-region residues according to Kabat); however, Asn297 may also be located about ± 3 amino acids upstream or downstream of position 297, i.e., between positions 294

and 300, due to minor sequence variations in antibodies. Such fucosylation variants may have improved ADCC function. See, e.g., US 2003/0157108; US 2004/0093621. Examples of publications related to "defucosylated" or "fucose-deficient" antibody variants include: US 2003/0157108; WO 2000/61739; WO 2001/29246; US 2003/0115614; US 2002/0164328; US 2004/0093621; US 2004/0132140; US 2004/0110704; US 2004/0110282; US 2004/0109865; WO 2003/085119; WO 2003/084570; WO 2005/035586; WO 2005/035778; WO 2005/053742; WO 2002/031140; Okazaki, A. et al., J. Mol. Biol. 336 (2004) 1239-1249; Yamane-Ohnuki, N. et al., Biotech. Bioeng. 87 (2004) 614-622. Examples of cell lines capable of producing defucosylated antibodies include Lec13 CHO cells deficient in protein fucosylation (Ripka, J. et al., Arch. Biochem. Biophys. 249 (1986) 533-545; US 2003/0157108; and WO 2004/056312, especially at Example 11), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene, *FUT8,* knockout CHO cells (see, e.g., Yamane-Ohnuki, N. et al., Biotech. Bioeng. 87 (2004) 614-622; Kanda, Y. et al., Biotechnol. Bioeng. 94 (2006) 680-688; and WO 2003/085107).

Antibodies variants are further provided with bisected oligosaccharides, e.g., in which a biantennary oligosaccharide attached to the Fc region of the antibody is bisected by GlcNAc. Such antibody variants may have reduced fucosylation and/or improved ADCC function. Examples of such antibody variants are described, e.g., in WO 2003/011878; US 6,602,684; and US 2005/0123546. Antibody variants with at least one galactose residue in the oligosaccharide attached to the Fc region are also provided. Such antibody variants may have improved CDC function. Such antibody variants are described, e.g., in WO 1997/30087; WO 1998/58964; and WO 1999/22764.

c) Fc-region variants

In certain embodiments, one or more amino acid modifications may be introduced into the Fc-region of an antibody provided herein, thereby generating an Fc-region variant. The Fc-region variant may comprise a human Fc-region sequence (*e.g.*, a human IgG1, IgG2, IgG3 or IgG4 Fc-region) comprising an amino acid modification (*e.g.* a substitution) at one or more amino acid positions.

In certain embodiments, herein is provided an antibody variant that possesses some but not all effector functions, which make it a desirable candidate for applications in which the half-life of the antibody *in vivo* is important yet certain effector

functions (such as complement and ADCC) are unnecessary or deleterious. *In vitro* and/or *in vivo* cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity), but retains FcRn binding ability. The primary cells for mediating ADCC, NK cells, express Fc(RIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch, J.V. and Kinet, J.P., Annu. Rev. Immunol. 9 (1991) 457-492. Non-limiting examples of *in vitro* assays to assess ADCC activity of a molecule of interest is described in US 5,500,362 (see, e.g. Hellstrom, I. et al., Proc. Natl. Acad. Sci. USA 83 (1986) 7059-7063; and Hellstrom, I. et al., Proc. Natl. Acad. Sci. USA 82 (1985) 1499-1502); US 5,821,337 (see Bruggemann, M. et al., J. Exp. Med. 166 (1987) 1351-1361). Alternatively, non-radioactive assays methods may be employed (see, for example, ACTI™ non-radioactive cytotoxicity assay for flow cytometry (CellTechnology, Inc. Mountain View, CA; and CytoTox 96® non-radioactive cytotoxicity assay (Promega, Madison, WI). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, *e.g.*, in an animal model such as that disclosed in Clynes, R. et al., Proc. Natl. Acad. Sci. USA 95 (1998) 652-656. C1q binding assays may also be carried out to confirm that the antibody is unable to bind C1q and hence lacks CDC activity. See, e.g., C1q and C3c binding ELISA in WO 2006/029879 and WO 2005/100402. To assess complement activation, a CDC assay may be performed (see, for example, Gazzano-Santoro, H. et al., J. Immunol. Methods 202 (1996) 163-171; Cragg, M.S. et al., Blood 101 (2003) 1045-1052; and Cragg, M.S. and M.J. Glennie, Blood 103 (2004) 2738-2743). FcRn binding and *in vivo* clearance/half-life determinations can also be performed using methods known in the art (see, e.g., Petkova, S.B. et al., Int. Immunol. 18 (2006: 1759-1769).

Antibodies with reduced effector function include those with substitution of one or more of Fc-region residues 238, 265, 269, 270, 297, 327 and 329 (US 6,737,056). Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327, including the so-called "DANA" Fc mutant with substitution of residues 265 and 297 to alanine (US 7,332,581).

Certain antibody variants with improved or diminished binding to FcRs are described. (See, e.g., US 6,737,056; WO 2004/056312, and Shields, R.L. et al., J. Biol. Chem. 276 (2001) 6591-6604)

In certain embodiments, an antibody variant comprises an Fc-region with one or more amino acid substitutions which improve ADCC, e.g., substitutions at positions 298, 333, and/or 334 of the Fc-region (EU numbering of residues).

In some embodiments, alterations are made in the Fc-region that result in altered (*i.e.*, either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC), e.g., as described in US 6,194,551, WO 99/51642, and Idusogie, E.E. et al., J. Immunol. 164 (2000) 4178-4184.

Antibodies with increased half-lives and improved binding to the neonatal Fc receptor (FcRn), which is responsible for the transfer of maternal IgGs to the fetus (Guyer, R.L. et al., J. Immunol. 117 (1976) 587-593, and Kim, J.K. et al., J. Immunol. 24 (1994) 2429-2434), are described in US 2005/0014934. Those antibodies comprise an Fc-region with one or more substitutions therein which improve binding of the Fc-region to FcRn. Such Fc variants include those with substitutions at one or more of Fc-region residues: 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424 or 434, e.g., substitution of Fc-region residue 434 (US 7,371,826).

See also Duncan, A.R. and Winter, G., Nature 322 (1988) 738-740; US 5,648,260; US 5,624,821; and WO 94/29351 concerning other examples of Fc-region variants.

d) Cysteine engineered antibody variants

In certain embodiments, it may be desirable to create cysteine engineered antibodies, e.g., "thioMAbs," in which one or more residues of an antibody are substituted with cysteine residues. In particular embodiments, the substituted residues occur at accessible sites of the antibody. By substituting those residues with cysteine, reactive thiol groups are thereby positioned at accessible sites of the antibody and may be used to conjugate the antibody to other moieties, such as drug moieties or linker-drug moieties, to create an immunoconjugate, as described further herein. In certain embodiments, any one or more of the following residues may be substituted with cysteine: V205 (Kabat numbering) of the light chain; A118 (EU numbering) of the heavy chain; and S400 (EU numbering) of the heavy chain

Fc region. Cysteine engineered antibodies may be generated as described, e.g., in US 7,521,541.

e) Antibody Derivatives

In certain embodiments, an antibody provided herein may be further modified to contain additional non-proteinaceous moieties that are known in the art and readily available. The moieties suitable for derivatization of the antibody include but are not limited to water soluble polymers. Non-limiting examples of water soluble polymers include, but are not limited to, polyethylene glycol (PEG), copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propropylene glycol homopolymers, prolypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. The polymer may be of any molecular weight, and may be branched or unbranched. The number of polymers attached to the antibody may vary, and if more than one polymer is attached, they can be the same or different molecules. In general, the number and/or type of polymers used for derivatization can be determined based on considerations including, but not limited to, the particular properties or functions of the antibody to be improved, whether the antibody derivative will be used in a therapy under defined conditions, etc.

In another embodiment, conjugates of an antibody and non-proteinaceous moiety that may be selectively heated by exposure to radiation are provided. In one embodiment, the non-proteinaceous moiety is a carbon nanotube (Kam, N.W. et al., Proc. Natl. Acad. Sci. USA 102 (2005) 11600-11605). The radiation may be of any wavelength, and includes, but is not limited to, wavelengths that do not harm ordinary cells, but which heat the non-proteinaceous moiety to a temperature at which cells proximal to the antibody-non-proteinaceous moiety are killed.

B. Recombinant Methods and Compositions

Antibodies may be produced using recombinant methods and compositions, e.g., as described in US 4,816,567. In one embodiment, isolated nucleic acid encoding an

anti-human CD19 antibody described herein is provided. Such nucleic acid may encode an amino acid sequence comprising the VL and/or an amino acid sequence comprising the VH of the antibody (e.g., the light and/or heavy chains of the antibody). In a further embodiment, one or more vectors (e.g., expression vectors) comprising such nucleic acid are provided. In a further embodiment, a host cell comprising such nucleic acid is provided. In one such embodiment, a host cell comprises (e.g., has been transformed with): (1) a vector comprising a nucleic acid that encodes an amino acid sequence comprising the VL of the antibody and an amino acid sequence comprising the VH of the antibody, or (2) a first vector comprising a nucleic acid that encodes an amino acid sequence comprising the VL of the antibody and a second vector comprising a nucleic acid that encodes an amino acid sequence comprising the VH of the antibody. In one embodiment, the host cell is eukaryotic, e.g. a Chinese Hamster Ovary (CHO) cell or lymphoid cell (e.g., Y0, NS0, Sp20 cell). In one embodiment, a method of making an anti-human CD19 antibody is provided, wherein the method comprises culturing a host cell comprising a nucleic acid encoding the antibody, as provided above, under conditions suitable for expression of the antibody, and optionally recovering the antibody from the host cell (or host cell culture medium).

For recombinant production of an anti-human CD19 antibody, nucleic acid encoding an antibody, e.g., as described above, is isolated and inserted into one or more vectors for further cloning and/or expression in a host cell. Such nucleic acid may be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the antibody).

Suitable host cells for cloning or expression of antibody-encoding vectors include prokaryotic or eukaryotic cells described herein. For example, antibodies may be produced in bacteria, in particular when glycosylation and Fc effector function are not needed. For expression of antibody fragments and polypeptides in bacteria, see, e.g., US 5,648,237, US 5,789,199, and US 5,840,523. (See also Charlton, K.A., In: Methods in Molecular Biology, Vol. 248, Lo, B.K.C. (ed.), Humana Press, Totowa, NJ (2003), pp. 245-254, describing expression of antibody fragments in *E. coli*.) After expression, the antibody may be isolated from the bacterial cell paste in a soluble fraction and can be further purified.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for antibody-encoding vectors, including

fungi and yeast strains whose glycosylation pathways have been "humanized," resulting in the production of an antibody with a partially or fully human glycosylation pattern. See Gerngross, T.U., Nat. Biotech. 22 (2004) 1409-1414; and Li, H. et al., Nat. Biotech. 24 (2006) 210-215.

Suitable host cells for the expression of glycosylated antibody are also derived from multicellular organisms (invertebrates and vertebrates). Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures can also be utilized as hosts. See, e.g., US 5,959,177, US 6,040,498, US 6,420,548, US 7,125,978, and US 6,417,429 (describing PLANTIBODIES™ technology for producing antibodies in transgenic plants).

Vertebrate cells may also be used as hosts. For example, mammalian cell lines that are adapted to grow in suspension may be useful. Other examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7); human embryonic kidney line (293 or 293 cells as described, e.g., in Graham, F.L. et al., J. Gen Virol. 36 (1977) 59-74); baby hamster kidney cells (BHK); mouse sertoli cells (TM4 cells as described, e.g., in Mather, J.P., Biol. Reprod. 23 (1980) 243-252); monkey kidney cells (CV1); African green monkey kidney cells (VERO-76); human cervical carcinoma cells (HELA); canine kidney cells (MDCK; buffalo rat liver cells (BRL 3A); human lung cells (W138); human liver cells (Hep G2); mouse mammary tumor (MMT 060562); TRI cells, as described, e.g., in Mather, J.P. et al., Annals N.Y. Acad. Sci. 383 (1982) 44-68; MRC 5 cells; and FS4 cells. Other useful mammalian host cell lines include Chinese hamster ovary (CHO) cells, including $DHFR^-$ CHO cells (Urlaub, G. et al., Proc. Natl. Acad. Sci. USA 77 (1980) 4216-4220); and myeloma cell lines such as Y0, NS0 and Sp2/0. For a review of certain mammalian host cell lines suitable for antibody production, see, e.g., Yazaki, P. and Wu, A.M., Methods in Molecular Biology, Vol. 248, Lo, B.K.C. (ed.), Humana Press, Totowa, NJ (2004), pp. 255-268.

C. Assays

Anti-human CD19 antibodies provided herein may be identified, screened for, or characterized for their physical/chemical properties and/or biological activities by various assays known in the art.

1. Binding assays and other assays

In one aspect, an antibody as reported herein is tested for its antigen binding activity, e.g., by known methods such as ELISA, Western blot, etc.

2. Activity assays

In one aspect, assays are provided for identifying anti-human CD19 antibodies thereof having biological activity. Biological activity may include, e.g., inhibition of B-cell proliferation or killing of B-cells. Antibodies having such biological activity in vivo and/or in vitro are also provided.

In certain embodiments, an antibody as reported herein is tested for such biological activity.

D. Immunoconjugates

Herein are also provided immunoconjugates comprising an anti-human CD19 antibody as reported herein conjugated to one or more cytotoxic agents, such as chemotherapeutic agents or drugs, growth inhibitory agents, toxins (e.g., protein toxins, enzymatically active toxins of bacterial, fungal, plant, or animal origin, or fragments thereof), or radioactive isotopes.

In one embodiment, an immunoconjugate is an antibody-drug conjugate (ADC) in which an antibody is conjugated to one or more drugs, including but not limited to a maytansinoid (see US 5,208,020, US 5,416,064 and EP 0 425 235 B1); an auristatin such as monomethyl auristatin drug moieties DE and DF (MMAE and MMAF) (see US 5,635,483, US 5,780,588, and US 7,498,298); a dolastatin; a calicheamicin or derivative thereof (see US 5,712,374, US 5,714,586, US 5,739,116, US 5,767,285, US 5,770,701, US 5,770,710, US 5,773,001, and US 5,877,296; Hinman, L.M. et al., Cancer Res. 53 (1993) 3336-3342; and Lode, H.N. et al., Cancer Res. 58 (1998) 2925-2928); an anthracycline such as daunomycin or doxorubicin (see Kratz, F. et al., Curr. Med. Chem. 13 (2006) 477-523; Jeffrey, S.C. et al., Bioorg. Med. Chem. Lett. 16 (2006) 358-362; Torgov,

M.Y. et al., Bioconjug. Chem. 16 (2005) 717-721; Nagy, A. et al., Proc. Natl. Acad. Sci. USA 97 (2000) 829-834; Dubowchik, G.M. et al., Bioorg. & Med. Chem. Letters 12 (2002) 1529-1532; King, H.D. et al., J. Med. Chem. 45 (20029 4336-4343; and US 6,630,579); methotrexate; vindesine; a taxane such as docetaxel, paclitaxel, larotaxel, tesetaxel, and ortataxel; a trichothecene; and CC1065.

In another embodiment, an immunoconjugate comprises an antibody as described herein conjugated to an enzymatically active toxin or fragment thereof, including but not limited to diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

In another embodiment, an immunoconjugate comprises an antibody as described herein conjugated to a radioactive atom to form a radioconjugate. A variety of radioactive isotopes are available for the production of radioconjugates. Examples include At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32}, Pb^{212} and radioactive isotopes of Lu. When the radioconjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example TC^{99m} or I^{123}, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, MRI), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

Conjugates of an antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta, E.S. et al., Science 238 (1987) 1098-1104. Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triamine pentaacetic acid (MX-DTPA) is

an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO 94/11026. The linker may be a "cleavable linker" facilitating release of a cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari, R.V. et al., Cancer Res. 52 (1992) 127-131; US 5,208,020) may be used.

The immunoconjugates or ADCs herein expressly contemplate, but are not limited to such conjugates prepared with cross-linker reagents including, but not limited to, BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate) which are commercially available (e.g., from Pierce Biotechnology, Inc., Rockford, IL., U.S.A).

E. Methods and Compositions for Diagnostics and Detection

In certain embodiments, any of the anti-human CD19 antibodies provided herein is useful for detecting the presence of human CD19 presenting cells in a biological sample. The term "detecting" as used herein encompasses quantitative or qualitative detection. In certain embodiments, a biological sample comprises a cell or tissue, such as e.g. blood, blood serum, or blood plasma.

In one embodiment, an anti- human CD19 antibody for use in a method of diagnosis or detection is provided. In a further aspect, a method of detecting the presence of human CD19 presenting cells in a biological sample is provided. In certain embodiments, the method comprises contacting the biological sample with an anti-human CD19 antibody as described herein under conditions permissive for binding of the anti-human CD19 antibody to human CD19, and detecting whether a complex is formed between the anti-human CD19 antibody and human CD19. Such method may be an *in vitro* or *in vivo* method. In one embodiment, an anti-human CD19 antibody is used to select subjects eligible for therapy with an anti-human CD19 antibody, e.g. where human CD19 is a biomarker for selection of patients.

Exemplary disorders that may be diagnosed using an antibody as reported herein include B-cell cancers, such as B-cell lymphoma and B-cell leukemias except for multiple myeloma, e.g. non-Hodgkin lymphoma and acute lymphoblastic leukemia.

In certain embodiments, labeled anti-human CD19 antibodies are provided. Labels include, but are not limited to, labels or moieties that are detected directly (such as fluorescent, chromophoric, electron-dense, chemiluminescent, and radioactive labels), as well as moieties, such as enzymes or ligands, that are detected indirectly, e.g., through an enzymatic reaction or molecular interaction. Exemplary labels include, but are not limited to, the radioisotopes ^{32}P, ^{14}C, ^{125}I, ^{3}H, and ^{131}I, fluorophores such as rare earth chelates or fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, luceriferases, e.g., firefly luciferase and bacterial luciferase (US 4,737,456), luciferin, 2,3-dihydrophthalazinediones, horseradish peroxidase (HRP), alkaline phosphatase, β-galactosidase, glucoamylase, lysozyme, saccharide oxidases, e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase, heterocyclic oxidases such as uricase and xanthine oxidase, coupled with an enzyme that employs hydrogen peroxide to oxidize a dye precursor such as HRP, lactoperoxidase, or microperoxidase, biotin/avidin, spin labels, bacteriophage labels, stable free radicals, and the like.

F. Pharmaceutical Formulations

Pharmaceutical formulations of an anti-human CD19 antibody as reported herein are prepared by mixing such antibody having the desired degree of purity with one or more optional pharmaceutically acceptable carriers (Remington's Pharmaceutical Sciences, 16th edition, Osol, A. (ed.) (1980)), in the form of lyophilized formulations or aqueous solutions. Pharmaceutically acceptable carriers are generally nontoxic to recipients at the dosages and concentrations employed, and include, but are not limited to: buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyl dimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride; benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as poly(vinylpyrrolidone); amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal

complexes (*e.g.* Zn-protein complexes); and/or non-ionic surfactants such as polyethylene glycol (PEG). Exemplary pharmaceutically acceptable carriers herein further include interstitial drug dispersion agents such as soluble neutral-active hyaluronidase glycoproteins (sHASEGP), for example, human soluble PH-20 hyaluronidase glycoproteins, such as rhuPH20 (HYLENEX®, Baxter International, Inc.). Certain exemplary sHASEGPs and methods of use, including rhuPH20, are described in US 2005/0260186 and US 2006/0104968. In one aspect, a sHASEGP is combined with one or more additional glycosaminoglycanases such as chondroitinases.

Exemplary lyophilized antibody formulations are described in US 6,267,958. Aqueous antibody formulations include those described in US 6,171,586 and WO 2006/044908, the latter formulations including a histidine-acetate buffer.

The formulation herein may also contain more than one active ingredients as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Such active ingredients are suitably present in combination in amounts that are effective for the purpose intended.

Active ingredients may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methyl methacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. (ed.) (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.* films, or microcapsules.

The formulations to be used for *in vivo* administration are generally sterile. Sterility may be readily accomplished, e.g., by filtration through sterile filtration membranes.

G. Therapeutic Methods and Compositions

Any of the anti-human CD19 antibodies provided herein may be used in therapeutic methods, either alone or in combination, either as monospecific antibody or as multispecific antibody.

CD19 is expressed on most B-cells (pan-B-cell marker) with the exception of stem cells and plasma cells, and is frequently expressed on most human B-cell malignancies (tumor associated antigen), such as lymphoma and leukemias except for multiple myeloma, e.g. in non-Hodgkin lymphoma and acute lymphoblastic leukemia.

Bispecific antibodies recognizing two cell surface proteins on different cell populations hold the promise to redirect cytotoxic immune cells for destruction of pathogenic target cells.

In one aspect, an anti-human CD19 antibody for use as a medicament is provided. In further aspects, an anti-human CD19 antibody for use in treating a B-cell cancer is provided. In certain embodiments, an anti-human CD19 antibody for use in a method of treatment is provided. In certain embodiments, herein is provided an anti-human CD19 antibody for use in a method of treating an individual having a B-cell cancer comprising administering to the individual an effective amount of the anti-human CD19 antibody. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent. In further embodiments, herein is provided an anti-human CD19 antibody for use depleting B-cells. In certain embodiments, herein is provided an anti-human CD19 antibody for use in a method of depleting B-cells in an individual comprising administering to the individual an effective of the anti-human CD19 antibody to deplete B-cells. An "individual" according to any of the above embodiments is preferably a human. The B-cell cancer is in one embodiment a B-cell lymphoma or a B-cell leukemia. In one embodiment the B-cell cancer is non-Hodgkin lymphoma or acute lymphoblastic leukemia.

In further aspects, an anti-human CD19 antibody for use in cancer immunotherapy is provided. In certain embodiments, an anti-human CD19 antibody for use in a method of cancer immunotherapy is provided. An "individual" according to any of the above embodiments is preferably a human.

In a further aspect, herein is provided for the use of an anti-human CD19 antibody in the manufacture or preparation of a medicament. In one embodiment, the medicament is for treatment of a B-cell cancer. In a further embodiment, the medicament is for use in a method of treating a B-cell cancer comprising administering to an individual having a B-cell cancer an effective amount of the medicament. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, e.g., as described below. In a further embodiment, the medicament is for depleting B-cells. In a further embodiment, the medicament is for use in a method of depleting B-cells in an individual comprising administering to the individual an amount effective of the medicament to deplete B-cells. An "individual" according to any of the above embodiments may be a human. The B-cell cancer is in one embodiment a B-cell lymphoma or a B-cell leukemia. In one embodiment the B-cell cancer is non-Hodgkin lymphoma or acute lymphoblastic leukemia.

In a further aspect, herein is provided a method for treating a B-cell cancer. In one embodiment, the method comprises administering to an individual having such B-cell cancer an effective amount of an anti-human CD19 antibody. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, as described below. An "individual" according to any of the above embodiments may be a human. The B-cell cancer is in one embodiment a B-cell lymphoma or a B-cell leukemia. In one embodiment the B-cell cancer is non-Hodgkin lymphoma or acute lymphoblastic leukemia.

In a further aspect, herein is provided a method for depleting B-cells in an individual. In one embodiment, the method comprises administering to the individual an effective amount of an anti-human CD19 antibody to deplete B-cells. In one embodiment, an "individual" is a human. The B-cell cancer is in one embodiment a B-cell lymphoma or a B-cell leukemia. In one embodiment the B-cell cancer is non-Hodgkin lymphoma or acute lymphoblastic leukemia.

In a further aspect, herein is provided pharmaceutical formulations comprising any of the anti-human CD19 antibodies as reported herein, e.g., for use in any of the above therapeutic methods. In one embodiment, a pharmaceutical formulation comprises any of the anti-human CD19 antibodies as reported herein and a pharmaceutically acceptable carrier. In another embodiment, a pharmaceutical

formulation comprises any of the anti-human CD19 antibodies as reported herein and at least one additional therapeutic agent.

Antibodies as reported herein can be used either alone or in combination with other agents in a therapy. For instance, an antibody as reported herein may be co-administered with at least one additional therapeutic agent.

Such combination therapies noted above encompass combined administration (where two or more therapeutic agents are included in the same or separate formulations), and separate administration, in which case, administration of the antibody as reported herein can occur prior to, simultaneously, and/or following, administration of the additional therapeutic agent or agents. In one embodiment, administration of the anti-human CD19 antibody and administration of an additional therapeutic agent occur within about one month, or within about one, two or three weeks, or within about one, two, three, four, five, or six days, of each other.

An antibody as reported herein (and any additional therapeutic agent) can be administered by any suitable means, including parenteral, intrapulmonary, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral infusions include intramuscular, intravenous, intraarterial, intraperitoneal, or subcutaneous administration. Dosing can be by any suitable route, e.g. by injections, such as intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. Various dosing schedules including but not limited to single or multiple administrations over various time-points, bolus administration, and pulse infusion are contemplated herein.

Antibodies as reported herein would be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The antibody need not be, but is optionally formulated with one or more agents currently used to prevent or treat the disorder in question. The effective amount of such other agents depends on the amount of antibody present in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as described herein, or about from 1

to 99% of the dosages described herein, or in any dosage and by any route that is empirically/clinically determined to be appropriate.

For the prevention or treatment of disease, the appropriate dosage of an antibody as reported herein (when used alone or in combination with one or more other additional therapeutic agents) will depend on the type of disease to be treated, the type of antibody, the severity and course of the disease, whether the antibody is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, and the discretion of the attending physician. The antibody is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 µg/kg to 15 mg/kg (e.g. 0.5 mg/kg - 10 mg/kg) of antibody can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. One exemplary dosage of the antibody would be in the range from about 0.05 mg/kg to about 10 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. Such doses may be administered intermittently, e.g. every week or every three weeks (*e.g.* such that the patient receives from about two to about twenty, or *e.g.* about six doses of the antibody). An initial higher loading dose, followed by one or more lower doses may be administered. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

Herein are further provided methods for treating an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, and a bone disease, comprising administering to a patient diagnosed as having such disease (and therefore being in need of such a therapy) an antibody specifically binding to human CD19 as reported herein. The antibody may be administered alone, in a pharmaceutical composition, or alternatively in combination with other medicaments for treating an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease. The antibody is administered in a pharmaceutically effective amount.

Herein are further provided the use of an antibody as reported herein for the treatment of an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis or a bone disease, and for the manufacture of a pharmaceutical composition comprising an antibody as reported herein. In addition, herein is provided a method for the manufacture of a pharmaceutical composition comprising an antibody as reported herein.

Herein are further provided an antibody as reported herein for the treatment of an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease.

Further provided herein is the use of an antibody as reported herein for the manufacture of a pharmaceutical composition for the treatment of an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease. The antibody is used in a pharmaceutically effective amount.

Further provided herein is the use of an antibody as reported herein for the manufacture of a pharmaceutical composition for the treatment of an inflammatory disease, an autoimmune disease, rheumatoid arthritis, lupus, psoriasis, or a bone disease. The antibody is used in a pharmaceutically effective amount.

It is understood that any of the above formulations or therapeutic methods may be carried out using an immunoconjugate as reported herein in place of or in addition to an anti-human CD19 antibody.

III. Articles of Manufacture

In another aspect, an article of manufacture containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an antibody as reported herein. The label or package insert indicates that the composition is used for treating the condition of choice.

Moreover, the article of manufacture may comprise (a) a first container with a composition contained therein, wherein the composition comprises an antibody as reported herein; and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. The article of manufacture in this embodiment may further comprise a package insert indicating that the compositions can be used to treat a particular condition. Alternatively, or additionally, the article of manufacture may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

It is understood that any of the above articles of manufacture may include an immunoconjugate as reported herein in place of or in addition to an anti-human CD19 antibody.

IV. Description of the Sequence Listing

SEQ ID NO: 1	murine anti-human CD19 antibody 8B8 heavy chain variable domain
SEQ ID NO: 2	murine anti-human CD19 antibody 8B8 light chain variable domain
SEQ ID NO: 3	murine anti-human CD19 antibody 8B8 HVR-H1
SEQ ID NO: 4	murine anti-human CD19 antibody 8B8 HVR-H2
SEQ ID NO: 5	murine anti-human CD19 antibody 8B8 HVR-H3
SEQ ID NO: 6	murine anti-human CD19 antibody 8B8 HVR-L1
SEQ ID NO: 7	murine anti-human CD19 antibody 8B8 HVR-L2
SEQ ID NO: 8	murine anti-human CD19 antibody 8B8 HVR-L3
SEQ ID NO: 9	humanized heavy chain variable domain
SEQ ID NO: 10-28	alternating the sequences of humanized light chain variable domain variant and humanized HVR-L1 variant

V. Antibody Nomenclature

	sequence number							
antibody or antibody variable region	heavy chain variable domain (VH)	light chain variable domain (VL)	HVR-H1	HVR-H2	HVR-H3	HVR-L1	HVR-L2	HVR-L3
0:wt	1	2	3	4	5	6	7	8
1:N27dH	9	10	3	11	5	12	7	8
2:N27dQ	9	13	3	11	5	14	7	8
3:S27eA	9	15	3	11	5	16	7	8
4:S27eV	9	17	3	11	5	18	7	8
5:S27eP	9	19	3	11	5	20	7	8
6:N28Q	9	21	3	11	5	22	7	8
7:G29A	9	23	3	11	5	24	7	8
8:G29V	9	25	3	11	5	26	7	8
9:S27eP N28S	9	27	3	11	5	28	7	8

VI. EXAMPLES

The following are examples of methods and compositions of the invention. It is understood that various other embodiments may be practiced, given the general description provided above.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literature cited herein are expressly incorporated in their entirety by reference.

Example 1

Immunization and generation of mouse anti-human CD19 antibodies (hybridomas)

Balb/c mice were immunized six times and boosted with CD19-transfected HEK293 cells (mean receptor density 35,000 per cell). The immune response was

monitored by testing serum samples with a CD19-cell-ELISA on human CD19-transfected NIH-3T3 cells. Spleen cells from mice with sufficient titers of anti-human CD19 antibody were used for immortalization by fusion with mouse myeloma cell line P3X63 Ag8.653. Three fusions were carried out and hybridoma supernatants screened by cell-ELISA on human CD19-transfected NIH-3T3 cells and FACS binding assay using Daudi ($CD19^+$) and $CD19^-$ cells for anti-human CD19 specific antibodies.

Example 2

Hybridoma screening and cell biological functional evaluation of anti-CD19 antibody

Cell-ELISA for screening antibodies against hCD19

A cell ELISA was applied for screening of hybridomas, and to identify those hybridomas that secrete antibodies against human-CD19. NIH3T3 cells transfected with human-CD19 were used as positive cells; non-transfected NIH3T3 cells were used as negative control cells. For the assessment of the positive hybridomas the OD ratio between transfected and non-transfected NIH3T3 cells was quantified.

- Culture Medium: DMEM high glucose (4.5 mg/ml), 10 % FCS, Na-Pyruvate, NEAA, Glutamine
- Antibodies positive control: anti CD19 monoclonal antibody (IgG1) Pharmingen Cat# 555409 c = 1 mg/ml
- Detection antibody: Goat anti-Mouse IgG (H+L) HRP Conjugate Bio-Rad Cat# 170-06516
- Dilution 1: 2000 in 1x ELISA Blocking Reagent
- Other reagents: Fibronectin Roche Cat# 838039 c = 1 mg/ml
- Glutardialdehyde: 25 % stock solution // Grade Agar Scientific #R102 final concentration: 0.05 % in PBS
- ELISA Blocking Reagent: 10x stock solution // Roche Cat# 1112589
- TMB substrate: Roche Cat# 11432559
- Stop Solution: 1 M H_2SO_4
- BioRad Cat# 170-6516 Dilution 1: 2000 in 1x ELISA Blocking Reagent

Day 1:

- Fibronectin coating: 5 µg/cm² in PBS; 96well plate = 32 cm²; 160 µg/plate in 6 ml

- PBS, 50 µl/well
- incubate 45 min at RT, aspirate coating solution
- Seed 1.25 x 10^4 cells/well in 50 µl culture medium in a 96well plate
- incubate 40 hours at 37 °C
- add to upper half of the plate: NIH3T3 cells expressing CD19
- add to lower half of the plate: non-transfected NIH3T3 cells

Day 3:

- Addition of positive control antibody or samples (supernatant or mouse serum) in 50 µl culture medium
- incubate for 2 h at 4 °C
- Remove medium, fix cells with 100 µl Glutardialdehyde (0.05 % in PBS)
- Wash two times with 200 µl PBS
- Addition of detection antibody 1:2000, 50 µl/well
- incubate 2 h at RT
- wash three times with 200 µl PBS
- add 50 µl TMB, incubate for 30 min. at RT,
- stop by addition of 25 µl 1 M H_2SO_4; read extinction at 450nm/620nm
- Calculation of results: ratio OD NIH3T3 CD19 : OD NIH3T3 non-transfected

Example 3

Humanization of anti-CD19 antibody

The CD19 binding specificity of the murine antibody was transferred onto a human acceptor framework to eliminate potential immunogenicity issues arising from sequence stretches that the human body will recognize as foreign. This was done by engrafting the entire complementary determining regions (CDR) of the murine (donor) antibody onto a human (acceptor) antibody framework, and is called CDR-grafting or antibody humanization.

The murine amino acid sequence was aligned with a collection of human germ-line antibody V genes, and sorted according to sequence identity and homology. Before selecting one particular acceptor sequence, the so-called canonical loop structures of the donor antibody have to be determined (Morea, V., et al., Methods, Vol 20, Issue 3 (2000) 267-279). These canonical loop structures are determined by the type of residues present at the so-called canonical positions. These positions lie (partially) outside of the CDR regions, and have to be kept functionally equivalent in the final construct in order to retain the CDR conformation of the parental

(donor) antibody. The human germ-line sequence VBASE_VH1_1 was chosen as the acceptor for the heavy chain and sequence VBASE_VK2_5 was chosen for the light chain. This resulted in the wild-type humanized antibody.

Example 4

Expression of CD19 binding antibodies

The antibody variable domain encoding sequences were generated by gene syntheses.

For the introduction of the respective point mutations a 33mer primer based quick change reaction was performed. All sequences were verified by sequencing (SequiServe, Vaterstetten, Germany). All sequences were cloned into vectors that enable selection and propagation in E. coli (origin of replication from the vector pUC18, beta-lactamase for ampicillin resistance). These vectors additionally contain cassettes that enable expression in mammalian cells (origin of replication, oriP, of Epstein - Barr virus (EBV), the immediate early enhancer and promoter from the human cytomegalovirus (HCMV) and a polyadenylation sequence).

All gene segments that code for antibody light and heavy chains are preceded by a DNA sequence coding for a signal peptide (MGWSCIILFLVATATGVHS; SEQ ID NO: 29). The proteins were expressed by transient transfection human embryonic kidney HEK 293 cells in suspension. These cells were cultivated at 37°C and 8% CO_2. On the day of transfection, cells were seeded in fresh medium at a density of 1–2×10^6 viable cells/mL. Equimolar amounts of both heavy and light chain plasmid DNAs were co-transfected. Cell culture supernatants were harvested 7 days after transfection, centrifuged (14,000 × g for 45 min at 4°C), and subsequently filtrated through a 0.22-µm filter. These supernatants could be frozen and stored at -20 °C before purification.

Example 5

Purification of CD19 binding antibodies

General method:

Cell free fermentation supernatant (HEK 293F) is loaded onto a pre-equilibrated (phosphate buffered saline, PBS) protein A affinity column (MabSelect^{TM}SuRe, GE Healthcare, 8x100mm) with a contact time of 5 minutes. After washing (PBS, 5 column volumes) the antibody is eluted with 25 mM citric acid /NaOH (pH 3.0).

The eluate is adjusted to pH 5.5 with 1 M Tris and incubated overnight at 4°C. Thereafter a final filtration (0.45µm) is performed:

Purification of anti-human CD19 antibody variant 5 (S27eP):

Cell free fermentation supernatant (244 ml, HEK 293F) was loaded onto a pre-equilibrated (phosphate buffered saline, PBS) protein A affinity column (MabSelect^{TM}SuRe, GE Healthcare, 8x100mm) with a contact time of 5 minutes. After washing (PBS, 5 column volumes) the antibody was eluted with 25 mM citric acid /NaOH (pH 3.0). The eluate was adjusted to pH 5.5 with 1 M Tris and incubated overnight at 4°C. Final filtration (0.45µm) returned 31.1 mg (5.7 ml, 5.45 mg/ml) 99.0% (SEC) pure product.

Purification of anti-human CD19 antibody variant 9 (S27eP/N28S):

Cell free fermentation supernatant (260 ml, HEK 293F) was loaded onto a pre-equilibrated (PBS) protein A affinity column (MabSelect^{TM}SuRe, GE Healthcare, 8x100mm) with a contact time of 5 minutes. After washing (PBS, 5 column volumes) the target protein was eluted with 25 mM citric acid /NaOH (pH 3.0). The eluate was adjusted to pH 5.5 with 1 M Tris (pH 9.0) and incubated overnight at 4°C. Final filtration (0.2µm) returned 9.1 mg (5.2 ml, 1.75 mg/ml) 98.0% (SEC) pure product.

Example 6

Provision of CD19 ECD expressing cells and binding of the antibodies thereto

HEK293 cells were transfected with 1 µg of plasmid DNA per 1.5 x 10^6 cells using LipofectAmine 2000 and incubated thereafter for 48 hours at 37°C. The plasmids encoded either human CD19 (PEEPLVVKVE EGDNAVLQCL KGTSDGPTQQ LTWSRESPLK PFLKLSLGLP GLGIHMRPLA IWLFIFNVSQ QMGGFYLCQP GPPSEKAWQP GWTVNVEGSG ELFRWNVSDL GGLGCGLKNR SSEGPSSPSG KLMSPKLYVW AKDRPEIWEG EPPCLPPRDS LNQSLSQDLT MAPGSTLWLS CGVPPDSVSR GPLSWTHVHP KGPKSLLSLE LKDDRPARDM WVMETGLLLP RATAQDAGKY YCHRGNLTMS FHLEITARPV LWHWLLRTGG WK; SEQ ID NO: 30) or cynomolgus monkey CD 19 (PQEPLVVKVE EGDNAVLQCL EGTSDGPTQQ LVWCRDSPFE PFLNLSLGLP GMGIRMGPLG IWLLIFNVSN QTGGFYLCQP GLPSEKAWQP GWTVSVEGSG ELFRWNVSDL GGLGCGLKNR SSEGPSSPSG KLNSSQLYVW AKDRPEMWEG EPVCGPPRDS LNQSLSQDLT MAPGSTLWLS CGVPPDSVSR GPLSWTHVRP KGPKSSLLSL ELKDDRPDRD

MWVVDTGLLL TRATAQDAGK YYCHRGNWTK SFYLEITARP ALWHWLLRIG GWKV; SEQ ID NO: 31) extracellular domain (ECD) fused to the human PSCA GPI anchor sequence (DTDLCNASGA HALQPAAAIL ALLPALGLLL WGPGQL; SEQ ID NO: 32) for extracellular presentation. The respective transfected cells were washed twice in FACS buffer (PBS containing 5% fetal bovine serum (FCS)) and resuspended in FACS buffer to a final concentration of $2*10^6$ cells/mL corresponding to $5.0*10^4$ cells/25 µL/well. The starting concentration of the antibodies was set to 60 µg/mL (2x final concentration) and then diluted in a 1:3 (v/v) titration series. The primary antibody was incubated on the cells for one hour at room temperature, followed by two wash steps. For secondary detection, anti-huIgG (H+L) antibody conjugated to Alexa488 in a concentration of 30 µg/mL was used. The secondary antibody was incubated for one hour at room temperature. Subsequently, the cells were washed twice and resuspended in 70 µL/well FACS buffer and analyzed using a BD FACS Canto.

The respective EC_{50} values for the humanized wild-type antibody and variants 5 (S27eP) and 9 (S27eP/M28S) are shown in the following Table.

	wt [µg/mL]	**variant 5 [µg/mL]**	**variant 9 [µg/mL]**
human CD19-ECD	0.087	0.084	0.089
cynomolgus CD19-ECD	0.313	0.255	0.435

Example 7

Mass Spectrometry (LC-MS/MS)

The antibody material (approximately 80 µg) was denatured in 200 mM histidine-HCl buffer (pH 6.0) comprising approximately 7 M Guanidinium-HCl, reduced using 10 mM TCEP, and buffer exchanged to 200 mM histidine-HCl (pH 6.0) using Zeba Spin Columns 7K MWCO (Thermo Scientific). Finally, the material was digested with 2.5 µg trypsin or thermolysin (Promega) for 16 hours at 37°C. Data acquisition was performed with a RP-UPLC gradient on a ACQUITY BEH300 C18 column (Waters) using a NanoAcquity UPLC system (Waters) followed by CID based MS/MS on an Orbitrap Fusion Tribrid mass spectrometer (Thermo Scientific) with an TriVersa NanoMate (Advion) as NanoElectrospray ionization source. The data were evaluated using Mascot MS/MS Ion Searches (Matrix Science) and Peptide Analyzer (Roche Diagnostics GmbH), in-house MS data evaluation software. Quantification was performed by integration of extracted ion current chromatograms of the corresponding peptides.

Results:

The level of deamidation and succinimide formation upon incubation at 37 °C for 2 weeks at pH 7.4 in PBS buffer of the wild-type humanized anti-CD19 antibody (variant 0: wt) is shown in the following Table (used fragment: SSQSLENSNGNTYLNWYLQKPGQSPQLLIYR; SEQ ID NO: 35).

sample	**deamidated form [%]**	**succinimide formation [%]**
reference	~8	0
incubated at 37 °C for 2 weeks at pH 7.4 in PBS buffer	26-32	0

The level of deamidation and succinimide formation upon incubation of the humanized anti-CD19 antibody variant 5 (S27eP) is shown in the following Table (used fragment: SSQSLENPNGNTYLNWYLQKPGQSPQLLIYR; SEQ ID NO: 35).

sample	**deamidated form [%]**	**succinimide formation [%]**
reference	2	2
incubated at 37 °C for 2 weeks at pH 7.4 in PBS buffer	7	0
incubated at 40 °C for 2 weeks at pH 6.0 in histidine/NaCl buffer	4	2

The level of deamidation and succinimide formation upon incubation of the humanized anti-CD19 antibody variant 3 (S27eA) is shown in the following Table (used fragment: SSQSLENANGNTYLNWYLQKPGQSPQLLIYR; SEQ ID NO: 35).

sample	**deamidated form [%]**	**succinimide formation [%]**
reference	7	2
incubated at 37 °C for 2 weeks at pH 7.4 in PBS buffer	23	1
incubated at 40 °C for 2 weeks at pH 6.0 in histidine/NaCl buffer	13	1

The level of deamidation and succinimide formation upon incubation of the humanized anti-CD19 antibody variant 7 (G29A) is shown in the following Table (used fragment: SSQSLENSNANTYLNWYLQKPGQSPQLLIYR; SEQ ID NO: 35).

sample	deamidated form [%]	succinimide formation [%]
reference	8	0
incubated at 37 °C for 2 weeks at pH 7.4 in PBS buffer	45	0.5
incubated at 40 °C for 2 weeks at pH 6.0 in histidine/NaCl buffer	13	0

Example 8

CD19 affinity determination

A surface plasmon resonance (SPR) based assay was used to determine the kinetic parameters of the binding between the anti-human CD19 antibodies and the extracellular domain of recombinant human CD19 receptor.

Protocol 1:

To capture the anti-human CD19 antibody an anti-human F(ab)'2 antibody fragment as capture antibody was used (Jackson Immuno Research; order code: 109-006-006). Of the capture antibody 20 µg/mL were immobilized onto a CM5 chip (GE Healthcare; BR-1005-30) at pH 4.5 by using an amine coupling kit according to the manufacturer instructions (GE Healthcare). The sample and running buffers were HBS-EP+ (GE Healthcare; BR-1006-69). The flow cell was set to 25 °C. The sample block was set to 12 °C. Both were primed with running buffer. The anti-human CD19 antibody was captured by injecting a 35 nM solution for 60 sec. at a flow of 20 µL/min. Association was measured by injection of recombinant human CD19 ECD in various concentrations in solution for 120 sec. at a flow of 50 µL/min, starting with 900 nM in 1:3 dilutions and five concentrations in total. The dissociation phase was monitored for up to 600 sec. and triggered by switching from the sample solution to running buffer. The surface was regenerated two times by 60 sec. and 30 sec. washing with a 10 mM glycine solution (pH 1.5) at a flow rate of 30 µL/min. Bulk refractive index differences were corrected by subtracting the response obtained from a goat anti-human

F(ab)'2 surface. Blank injections are also subtracted (= double referencing). For calculation of apparent KD and other kinetic parameters the Langmuir 1:1 model was used.

Protocol 2:

To capture the anti-human CD19 antibody an anti-human Fab capture antibody was used. First 30 µg/mL goat anti-human Fab antibody (Order Code: 28958325; GE Healthcare Bio-Sciences AB) was immobilized onto a CM5 chip (GE Healthcare; BR-1005-30) at pH 5.0 by using an amine coupling kit (GE Healthcare) according to the manufacturer's instructions. The sample and running buffer was HBS-EP+ (GE Healthcare; BR-1006-69). The flow cell was set to 25 °C. The sample block was set to 12 °C. Both were primed with running buffer. The anti-human CD19 antibody was captured by injecting a 10 nM solution for 60 sec. at a flow of 10 µL/min. Association was measured by injection of recombinant human CD19 ECD for 90 sec. at a flow rate of 10 µL/min at a concentration of 250 nM. The dissociation phase was monitored for up to 60 sec. and triggered by switching from the sample solution to running buffer. The surface was regenerated by 60 sec. washing with a 10 mM glycine solution (pH 2.1) at a flow rate of 10 µL/min. Bulk refracting index differences were corrected by subtracting the response from a blank surface.

Calculation:

The relative binding of a sample is the ratio calculated from the capture level and binding level (RU binding divided by RU capture):

$$rel_binding = \frac{binding_level}{capture_level}$$

The relative active concentration of the sample is the ratio of a sample as compared to a reference sample:

$$rel_active_conc = \frac{rel_binding_{sample}}{rel_binding_{reference}}$$

Patent Claims

1. An antibody that specifically binds to human CD19, wherein the antibody comprises
(a) HVR-H1 comprising the amino acid sequence of SEQ ID NO: 03,
(b) HVR-H2 comprising the amino acid sequence of SEQ ID NO: 11,
(c) HVR-H3 comprising the amino acid sequence of SEQ ID NO: 05,
(d) HVR-L1 comprising the amino acid sequence of SEQ ID NO: 20 or 28,
(e) HVR-L2 comprising the amino acid sequence of SEQ ID NO: 07, and
(f) HVR-L3 comprising the amino acid sequence of SEQ ID NO: 08.

2. The antibody according to claim 1, wherein the antibody is a monoclonal antibody.

3. The antibody according to any one of claims 1 to 2, wherein the antibody is a human, humanized or chimeric antibody.

4. The antibody according to any one of claim 1 to 3, wherein the antibody is an antibody fragment that specifically binds to human CD19.

5. The antibody according to any one of claims 1 to 4, wherein the antibody comprises
(a) a VH sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 09 and a VL sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 19, or
(b) a VH sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 09 and a VL sequence having at least 95 % sequence identity to the amino acid sequence of SEQ ID NO: 27,or
(c) a VH sequence and a VL sequence as in (a) or (b).

6. A pharmaceutical formulation comprising the antibody according to any one of claims 1 to 5 and a pharmaceutically acceptable carrier.

7. The antibody according to any one of claims 1 to 5 for use as a medicament.

8. The antibody according to any one of claims 1 to 5 for the treatment of B-cell cancer.

9. The antibody according to any one of claims 1 to 5 for use in the depletion of B-cells.

10. Use of the antibody according to any one of claims 1 to 5 in the manufacture of a medicament.

11. The use according to claim 10, wherein the medicament is for the treatment of a B-cell cancer.

12. The use according to claim 10, wherein the medicament is for the depletion of B-cells.

13. A method of treating an individual having a B-cell cancer comprising administering to the individual an effective amount of the antibody according to any one of claims 1 to 5.

14. A method of depleting B-cells in an individual comprising administering to the individual an effective amount of the antibody according to any one of claims 1 to 5 to deplete B-cells.