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(54) **Title**: ANTI-CEACAM5 ANTIBODIES AND USES THEREOF

(57) **Abstract**: The present disclosure discloses antibodies which bind human and Macaca fascicularis CEACAM5 proteins, as well as isolated nucleic acids, vectors and host cells comprising a sequence encoding said antibodies. The disclosure also discloses immunoconjugates comprising said antibodies conjugated or linked to a growth-inhibitory agent, and to pharmaceutical compositions comprising antibodies, or immunoconjugates of the disclosure. The antibodies or immunoconjugates of the disclosure are used for the treatment of cancer or for diagnostic purposes.

ANTI-CEACAM5 ANTIBODIES AND USES THEREOF

The present invention discloses antibodies which specifically bind human and *Macaca fascicularis* CEACAM5 proteins as well as isolated nucleic acids, vectors and host cells comprising a sequence encoding said antibodies. The invention also discloses immunoconjugates comprising said antibodies conjugated or linked to a growth-inhibitory agent, and to pharmaceutical compositions comprising antibodies or immunoconjugates of the invention. The invention discloses the use of the antibodies or immunoconjugates of the invention for the treatment of cancer or for diagnostic purposes.

Carcino-embryonic antigen (CEA) is a glycoprotein involved in cell adhesion. CEA was first identified in 1965 (Gold and Freedman, J Exp Med, 121, 439, 1965) as a protein normally expressed by fetal gut during the first six months of gestation, and found in cancers of the pancreas, liver and colon. The CEA family belongs to the immunoglobulin superfamily. The CEA family, which consists of 18 genes, is sub-divided in two sub-groups of proteins: the carcinoembryonic antigen-related cell adhesion molecule (CEACAM) sub-group and the pregnancy-specific glycoprotein subgroup (Kammerer & Zimmermann, BMC Biology 2010, 8:12).

In humans, the CEACAM sub-group consists of 7 members: CEACAM1, CEACAM3, CEACAM4, CEACAM5, CEACAM6, CEACAM7, CEACAM8. Numerous studies have shown that CEACAM5, identical to the originally identified CEA, is highly expressed on the surface of colorectal, gastric, lung, breast, prostate, ovary, cervix, and bladder tumor cells and weakly expressed in few normal epithelial tissues such as columnar epithelial and goblet cells in colon, mucous neck cells in the stomach and squamous epithelial cells in esophagus and cervix (Hammarström et al, 2002, in "Tumor markers, Physiology, Pathobiology, Technology and Clinical Applications" Eds. Diamandis E. P. et al., AACC Press, Washington pp 375). Thus, CEACAM5 may constitute a therapeutic target suitable for tumor specific targeting approaches, such as immunoconjugates. The present invention provides monoclonal antibodies directed against CEACAM5, and shows that they can be conjugated to a cytotoxic agent to induce a cytotoxic activity able to kill tumor cells *in vitro* and to induce tumor regression *in vivo*.

The extracellular domains of CEACAM family members are composed of

repeated immunoglobulin-like (Ig-like) domains which have been categorized in 3 types, A, B and N, according to sequence homologies. CEACAM5 contains seven such domains, namely N, A1, B1, A2, B2, A3 and B3.

CEACAM5 A1, A2 and A3 domains, on one hand, and B1, B2 and B3 domains, on the other hand, show high sequence homologies, the A domains of human CEACAM5 presenting from 84 to 87% pairwise sequence similarity, and the B domains from 69 to 80%. Furthermore, other human CEACAM members presenting A and/or B domains in their structure, namely CEACAM1, CEACAM6, CEACAM7 and CEACAM8, show homology with human CEACAM5. In particular, the A and B domains of human CEACAM6 protein display sequence homologies with A1 and A3 domains, and any of B1 to B3 domains of human CEACAM5, respectively, which are even higher than observed among the A domains and the B domains of human CEACAM5.

Numerous anti-CEA antibodies were generated in view of CEA-targeted diagnostic or therapeutic purposes. Specificity towards related antigens has always been mentioned as a concern in this field, as an example by Sharkey et al (1990, Cancer Research 50, 2823). Due to the above mentioned homologies some of previously described antibodies may demonstrate binding to repetitive epitopes of CEACAM5 present in the different immunoglobulin domains show cross-reactivity to other CEACAM members such as CEACAM1, CEACAM6, CEACAM7, or CEACAM8, lacking specificity to CEACAM5. The specificity of the anti-CEACAM5 antibody is desired in view of CEA-targeted therapies such that it binds to human CEACAM5-expressing tumor cells but does not bind to some normal tissues expressing the others CEACAM members. It is noteworthy that CEACAM1, CEACAM6 and CEACAM8 have been described as expressed by neutrophils of human and non-human primates (Ebrahimmnejad et al, 2000, Exp Cell Res, 260, 365; Zhao et al, 2004, J Immunol Methods 293, 207; Strickland et al, 2009 J Pathol, 218, 380) where they have been shown to regulate granulopoiesis and to play a role in immune response.

An anti-CEACAM6 antibody drug conjugate has been described, such as the maytansinoid anti-CEACAM6 antibody developed by Genentech (Strickland et al, 2009 J Pathol, 218, 380), which has been shown to induce CEACAM6-dependent haematopoietic toxicity in non-human primates. This toxicity, attributed to accumulation of the antibody drug conjugate in bone marrow and depletion of

granulocytes and their cell precursors, was considered by the authors as a major safety concern. So, more precisely, for therapeutic purposes, cross-reactivity of an anti-CEACAM5 antibody with CEACAM1, CEACAM6, CEACAM7, or CEACAM8 may decrease the therapeutic index of the compound by increased toxicity on normal tissues. Thus, there is a strong advantage in obtaining antibodies specifically directed to CEACAM5 that would not cross-react with other molecules of the CEACAM family, especially for use as an antibody drug conjugate (ADC) or with any other mode of action resulting in killing the target cell.

Moreover, as CEACAM5 is described to be expressed, although at low level, in some normal cell tissues, it is critical to develop anti-CEACAM5 antibodies capable of binding to human CEACAM5 as well as to cynomolgus monkey (*Macaca fascicularis*) CEACAM5, as such antibodies may be readily tested in preclinical toxicological studies in cynomolgus monkeys to evaluate their safety profile. Since it has been shown that the efficiency of therapeutic antibodies may be dependent on the localization of the epitope in the target, both in the case of functional antibodies (Doern et al. 2009, J. Biol. Chem 284 10254) and in the case where effector functions are involved (Beers et al. Semin Hematol 47:107–114), a human/monkey cross-reactive antibody has to be shown to bind epitopes in the same repeated Ig-like homologous domain of human and cynomolgus monkey proteins.

Combining the need for species cross-reactivity of such antibodies with the specificity for human and *Macaca fascicularis* CEACAM5, *i.e.* no cross reactivity with other *Macaca fascicularis* and human CEACAM members, adds a further degree of complexity, given the overall sequence homologies between human and *Macaca fascicularis* CEACAM proteins.

Indeed, global pairwise alignment of *Macaca fascicularis* CEACAM5 sequence with human CEACAM5 sequence (AAA51967.1/GI:180223, 702 amino acids) indicated only 78.5% identity. *Macaca fascicularis* CEACAM1, CEACAM5, and CEACAM6 genes were cloned and a global alignment of human and *Macaca fascicularis* A, B and N domains was performed. This alignment predicted that there are very few regions, if any, to localize an ideal epitope that would be common to human and macaque CEACAM5 and not shared with any other family member. For these reasons developing antibodies cross-reactive between human and *Macaca fascicularis* CEACAM5 without cross-reactivity with other human and *Macaca fascicularis* CEACAM members was expected to have a low probability of success.

Noteworthy, previously described anti-CEACAM5 antibodies are almost never documented for *Macaca fascicularis* cross-reactivity, with very few exceptions (MT111, see below).

Anti-human CEACAM5 antibodies have already been used in clinical trials, such as Immunomedics labetuzumab (also known as hMN14, Sharkey et al, 1995, Cancer Research 55, 5935). This antibody has been shown not to bind to related antigens, but is not cross-reacting with CEACAM5 from *Macaca fascicularis*. Noteworthy , Micromet's MT111 antibody (also known as MEDI-565 antibody of MedImmune) is a bi-specific antibody binding to human CEACAM5 and human CD3 (Peng et al., PLoS ONE 7(5): e3641; WO 2007/071426). MT111 is said to have been created by fusion of a single chain variable fragment (scFv) from an antibody that recognizes human and cynomolgus CEACAM5 with scFv from an antibody that recognize human CD3 (poster of Oberst et al., AACR Annual Meeting April 2009 Denver, CO). It has also been reported that MT111 does not bind other CEACAM family members (Peng et al., PLoS ONE 7(5): e3641). MT111 binds to a conformational epitope in the A2 domain of human CEACAM5. This conformational epitope is missing in a splice variant of human CEACAM5, which is expressed concomitantly with full-length CEACAM5 on tumors (Peng et al., PLoS ONE 7(5): e3641). In addition, there is no evidence that MT111 binds to the same epitope in *Macaca fascicularis* CEACAM5.

In an attempt to produce new antibodies against CEACAM5 surface protein with optimal characteristics for therapeutic purposes, the inventors have immunized mice with recombinant proteins and with tumour cells. They have screened hundreds of hybridoma using ELISA on several recombinant proteins of the CEACAM family, and flow cytometry with relevant cell lines, in order to select only immunoglobulins (IgGs) with the advantageous profile. Unexpectedly, they were able to select hybridoma clones and produce corresponding mature IgGs that comprise all of the desired features. They specifically bind to the A3-B3 domain of human CEACAM5 with a high affinity and do not recognize human CEACAM1, CEACAM6, CEACAM7 and CEACAM8 proteins. In a cellular context, these antibodies display high affinity for tumor cells (in the nanomolar range). Moreover these antibodies also bind to *Macaca fascicularis* CEACAM5 protein with a ratio of affinity monkey/human less than or equal to 10. Antibodies of the invention specifically bind to the A3-B3 domain of *Macaca fascicularis* CEACAM5 and do not recognize other *Macaca fascicularis* CEACAM members.

By targeting the A3-B3 domain of CEACAM5, these antibodies have increased tumour-targeting potential, as they have the capacity to bind both full-length human CEACAM5 and to its splice variant identified by Peng et al. (PLoS ONE 7(5): e3641).

Finally, CEACAM5 is described in literature as a poorly internalizing surface protein (reviewed in Schmidt et al, 2008, Cancer Immunol. Immunother. 57, 1879), and therefore may not be a favorable target for antibody drug conjugates. In spite of what has been reported in the prior art, the inventors have shown that the antibodies they have produced are able to internalize the CEACAM5-antibody complex after binding, and to induce cytotoxic activity on tumor cells in vitro when combined to a cytotoxic agent. The same antibodies combined to a cytotoxic agent are also able to markedly inhibit tumor growth in mice bearing human primary colon and stomach tumors.

Definitions

As used herein "CEACAM5" designates the "carcino-embryonic antigen-related cell adhesion molecule 5", also known as "CD66e" (Cluster of Differentiation 66e) or CEA. CEACAM5 is a glycoprotein involved in cell adhesion. CEACAM5 is highly expressed in particular on the surface of colorectal, gastric, lung and uterine tumor cells.

A reference sequence of full length human CEACAM5, including signal peptide (positions 1-34) and propeptide (positions 686-702), is available from the GenBank database under accession number AAA51967.1 (SEQ ID NO:52) Five non synonymous SNPs have been identified with a frequency higher than 2% in caucasian population, four of them being localised in the N domain (at positions 80, 83, 112, 113), the last one in the A2 domain (at position 398) of human CECAM5 (SEQ ID NO:58). GenBank AAA51967.1 contains the major haplotype (I80, V83, I112, I113 and E398).

A sequence of the extracellular domain of *Macaca fascicularis* CEACAM5, cloned by the inventors, is disclosed in SEQ ID NO:53.

A "domain" may be any region of a protein, generally defined on the basis of sequence homologies and often related to a specific structural or functional entity. CEACAM family members are known to be composed of Ig-like domains. The term domain is used in this document to designate either individual Ig-like domains, such as "N-domain" or for groups of consecutive domains, such as "A3-B3 domain".

Domain organisation of human CEACAM5 is as follows (based on GenBank AAA51967.1 sequence; SEQ ID NO:52) :

Human CEACAM5 domains	Positions on SEQ ID NO :52
Domain N	35 – 142
Domain A1	143 – 237
Domain B1	238 – 320
Domain A2	321 – 415
Domain B2	416 – 498
Domain A3	499 – 593
Domain B3	594 – 685

Accordingly, the A3-B3 domain of human CEACAM5 consists of amino acids at positions 499-685 of SEQ ID NO:52.

Domain organisation of *Macaca fascicularis* CEACAM5 is as follows (based on cloned extracellular domain sequence; SEQ ID NO:53) :

Macaca fascicularis CEACAM5 domains	Positions on SEQ ID NO :53
Domain N-A1-B1	–1 - 286
Domain A2-B2	–287 - 464
Domain A3-B3	465 - 654

Accordingly, the A3-B3 domain of *Macaca fascicularis* CEACAM5 consists of amino acids at positions 465-654 of SEQ ID NO:53.

A "coding sequence" or a sequence "encoding" an expression product, such as a RNA, polypeptide, protein, or enzyme, is a nucleotide sequence that, when expressed, results in the production of that RNA, polypeptide, protein, or enzyme, i.e., the nucleotide sequence encodes an amino acid sequence for that polypeptide, protein or enzyme. A coding sequence for a protein may include a start codon (usually

ATG) and a stop codon.

As used herein, references to specific proteins (e.g., antibodies) can include a polypeptide having a native amino acid sequence, as well as variants and modified forms regardless of their origin or mode of preparation. A protein which has a native amino acid sequence is a protein having the same amino acid sequence as obtained from nature. Such native sequence proteins can be isolated from nature or can be prepared using standard recombinant and/or synthetic methods. Native sequence proteins specifically encompass naturally occurring truncated or soluble forms, naturally occurring variant forms (e.g., alternatively spliced forms), naturally occurring allelic variants and forms including post-translational modifications. Native sequence proteins include proteins carrying post-translational modifications such as glycosylation, or phosphorylation, or other modifications of some amino acid residues.

The term "gene" means a DNA sequence that codes for, or corresponds to, a particular sequence of amino acids which comprises all or part of one or more proteins or enzymes, and may or may not include regulatory DNA sequences, such as promoter sequences, which determine for example the conditions under which the gene is expressed. Some genes, which are not structural genes, may be transcribed from DNA to RNA, but are not translated into an amino acid sequence. Other genes may function as regulators of structural genes or as regulators of DNA transcription. In particular, the term gene may be intended for the genomic sequence encoding a protein, i.e. a sequence comprising regulator, promoter, intron and exon sequences.

A sequence “at least 85% identical to a reference sequence” is a sequence having, on its entire length, 85%, or more, for instance 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with the entire length of the reference sequence.

A percentage of “sequence identity” may be determined by comparing the two sequences, optimally aligned over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the

percentage of sequence identity. Optimal alignment of sequences for comparison is conducted by global pairwise alignment, e.g. using the algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970). The percentage of sequence identity can be readily determined for instance using the program Needle, with the BLOSUM62 matrix, and the following parameters gap-open=10, gap-extend=0.5.

A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain R group with similar chemical properties (e.g., charge, size or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine, and isoleucine; 2) aliphatic-hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartic acid and glutamic acid; and 7) sulfur-containing side chains: cysteine and methionine. Conservative amino acids substitution groups can also be defined on the basis of amino acid size.

An “antibody” may be a natural or conventional antibody in which two heavy chains are linked to each other by disulfide bonds and each heavy chain is linked to a light chain by a disulfide bond. There are two types of light chain, lambda (l) and kappa (k). There are five main heavy chain classes (or isotypes) which determine the functional activity of an antibody molecule: IgM, IgD, IgG, IgA and IgE. Each chain contains distinct sequence domains. The light chain includes two domains or regions, a variable domain (VL) and a constant domain (CL). The heavy chain includes four domains, a variable domain (VH) and three constant domains (CH1, CH2 and CH3, collectively referred to as CH). The variable regions of both light (VL) and heavy (VH) chains determine binding recognition and specificity to the antigen. The constant region domains of the light (CL) and heavy (CH) chains confer important biological properties, such as antibody chain association, secretion, trans-placental mobility, complement binding, and binding to Fc receptors (FcR). The Fv fragment is the N-terminal part of the Fab fragment of an immunoglobulin and consists of the variable portions of one light chain and one heavy chain. The specificity of the antibody resides in the structural complementarity between the antibody combining site and the antigenic determinant. Antibody combining sites are made up of residues that are

primarily from the hypervariable or complementarity determining regions (CDRs). Occasionally, residues from nonhypervariable or framework regions (FR) influence the overall domain structure and hence the combining site. Complementarity Determining Regions or CDRs therefore refer to amino acid sequences which together define the binding affinity and specificity of the natural Fv region of a native immunoglobulin binding site. The light and heavy chains of an immunoglobulin each have three CDRs, designated CDR1-L, CDR2-L, CDR3-L and CDR1-H, CDR2-H, CDR3-H, respectively. A conventional antibody antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region.

"Framework Regions" (FRs) refer to amino acid sequences interposed between CDRs, i.e. to those portions of immunoglobulin light and heavy chain variable regions that are relatively conserved among different immunoglobulins in a single species. The light and heavy chains of an immunoglobulin each have four FRs, designated FR1-L, FR2-L, FR3-L, FR4-L, and FR1-H, FR2-H, FR3-H, FR4-H, respectively.

As used herein, a "human framework region" is a framework region that is substantially identical (about 85%, or more, for instance 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%) to the framework region of a naturally occurring human antibody.

In the context of the invention, CDR/FR definition in an immunoglobulin light or heavy chain is to be determined based on IMGT definition (Lefranc et al. Dev. Comp. Immunol., 2003, 27(1):55-77; www.imgt.org).

As used herein, the term "antibody" denotes conventional antibodies and fragments thereof, as well as single domain antibodies and fragments thereof, in particular variable heavy chain of single domain antibodies, and chimeric, humanised, bispecific or multispecific antibodies.

As used herein, antibody or immunoglobulin also includes "single domain antibodies" which have been more recently described and which are antibodies whose complementary determining regions are part of a single domain polypeptide. Examples of single domain antibodies include heavy chain antibodies, antibodies naturally devoid of light chains, single domain antibodies derived from conventional four-chain antibodies, engineered single domain antibodies. Single domain antibodies may be derived from any species including, but not limited to mouse, human, camel, llama, goat, rabbit, bovine. Single domain antibodies may be naturally occurring single domain antibodies known as heavy chain antibody devoid of light chains. In particular,

Camelidae species, for example camel, dromedary, llama, alpaca and guanaco, produce heavy chain antibodies naturally devoid of light chain. Camelid heavy chain antibodies also lack the CH1 domain.

The variable heavy chain of these single domain antibodies devoid of light chains are known in the art as "VHH" or "nanobody". Similar to conventional VH domains, VHHs contain four FRs and three CDRs. Nanobodies have advantages over conventional antibodies: they are about ten times smaller than IgG molecules, and as a consequence properly folded functional nanobodies can be produced by in vitro expression while achieving high yield. Furthermore, nanobodies are very stable, and resistant to the action of proteases. The properties and production of nanobodies have been reviewed by Harmsen and De Haard HJ (Appl. Microbiol. Biotechnol. 2007 Nov;77(1):13-22).

The term "monoclonal antibody" or "mAb" as used herein refers to an antibody molecule of a single amino acid sequence, which is directed against a specific antigen, and is not to be construed as requiring production of the antibody by any particular method. A monoclonal antibody may be produced by a single clone of B cells or hybridoma, but may also be recombinant, i.e. produced by protein engineering.

The term "chimeric antibody" refers to an engineered antibody which, in its broadest sense, contains one or more regions from one antibody and one or more regions from one or more other antibodies. In an embodiment, a chimeric antibody comprises a VH domain and a VL domain of an antibody derived from a non-human animal, in association with a CH domain and a CL domain of another antibody, in an embodiment, a human antibody. As the non-human animal, any animal such as mouse, rat, hamster, rabbit or the like can be used. A chimeric antibody may also denote a multispecific antibody having specificity for at least two different antigens.

The term "humanised antibody" refers to an antibody which is wholly or partially of non-human origin and which has been modified to replace certain amino acids, for instance in the framework regions of the VH and VL domains, in order to avoid or minimize an immune response in humans. The constant domains of a humanized antibody are most of the time human CH and CL domains.

"Fragments" of (conventional) antibodies comprise a portion of an intact antibody, in particular the antigen binding region or variable region of the intact antibody. Examples of antibody fragments include Fv, Fab, F(ab')2, Fab', dsFv,

(dsFv)2, scFv, sc(Fv)2, diabodies, bispecific and multispecific antibodies formed from antibody fragments. A fragment of a conventional antibody may also be a single domain antibody, such as a heavy chain antibody or VHH.

The term “Fab” denotes an antibody fragment having a molecular weight of about 50,000 and antigen binding activity, in which about a half of the N-terminal side of the heavy chain and the entire light chain are bound together through a disulfide bond. It is usually obtained among fragments by treating IgG with a protease, papaine.

The term “F(ab')2” refers to an antibody fragment having a molecular weight of about 100,000 and antigen binding activity, which is slightly larger than 2 identical Fab fragments bound via a disulfide bond of the hinge region. It is usually obtained among fragments by treating IgG with a protease, pepsin.

The term “Fab' “ refers to an antibody fragment having a molecular weight of about 50,000 and antigen binding activity, which is obtained by cutting a disulfide bond of the hinge region of the F(ab')2.

A single chain Fv ("scFv") polypeptide is a covalently linked VH::VL heterodimer which is usually expressed from a gene fusion including VH and VL encoding genes linked by a peptide-encoding linker. The human scFv fragment of the invention includes CDRs that are held in appropriate conformation, for instance by using gene recombination techniques. Divalent and multivalent antibody fragments can form either spontaneously by association of monovalent scFvs, or can be generated by coupling monovalent scFvs by a peptide linker, such as divalent $sc(Fv)_2$. “dsFv” is a VH::VL heterodimer stabilised by a disulphide bond. “(dsFv)2” denotes two dsFv coupled by a peptide linker.

The term “bispecific antibody” or “BsAb” denotes an antibody which combines the antigen-binding sites of two antibodies within a single molecule. Thus, BsAbs are able to bind two different antigens simultaneously. Genetic engineering has been used with increasing frequency to design, modify, and produce antibodies or antibody derivatives with a desired set of binding properties and effector functions as described for instance in EP 2 050 764 A1.

The term “multispecific antibody” denotes an antibody which combines the antigen-binding sites of two or more antibodies within a single molecule.

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a

light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains of the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites.

The term “hybridoma” denotes a cell, which is obtained by subjecting a B cell prepared by immunizing a non-human mammal with an antigen to cell fusion with a myeloma cell derived from a mouse or the like which produces a desired monoclonal antibody having an antigen specificity.

By "purified" and "isolated" it is meant, when referring to a polypeptide (i.e. the antibody of the invention) or a nucleotide sequence, that the indicated molecule is present in the substantial absence of other biological macromolecules of the same type. The term "purified" as used herein means at least 75%, 85%, 95%,, 96%, 97%, or 98% by weight, of biological macromolecules of the same type are present. An “isolated” nucleic acid molecule which encodes a particular polypeptide refers to a nucleic acid molecule which is substantially free of other nucleic acid molecules that do not encode the subject polypeptide; however, the molecule may include some additional bases or moieties which do not deleteriously affect the basic characteristics of the composition.

As used herein, the term “subject” denotes a mammal, such as a rodent, a feline, a canine, and a primate. Furthermore, a subject according to the invention is a human.

Antibodies

The inventors have succeeded in generating, screening and selecting specific mouse anti-CEACAM5 antibodies displaying high affinity for both human and *Macaca fascicularis* CEACAM5 protein, and which do not significantly cross-react with human CEACAM1, CEACAM6, CEACAM7 and CEACAM8 proteins, and with *Macaca fascicularis* CEACAM1, CEACAM6 and CEACAM8 proteins.

The inventors have determined the sequence of variable heavy and light chains of such monoclonal antibodies, the so-called antibodies MAb1, MAb2, MAb3, MAb4, and MAb5.

The so-called “antibody MAb1” comprises:

- a variable domain of heavy chain consisting of sequence EVMLVESGGGLVKPGGSLKLSCAAS**GFTFSSYA**MSWVRQTPEKRLEWVAT**ISSGG**

SYIYYLDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYC**ARPAYYGNPAMDY**WG QGTSVTVSS (SEQ ID NO:31, with CDRs shown in bold characters) in which FR1-H spans amino acid positions 1 to 25, CDR1-H spans amino acid positions 26 to 33 (SEQ ID NO:1), FR2-H spans amino acid positions 34 to 50, CDR2-H spans amino acid positions 51 to 58 (SEQ ID NO:2), FR3-H spans amino acid positions 59 to 96, CDR3-H spans amino acid positions 97 to 109 (SEQ ID NO:3), and FR4-H spans amino acid positions 110 to 120, and

- a variable domain of light chain consisting of sequence DILMTQSQKFMSTSVGDRVSVTCKAS**QNVGTN**VAWYQQKPGQSPKPLIY**SAS**YRYS GVPDRFTGSGSGTDFTLTISNVQSEDLAEYFC**QQYNSYPLYT**FGGGTKLEIK (SEQ ID NO:32, with CDRs shown in bold characters) in which FR1-L spans amino acid positions 1 to 26, CDR1-L spans amino acid positions 27 to 32 (SEQ ID NO:4), FR2-L spans amino acid positions 33 to 49, CDR2-L spans amino acid positions 50 to 52, FR3-L spans amino acid positions 53 to 88, CDR3-L spans amino acid positions 89 to 98 (SEQ ID NO:6), and FR4-L spans amino acid positions 99 to 108.

The so-called “antibody MAb2” comprises:

- a variable domain of heavy chain consisting of sequence EVQLQESGGVLVKPGGSLKLSCAAS**GFVFSSYD**MSWVRQTPEKRLEWVAY**ISSGG GIT**YFPDTVQGRFTVSRDNAKNTLYLQMNSLKSEDTAIYYC**AAHYFGSSGPFAY**WG QGTLVTVSA (SEQ ID NO:33, with CDRs shown in bold characters) in which FR1-H spans amino acid positions 1 to 25, CDR1-H spans amino acid positions 26 to 33 (SEQ ID NO:7), FR2-H spans amino acid positions 34 to 50, CDR2-H spans amino acid positions 51 to 58 (SEQ ID NO:8), FR3-H spans amino acid positions 59 to 96, CDR3-H spans amino acid positions 97 to 109 (SEQ ID NO:9), and FR4-H spans amino acid positions 110 to 120, and

- a variable domain of light chain consisting of sequence DIQMTQSPASLSASVGETVTITCRAS**ENIFSY**LAWYQQKQGKSPQLLVY**NTK**TLAEG VPSRFSGSGSGTQFSLKINSLQPEDFGSYYC**QHHYGTPFT**FGSGTKLEIK (SEQ ID NO:34, with CDRs shown in bold characters) in which FR1-L spans amino acid positions 1 to 26, CDR1-L spans amino acid positions 27 to 32 (SEQ ID NO:10), FR2-L spans amino acid positions 33 to 49, CDR2-L spans amino acid positions 50 to 52, FR3-L spans amino acid positions 53 to 88, CDR3-L spans amino acid positions 89 to 97 (SEQ ID NO:12), and FR4-L spans amino acid positions 98 to 107.

A variant of antibody MAb2 was also generated by introducing a K52R

substitution in the CDR2-L. This variant, which is called herein "Mab2$_{K52R}$", has essentially the same affinity for human and *Macaca fascicularis* CEACAM5 as MAb2.

The so-called "antibody MAb3" comprises:

- a variable domain of heavy chain consisting of sequence EVKLVESGGGLVKPGGSLTLPCAAS**GFTFSRYA**MSWVRQTPEKRLEWVAS**ISSGG DT**YYPDSVKGRFTVSRDNARNILFLQMSSLRSEDTGMYYC**ARVNYYDSSFLDW**WG QGTTLTVSS (SEQ ID NO:35, with CDRs shown in bold characters) in which FR1-H spans amino acid positions 1 to 25, CDR1-H spans amino acid positions 26 to 33 (SEQ ID NO:13), FR2-H spans amino acid positions 34 to 50, CDR2-H spans amino acid positions 51 to 57 (SEQ ID NO:14), FR3-H spans amino acid positions 58 to 95, CDR3-H spans amino acid positions 96 to 108 (SEQ ID NO:15), and FR4-H spans amino acid positions 109 to 119, and

- a variable domain of light chain consisting of sequence DIVMTQSQRFMSTLEGDRVSVTCKAS**QNVGTN**VAWYQQKPGQSPKALIY**SAS**YRY SGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFC**QQYNNYPLYT**FGGGTKLEIK (SEQ ID NO:36, with CDRs shown in bold characters) in which FR1-L spans amino acid positions 1 to 26, CDR1-L spans amino acid positions 27 to 32 (SEQ ID NO:16), FR2-L spans amino acid positions 33 to 49, CDR2-L spans amino acid positions 50 to 52, FR3-L spans amino acid positions 53 to 88, CDR3-L spans amino acid positions 89 to 98 (SEQ ID NO:18), and FR4-L spans amino acid positions 99 to 108.

The so-called "antibody MAb4" comprises:

- a variable domain of heavy chain consisting of sequence EVQLVESGGGLVKPGGSLKLSCAAS**GFTFSSYD**MSWVRQTPEKRLEWVAF**ISSYG GRT**YYADTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYC**AAHYFGTSGPFAY**WG QGTLVTVSA (SEQ ID NO:37, with CDRs shown in bold characters) in which FR1-H spans amino acid positions 1 to 25, CDR1-H spans amino acid positions 26 to 33 (SEQ ID NO:19), FR2-H spans amino acid positions 34 to 50, CDR2-H spans amino acid positions 51 to 58 (SEQ ID NO:20), FR3-H spans amino acid positions 59 to 96, CDR3-H spans amino acid positions 97 to 109 (SEQ ID NO:21), and FR4-H spans amino acid positions 110 to 120, and

- a variable domain of light chain consisting of sequence DIQMTQSPASLSASVGETVTITCRAS**ENIYSY**FAWYQQKQGKSPQLLVY**NAK**ILAEG VPSRFSGSGSGTQFSLKINSLQPEDFGTYYC**QHHYGIPFT**FGSGTKLELK (SEQ ID NO:38, with CDRs shown in bold characters) in which FR1-L spans amino acid

positions 1 to 26, CDR1-L spans amino acid positions 27 to 32 (SEQ ID NO:22), FR2-L spans amino acid positions 33 to 49, CDR2-L spans amino acid positions 50 to 52, FR3-L spans amino acid positions 53 to 88, CDR3-L spans amino acid positions 89 to 97 (SEQ ID NO:24), and FR4-L spans amino acid positions 98 to 107.

The so-called "antibody MAb5" comprises:

- a variable domain of heavy chain consisting of sequence ELQLVESGGVLVKPGGSLKLSCAAS**GFAFSSYD**MSWVRQTPEKRLEWVTY**INSGG GIT**YYPDTVKGRFTISRDNARNTLYLQMSSLKSEDTAIYYC**TAHYFGSSGPFAY**WGQ GTLVTVSA (SEQ ID NO:39, with CDRs shown in bold characters) in which FR1-H spans amino acid positions 1 to 25, CDR1-H spans amino acid positions 26 to 33 (SEQ ID NO:25), FR2-H spans amino acid positions 34 to 50, CDR2-H spans amino acid positions 51 to 58 (SEQ ID NO:26), FR3-H spans amino acid positions 59 to 96, CDR3-H spans amino acid positions 97 to 109 (SEQ ID NO:27), and FR4-H spans amino acid positions 110 to 120, and

- a variable domain of light chain consisting of sequence DIQMTQSPASLSASVGETVTITCRAS**ENIYSY**LAWYQQKQGKSPQLLVY**NAK**TLTEG VPSRFSGSGSGTQFSLKINSLQPEDFGSYYC**QHHYGTPFT**FGSGTKLEIK (SEQ ID NO:40, with CDRs shown in bold characters) in which FR1-L spans amino acid positions 1 to 26, CDR1-L spans amino acid positions 27 to 32 (SEQ ID NO:28), FR2-L spans amino acid positions 33 to 49, CDR2-L spans amino acid positions 50 to 52, FR3-L spans amino acid positions 53 to 88, CDR3-L spans amino acid positions 89 to 97 (SEQ ID NO:30), and FR4-L spans amino acid positions 98 to 107.

Therefore, the invention relates to an antibody which binds to human and *Macaca fascicularis* CEACAM5.

In an embodiment the antibody of the invention binds to the A3-B3 domains of human and *Macaca fascicularis* CEACAM5. More specifically, the antibody can bind to the human and *Macaca fascicularis* A3-B3 domains indifferently whether expressed in isolated form, or present in a soluble extracellular domain or membrane-anchored full-length CEACAM5 protein.

The specificity of the antibodies for the A3-B3 domain of human CEACAM5 is advantageous as no SNP with a frequency higher than 2% in caucasian population was reported in this domain, which minimizes the risk that the antibodies' epitope(s) on CEACAM5 be altered in part of the population.

The invention also provides for an antibody which competes for binding to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins with an antibody comprising the variable heavy and light chains of an antibody selected from the group consisting of the so-called antibodies MAb1, MAb2, $MAb2_{K52R,}$ MAb3, MAb4, and MAb5, i.e. selected from the group consisting of:

a) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:31 and a variable domain of light chain of sequence of sequence SEQ ID NO:32;

b) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:33 and a variable domain of light chain of sequence of sequence SEQ ID NO:34;

c) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:33 and a variable domain of light chain of sequence of sequence SEQ ID NO:34 in which K at position 52 has been replaced by R;

d) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:35 and a variable domain of light chain of sequence of sequence SEQ ID NO:36;

e) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:37 and a variable domain of light chain of sequence of sequence SEQ ID NO:38; and

f) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:39 and a variable domain of light chain of sequence of sequence SEQ ID NO:40.

The ability of a candidate antibody to compete for binding to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins with an antibody comprising the variable heavy and light chains of an antibody selected from the group consisting of the antibodies MAb1, MAb2, MAb3, MAb4, and MAb5 (hereafter a “reference” antibody) may be readily assayed, for instance, by competitive ELISA wherein the antigen (i.e. the A3-B3 domain of human or *Macaca fascicularis* CEACAM5, or a polypeptide comprising or consisting of a fragment of human or *Macaca fascicularis* CEACAM5 including the A3-B3 domain, in particular the extracellular domain of human or *Macaca fascicularis* CEACAM5) is bound to a solid support and two solutions containing the candidate antibody and the reference antibody, respectively,

are added and the antibodies are allowed to compete for binding to the antigen. The amount of reference antibody bound to the antigen may then be measured, and compared to the amount of reference antibody bound to the antigen when measured against a negative control (e.g. solution containing no antibody). An amount of bound reference antibody in presence of the candidate antibody decreased as compared to the amount of bound reference antibody in presence of the negative control indicates that the candidate antibody has competed with the reference antibody. Conveniently, the reference antibody may be labeled (e.g. fluorescently) to facilitate detection of bound reference antibody. Repeated measurements may be performed with serial dilutions of the candidate and/or reference antibody.

According to an embodiment, such an antibody, and for instance the antibody which competes for binding to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins with an antibody as defined in b), c), e) and f) above, binds to two regions of the A3-B3 domain of human CEACAM5 protein that consist of amino acids at positions 109-115 (SEQ ID NO:76) and amino acids at positions 131-143 (SEQ ID NO:77) of the A3-B3 domain of human CEACAM5 protein, respectively. Indeed, a conformational epitope for the MAb2 antibody has been identified to belong to the regions 109-115 and 131-143 of the A3-B3 domain of human CEACAM5 protein, and MAb2, MAb4 and MAb5 being structurally closely related, it is assumed by the inventors that said antibodies bind to the same epitope.

According to an embodiment, the antibody according to the invention is specific for the surface human and *Macaca fascicularis* CEACAM5 proteins. In an embodiment, the antibody of the invention does not bind to, or does not significantly cross-react with human CEACAM1, human CEACAM6, human CEACAM7, human CEACAM8, *Macaca fascicularis* CEACAM1, *Macaca fascicularis* CEACAM6 and *Macaca fascicularis* CEACAM8 proteins.

In particular, the antibody does not bind to, or does not significantly cross-react with the extracellular domain of the aformentionned human and *Macaca fascicularis* CEACAM proteins.

Human CEACAM1 full-length protein is available in GenBank database under accession number NP_001703.2 (SEQ ID NO:11). The extracellular domain of human CEACAM1 consists of amino acids at positions 35-428 of SEQ ID NO:11. Human CEACAM6 full-length protein is available in GenBank database under accession number NP_002474.3 (SEQ ID NO:71). The extracellular domain of human

CEACAM6 consists of amino acids at positions 35-327 of SEQ ID NO:71.

Human CEACAM7 full-length protein is available in GenBank database under accession number NP_008821.1 (SEQ ID NO:72). The extracellular domain of human CEACAM7 consists of amino acids at positions 36-248 of SEQ ID NO:72.

Human CEACAM8 full-length protein is available in GenBank database under accession number NP_001807.2 (SEQ ID NO:73). The extracellular domain of human CEACAM8 consists of amino acids at positions 35-332 of SEQ ID NO:73.

M.fascicularis CEACAM1 extracellular domain consists of amino acids at positions 35-428 of full-length protein, i.e. amino acids 1-394 of SEQ ID NO:57.

M.fascicularis CEACAM6 extracellular domain consists of amino acids at positions 35-327 of full-length protein, i.e. amino acids 1-293 of SEQ ID NO:61.

M.fascicularis CEACAM8 extracellular domain consists of amino acids at positions 35-332 of full-length protein, i.e. amino acids 1-298 of SEQ ID NO:63.

"Affinity" is defined, in theory, by the equilibrium association between the whole antibody and the antigen. It can be experimentally assessed by a variety of known methods, such as measuring association and dissociation rates with surface plasmon resonance or measuring the EC_{50} (or apparent K_D) in an immunochemical assay (ELISA, FACS). In these assays, the EC_{50} is the concentration of the antibody which induces a response halfway between the baseline and maximum after some specified exposure time on a defined concentration of antigen by ELISA (enzyme-linked immuno-sorbent assay) or cell expressing the antigen by FACS (Fluorescence Activated Cell Sorting).

A monoclonal antibody binding to antigen 1(Ag1) is "cross-reactive" to antigen 2 (Ag2) when the EC_{50}s are in a similar range for both antigens. In the present application, a monoclonal antibody binding to Ag1 is cross-reactive to Ag2 when the ratio of affinity of Ag2 to affinity of Ag1 is equal or less than 10 (for instance 5, 2, 1 or 0.5), affinities being measured with the same method for both antigens.

A monoclonal antibody binding to Ag1 is "not significantly cross-reactive" to Ag2 when the affinities are very different for the two antigens. Affinity for Ag2 may not be measurable if the binding response is too low. In the present application, a monoclonal antibody binding to Ag1 is not significantly cross-reactive to Ag2, when the binding response of the monoclonal antibody to Ag2 is less than 5% of the binding response of the same monoclonal antibody to Ag1 in the same experimental setting and at the same antibody concentration. In practice, the antibody concentration used

can be the EC_{50} or the concentration required to reach the saturation plateau obtained with Ag1.

A monoclonal antibody "binds specifically" to, or "is specific for" Ag1 when it is not significantly cross-reactive to Ag2. Accordingly, the antibody according to the invention has a ratio of affinity for human CEACAM5 to the affinity for *Macaca fascicularis* CEACAM5 which is ≤10, for instance ≤5, ≤2, ≤1, or ≤0.5. Thus, the polypeptide according to the invention may be used in toxicological studies performed in monkeys because the toxicity profile observed in monkeys would be relevant to anticipate potential adverse effects in humans

An embodiment of the invention has an affinity for human CEACAM5 or *Macaca fascicularis* CEACAM5, or both, which is ≤10nM, for instance ≤ 5nM, ≤ 3nM, ≤ 1nM or ≤ 0.1nM, for instance an affinity of 0.01 nM to 5 nM, or and affinity of 0.1 nM to 5 nM, or of 0.1 nM to 1 nM.

Affinity for human CEACAM5 or for *Macaca fascicularis* CEACAM5 may be determined as the EC50 value in an ELISA using soluble recombinant CEACAM5 as capture antigen.

The antibody of the invention may also have an apparent dissociation constant (apparent KD), as may be determined by FACS analysis on tumor cell line MKN45 (DSMZ, ACC 409) or on xenograft tumor cells deriving from patient (CR-IGR-034P available from Oncodesign Biotechnology, tumor collection CReMEC), which is ≤25nM, for instance ≤20nM, ≤10nM, ≤5nM, ≤3nM or ≤1nM. The apparent KD may be within the range 0.01-20 nM, or may be within the range 0.1-20nM, 0.1-10nM, or 0.1-5nM.

Additionally, antibodies according to the invention have been shown to be able to detect CEACAM5 expression by immunohistochemistry in frozen and formalin-fixed and paraffin embedded (FFPE) tissue sections.

Alignments of the sequences of the VH and VL regions of the MAb1, MAb2, MAb3, MAb4 and MAb5 antibodies are shown in Figure 7. The comparison of the CRD-H and CDR-L sequences indicates that, structurally, MAb2, MAb4 and MAb5, on one hand, and MAb1 and MAb3, on the other hand, are closely related, said antibodies probably binding to the same epitope. The comparison of the CRD-H and CDR-L sequences further identifies CDR positions that are strictly conserved between the two groups of antibodies and which are thus assumed to be important for

specificity, whereas other positions could support substitution.

It has been further identified by the inventors that residues at positions 101-109 of MAb2 VH (i.e. residues of CDR3-H) and residues at positions 47-54 and 88-104 of MAb2 VL (i.e. regions including CDR2-L and CDR3-L, respectively) make part, or form, the antibody paratope for human CEACAM5-A3B3 domain.

Furthermore, residues at positions 27, 28, 29, 31, 51, 52, 89, 90, 93, 94, 96, and 97 of MAb2 VL (i.e. within CDR1-L, CDR2-L and CDR3-L), and residues at positions 26 to 31, 51 to 58, 97, 103, 104, 107, and 109 of MAb2 VH (i.e. within CDR1-H, all of CDR2-H and within CDR3-H) have been identified by single acid substitutions as neutral for binding to human and cynomolgus CEACAM5 extracellular domains. In addition, residues at positions 30 and 92 of MAb2 VL (i.e. within CDR1-L and CDR3-L), and residues at positions 98 and 100 of MAb2 VH (i.e. within CDR3-H), have been shown to tolerate a conservative substitution. Since MAb2, MAb4 and MAb5 carry the same set of 6 CDRs or very closely related ones, it is considered that variations at the same positions of MAb4 or MAb5 in VH or VL or both VH and CLsequences will also result in variant antibodies maintaining the binding specificity and/or affinity for human and cynomolgus CEACAM5.

Noteworthy, all residues of CDR2-H being identified as neutral for binding to human and cynomolgus CEACAM5 extracellular domains, the inventors assumed that CDR2-H might not participate in the interaction. Accordingly, in the antibodies of the invention, CDR2-H could be any sequence of 6 to 10 amino acids, this being the regular length of CDR2-H sequences in human antibodies.

Accordingly, the antibody according to the invention comprises:

a) a CDR1-H consisting of sequence $X_1X_2X_3X_4X_5X_6YD$ (SEQ ID NO:83) wherein each of X_1, X_2, X_3, X_4, X_5 and X_6 is any amino acid; and

a CDR2-H consisting of a 6 to 10 amino acid-long sequence, preferably a 8 amino acid long sequence in which any amino acid may be present at any position; and

a CDR3-H consisting of sequence $X_1X_2HX_3FGX_4X_5GPX_6AX_7$ (SEQ ID NO:84) wherein each of X_1, X_4, X_5, X_6, and X_7 is any amino acid, X_2 is A or S, and X_3 is Y, F or W; and/or

b) a CDR1-L consisting of sequence $X_1X_2X_3X_4X_5Y$ (SEQ ID NO:85) wherein each of X_1, X_2, X_3 and X_5 is any amino acid,and X_4 is Y, F or W; and

a CDR2-L consisting of sequence NX_1X_2 wherein each of X_1 and X_2 is any

amino acid; and

a CDR3-L consisting of sequence $X_1X_2HX_3X_4X_5PX_6X_7$ (SEQ ID NO:86) wherein each of X_1, X_2, X_4, X_5, X_6 and X_7 is any amino acid, X_3 is Y, F or W.

In an embodiment, in the CDR1-H consisting of sequence $X_1X_2X_3X_4X_5X_6YD$ (SEQ ID NO:83), X_1 is G, or X_2 is F, or X_3 is T, A or V, or X_4 is F, or X_5 is S, or X_6 is S, or any combination thereof.

In an embodiment, the CDR2-H consists of sequence $IX_1SX_2GGX_3T$ (SEQ ID NO:79) wherein X_1 is S or N (in particular S), X_2 is Y or G (in particular G), X_3 is R or I. In a further embodiment X_3 is I.

In an embodiment, in the CDR3-H consisting of sequence $X_1X_2HX_3FGX_4X_5GPX_6AX_7$ (SEQ ID NO:84), X_1 is A or T, or X_4 is T or S, or X_5 is S, or X_6 is F, or X_7 is Y, or any combination thereof.

In an embodiment, in the CDR1-L consisting of sequence $X_1X_2X_3X_4X_5Y$ (SEQ ID NO:85), X_1 is E, or X_2 is N, or X_3 is I, or X_5 is S, or any combination thereof.

In an embodiment, the CDR2-L consists of sequence NX_1X_2 wherein X_1 is A or T, and X_2 is K or R.

In an embodiment, in the CDR3-L consisting of sequence $X_1X_2HX_3X_4X_5PX_6X_7$ (SEQ ID NO:86), X_1 is Q, or X_2 is H, or X_4 is G, or X_5 is T, or X_6 is F, or X_7 is T, or any combination thereof.According to an embodiment, the antibody according to the invention comprises :

a) a CDR1-H consisting of sequence GFX_1FSSYD (SEQ ID NO:78) wherein X_1 is T, A or V; and

a CDR2-H consisting of sequence $IX_1SX_2GGX_3T$ (SEQ ID NO:79) wherein X_1 is S or N (in particular S), X_2 is Y or G (in particular G), X_3 is R or I ; and

a CDR3-H consisting of sequence $X_1AHYFGX_2SGPFAY$ (SEQ ID NO:80) wherein X_1 is A or T (in particular A), and X_2 is T or S ; and/or

b) a CDR1-L consisting of sequence ENIFSY (SEQ ID NO:10) or ENIYSY (SEQ ID NO:22); and

a CDR2-L consisting of sequence NX_1X_2 wherein X_1 is A or T, and X_2 is K or R, in particular R; CDR2-L consisting in particular of NAK, NTK and NTR; and

a CDR3-L consisting of sequence QHHYGTPFT (SEQ ID NO:12) or QHHYGIPFT (SEQ ID NO:24).

According to an embodiment, in CDR2-H, X_1 is S or N, X_2 is G and X_3 is I.

According to an embodiment, CDR2-H consists of ISSGGGIT (SEQ ID NO:8),

ISSYGGRT (SEQ ID NO:20) or INSGGGIT (SEQ ID NO:26).

According to an embodiment, in CDR3-H, X_1 is A or T, and X_2 is S.

According to an embodiment, CDR3-H consists of AAHYFGSSGPFAY (SEQ ID NO:9), AAHYFGTSGPFAY (SEQ ID NO:21), or TAHYFGSSGPFAY (SEQ ID NO:27).

Any combination of these embodiments makes part of the invention.

Alternatively, the antibody according to the invention comprises:

a) a CDR1-H consisting of sequence GFTFSX_1YX_2 (SEQ ID NO:81) wherein X_1 is R or S, in particular S, and X_2 is A or D; and

a CDR2-H consisting of sequence ISSGG$X_1X_2X_3$ (SEQ ID NO:82) wherein X_1 is absent, S or G (in particular G), X_2 is D, Y or I, and X_3 is T or I; and

a CDR3-H consisting of sequence ARPAYYGNPAMDY (SEQ ID NO:3) or ARVNYYDSSFLDW (SEQ ID NO:15); and/or

b) a CDR1-L consisting of sequence QNVGTN (SEQ ID NO:4); and

a CDR2-L consisting of sequence SAS; and

a CDR3-L consisting of sequence QQYNSYPLYT (SEQ ID NO:6) or QQYNNYPLYT (SEQ ID NO:18).

According to an embodiment, CDR2-H consists of sequence ISSGGSYI (SEQ ID NO:2) or ISSGGDT (SEQ ID NO:14).

According to an embodiment, CDR2-H consists of sequence ISSGGSYI (SEQ ID NO:2) and CDR3-H of sequence ARPAYYGNPAMDY (SEQ ID NO:3).

According to an embodiment, CDR2-H consists of ISSGGDT (SEQ ID NO:14) and CDR3-H of sequence ARVNYYDSSFLDW (SEQ ID NO:15).

According to an embodiment, the antibody according to the invention comprises the CDR sequences of the heavy and/or light chains of one of so-called anti-CEACAM5 antibodies MAb1, MAb2, MAb2$_{K52R}$, MAb3, MAb4, and MAb5.

Therefore, the invention relates to an antibody which comprises:

a) CDR1-H of sequence GFTFSSYA (SEQ ID NO:1) or a sequence differing from SEQ ID NO:1 by one amino acid substitution; CDR2-H of sequence ISSGGSYI (SEQ ID NO:2) or a sequence differing from SEQ ID NO:2 by one or more amino acid substitutions; CDR3-H of sequence ARPAYYGNPAMDY (SEQ ID NO:3) or a sequence differing from SEQ ID NO:3 by one amino acid substitution; CDR1-L of sequence QNVGTN (SEQ ID NO:4) or a sequence

differing from SEQ ID NO:4 by one amino acid substitution; CDR2-L of sequence SAS or a sequence differing from SAS by one amino acid substitution and CDR3-L of sequence QQYNSYPLYT (SEQ ID NO:6) or a sequence differing from SEQ ID NO:6 by one amino acid substitution; or

b) a CDR1-H of sequence GFVFSSYD (SEQ ID NO:7) or a sequence differing from SEQ ID NO:7 by one amino acid substitution; CDR2-H of sequence ISSGGGIT (SEQ ID NO:8) or a sequence differing from SEQ ID NO:8 by one or more amino acid substitutions; CDR3-H of sequence AAHYFGSSGPFAY (SEQ ID NO:9) or a sequence differing from SEQ ID NO:9 by one or more amino acid substitutions; CDR1-L of sequence ENIFSY (SEQ ID NO:10) or a sequence differing from SEQ ID NO:10 by one amino acid substitution; CDR2-L of sequence NTK or NTR or a sequence differing from NTK or NTR by one amino acid substitution and CDR3-L of sequence QHHYGTPFT (SEQ ID NO:12) or a sequence differing from SEQ ID NO:12 by one amino acid substitution; or

c) a CDR1-H of sequence GFTFSRYA (SEQ ID NO:13) or a sequence differing from SEQ ID NO:13 by one amino acid substitution; CDR2-H of sequence ISSGGDT (SEQ ID NO:14) or a sequence differing from SEQ ID NO:14 by one or more amino acid substitutions; CDR3-H of sequence ARVNYYDSSFLDW (SEQ ID NO:15) or a sequence differing from SEQ ID NO:15 by one amino acid substitution; CDR1-L of sequence QNVGTN (SEQ ID NO:16) or a sequence differing from SEQ ID NO:16 by one amino acid substitution; CDR2-L of sequence SAS or a sequence differing from SAS by one amino acid substitution and CDR3-L of sequence QQYNNYPLYT (SEQ ID NO:18) or a sequence differing from SEQ ID NO:18 by one amino acid substitution; or

d) a CDR1-H of sequence GFTFSSYD (SEQ ID NO:19) or a sequence differing from SEQ ID NO:19 by one amino acid substitution; CDR2-H of sequence ISSYGGRT (SEQ ID NO:20) or a sequence differing from SEQ ID NO:20 by one or more amino acid substitutions; CDR3-H of sequence AAHYFGTSGPFAY (SEQ ID NO:21) or a sequence differing from SEQ ID NO:21 by one or more amino acid substitutions; CDR1-L of sequence ENIYSY (SEQ ID NO:22) or a sequence differing from SEQ ID NO:22 by one amino acid substitution; CDR2-L of sequence NAK or a sequence differing from NAK by one or more amino acid substitutions and CDR3-L of sequence

QHHYGIPFT (SEQ ID NO:24) or a sequence differing from SEQ ID NO:24 by one amino acid substitution; or

e) an antibody comprising a CDR1-H of sequence GFAFSSYD (SEQ ID NO:25) or a sequence differing from SEQ ID NO:25 by one amino acid substitution; CDR2-H of sequence INSGGGIT (SEQ ID NO:26) or a sequence differing from SEQ ID NO:26 by one or more amino acid substitutions; CDR3-H of sequence TAHYFGSSGPFAY (SEQ ID NO:27) or a sequence differing from SEQ ID NO:27 by one or more amino acid substitutions; CDR1-L of sequence ENIYSY (SEQ ID NO:28) or a sequence differing from SEQ ID NO:28 by one amino acid substitution; CDR2-L of sequence NAK; or a sequence differing from NAK by one or more amino acid substitutions and CDR3-L of sequence QHHYGTPFT (SEQ ID NO:30) or a sequence differing from SEQ ID NO:30 by one amino acid substitution.

One or more individual amino acids may be altered by substitution, in particular by conservative substitution, in one or more of the above CDR sequences. Such an alteration may be intended for example to remove a glycosylation site or a deamidation site, in connection with humanisation of the antibody.

Based on the alignments of the sequences of the VH and VL regions of the MAb1, MAb2, MAb3, MAb4 and MAb5, and based on single acid substitutions in a variant of MAb2 antibody, an amino acid may be substituted:

- in CDR1-H: at one or more of positions 1 to 6, for instance at position 3, of CDR1-H of sequence GFVFSSYD (SEQ ID NO:7), GFTFSSYD (SEQ ID NO:19) or GFAFSSYD (SEQ ID NO:25), or at position 6 of CDR1-H of sequence GFTFSSYA (SEQ ID NO:1) or GFTFSRYA (SEQ ID NO:13); and/or
- in CDR2-H, at one or more of any of the positions, or at one, two or three of positions 2, 4, and 7 of CDR2-H of sequence ISSGGGIT (SEQ ID NO:8), ISSYGGRT (SEQ ID NO:20) or INSGGGIT (SEQ ID NO:26), or at one, two or three of positions 6, 7 and 8 (where the sequence is 8 amino acid long) of CDR2-H of sequence ISSGGSYI (SEQ ID NO:2) or ISSGGDT (SEQ ID NO:14); and/or see above
- in CDR3-H, at one or more of positions 1, 7, 8, 11 and 13, for instance at one or two of positions 1 and 7 of CDR3-H of sequence AAHYFGSSGPFAY (SEQ ID NO:9), AAHYFGTSGPFAY (SEQ ID NO:21), or TAHYFGSSGPFAY (SEQ ID NO:27), or at position 3, 4, 7, 8, 9, 10, or 11 of sequence ARPAYYGNPAMDY (SEQ ID NO:3) or ARVNYYDSSFLDW (SEQ ID NO:15) ; and/or

- in CDR1-L, at one or more of positions 1 to 5, in particular at one or more of positions 1, 2, 3 and 5 or at position 4 of CDR1-L of sequence ENIFSY (SEQ ID NO:10) or ENIYSY (SEQ ID NO:28); and/or

- in CDR2-L, at positions 2 and/or 3 of sequence NAK, NTK or NTR, in particular at least at position 3 if K is present. In such a case, R for instance can be substituted for K at position 3 of CDR2-L ; and/or

- in CDR3-L, at one or more of positions 1, 2, 5, 6, 8 and 9, for instance at position 6 of CDR3-L of sequence QHHYGIPFT (SEQ ID NO:24) or QHHYGTPFT (SEQ ID NO:30), or at position 5 of CDR3-L of sequence QQYNSYPLYT (SEQ ID NO:6) or QQYNNYPLYT (SEQ ID NO:18).

According to an embodiment, in the antibodies of the invention:

- position 5 of CDR3-H of sequence AAHYFGSSGPFAY (SEQ ID NO:9), AAHYFGTSGPFAY (SEQ ID NO:21), or TAHYFGSSGPFAY (SEQ ID NO:27); and/or

- position 6 of CDR1-L of sequence ENIFSY (SEQ ID NO:10) or ENIYSY (SEQ ID NO:28); and/or

- position 3 of CDR3-L of sequence QHHYGIPFT (SEQ ID NO:24) or QHHYGTPFT (SEQ ID NO:30)

is (are) unmodified.

According to an embodiment, in CDR1-H of sequence GFVFSSYD (SEQ ID NO:7), GFTFSSYD (SEQ ID NO:19) or GFAFSSYD (SEQ ID NO:25), the amino acid which is substituted for the amino acid at position at position 3 of CDR1-H is selected from the group consisting of T, A or V.

According to an embodiment, in CDR1-H of sequence GFTFSSYA (SEQ ID NO:1) or GFTFSRYA (SEQ ID NO:13), the amino acid which is substituted for the amino acid at position 6 of CDR1-H is R or S.

According to an embodiment, in CDR3-H of sequence AAHYFGSSGPFAY (SEQ ID NO:9), AAHYFGTSGPFAY (SEQ ID NO:21), or TAHYFGSSGPFAY (SEQ ID NO:27), the amino acid which is substituted for the amino acid at position 1 of CDR3-H is A or T and/or the amino acid which is substituted for the amino acid at position 7 of CDR3-H is T or S.

According to an embodiment, in CDR3-H of sequence ARPAYYGNPAMDY (SEQ ID NO:3) or ARVNYYDSSFLDW (SEQ ID NO:15), the amino acid which is substituted for the amino acid at position 3 of CDR3-H is V or P, at position 4 is A or N, at position 7 is D or G, at position 8 is S or N, at position 9 is S or P, at position 10

is F or A, or at position 11 is W or Y.

According to an embodiment, the amino acid which is substituted for the amino acid at position 4 of CDR1-L is Y or F.

According to an embodiment, in CDR2-L of sequence NAK, NTK or NTR, the amino acid which is substituted for the amino acid at position 2 of CDR2-L is A or T.

According to an embodiment, in CDR3-L of sequence QQYNSYPLYT (SEQ ID NO:6) or QQYNNYPLYT (SEQ ID NO:18), the amino acid which is substituted for the amino acid at position 5 of CDR3-L is N or S.

According to an embodiment, in CDR3-L of sequence QHHYGIPFT (SEQ ID NO:24) or QHHYGTPFT (SEQ ID NO:30), the amino acid which is substituted for the amino acid at position 6 of CDR3-L is I or T.

Any combination of the above embodiments makes part of the invention.

In an embodiment the antibody according to the invention is a conventional antibody, such as a conventional monoclonal antibody, or an antibody fragment, a bispecific or multispecific antibody.

In an embodiment the antibody according to the invention comprises or consists of an IgG, or a fragment thereof.

The invention also provides antibodies as defined above further comprising at least the variable domain of heavy chain and/or the variable domain of light chain of one of the five so-called anti-CEACAM5 antibodies MAb1, MAb2, MAb3, MAb4, and MAb5.

Thus an embodiment of the invention relates to a antibody which comprises:

a) a variable domain of heavy chain of sequence SEQ ID NO:31 or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:32, or a sequence at least 85% identical thereto; or

b) a variable domain of heavy chain of sequence SEQ ID NO:33, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:34, or a sequence at least 85% identical thereto; or

c) a variable domain of heavy chain of sequence SEQ ID NO:35, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:36, or a sequence at least 85% identical thereto; or

d) a variable domain of heavy chain of sequence SEQ ID NO:37, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:38, or a sequence at least 85% identical thereto; or

e) a variable domain of heavy chain of sequence SEQ ID NO:39, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:40, or a sequence at least 85% identical thereto.For instance, the sequence of the variable domain of heavy or light chain may differ from the reference sequence SEQ ID NO:31, 32, 33, 34, 35, 36, 37, 38, 39 or 40, as appropriate, by one or more amino acid substitution(s), in particular by one or more conservative amino acid substitution(s) and/or substitution(s) with canonical residues. In an embodiment, the sequence of the variable domain of heavy or light chain may differ from the reference sequence SEQ ID NO:31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 by conservative amino acid substitution(s), only.

The sequence alterations as compared with sequence SEQ ID NO:31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 willbe present essentially in one or more of the framework regions, FR1-L, FR2-L, FR3-L, FR4-L and/or FR1-H, FR2-H, FR3-H, FR4-H.

However, amino acid substitutions in one or more CDRs are also possible. In an embodiment, the sequence of the variable domain of light chain may differ from sequence SEQ ID NO:34 at least by a K to R substitution at position 52 of SEQ ID NO:34 (in CDR2-L).

The antibody of the invention and a fragment thereof may be, respectively, a murine antibody and a fragment of a murine antibody.

The antibody may also be a chimeric antibody, and in an embodiment a murine/human antibody, e.g. an antibody comprising murine variable domains of heavy and light chains and a CH domain and a CL domain from a human antibody. The polypeptide may be a fragment of such an antibody.

According to an embodiment, the antibody of the invention is:

a) a chimeric antibody comprising, or consisting of, a heavy chain of sequence SEQ ID NO:41 or a sequence at least 85% identical thereto or a light chain of sequence of sequence SEQ ID NO:42 or a sequence at least 85% identical thereto (i.e heavy and/or light chain of chMAb1 as described in example 5); or a heavy chain and a light chain or,

b) a chimeric antibody comprising, or consisting of, a heavy chain of sequence SEQ ID NO:43 or a sequence at least 85% identical thereto or a light chain of sequence of sequence SEQ ID NO:44 or a sequence at least 85% identical thereto; (i.e heavy and/or light chain of chMAb2 as described in example 5); or or a heavy chain and a light chain or,

c) a chimeric antibody comprising, or consisting of, a heavy chain of sequence SEQ ID NO:45 or a sequence at least 85% identical thereto or a light chain of sequence of sequence SEQ ID NO:46 or a sequence at least 85% identical thereto; (i.e heavy and/or light chain of chMAb3 as described in example 5); or a heavy chain and a light chain or,

d) a chimeric antibody comprising, or consisting of, heavy chain of sequence SEQ ID NO:47 or a sequence at least 85% identical thereto or a light chain of sequence of sequence SEQ ID NO:48 or a sequence at least 85% identical thereto, (i.e heavy and/or light chain of chMAb4 as described in example 5); or or a heavy chain and a light chain or,

e) a chimeric antibody comprising, or consisting of, a heavy chain of sequence SEQ ID NO:49 or a sequence at least 85% identical thereto or a light chain of sequence of sequence SEQ ID NO:50 or a sequence at least 85% identical thereto (i.e heavy and/or light chain of chMAb5 as described in example 5), or or a heavy chain and a light chain or,

f) a fragment of the chimeric antibody defined in a), b), c), d) or e).

The antibody may also be a humanised antibody or a fragment of a humanised antibody. In an embodiment, the antibody of the invention may result from humanisation of any of the chimeric antibodies defined above in a), b), c), d), e) or f).

Numerous methods for humanisation of an antibody sequence are known in the art; see e.g. the review by Almagro & Fransson (2008) Front Biosci. 13: 1619-1633. One commonly used method is CDR grafting, or antibody reshaping, which involves grafting of the CDR sequences of a donor antibody, generally a mouse antibody, into the framework scaffold of a human antibody of different specificity. Since CDR grafting may reduce the binding specificity and affinity, and thus the biological activity, of a CDR grafted non-human antibody, back mutations may be introduced at selected positions of the CDR grafted antibody in order to retain the binding specificity and affinity of the parent antibody. Identification of positions for possible back mutations

can be performed using information available in the literature and in antibody databases. Amino acid residues that are candidates for back mutations are typically those that are located at the surface of an antibody molecule, while residues that are buried or that have a low degree of surface exposure will not normally be altered. An alternative humanization technique to CDR grafting and back mutation is resurfacing, in which non-surface exposed residues of non-human origin are retained, while surface residues are altered to human residues. Another alternative technique is known as “guided selection” (Jespers et al. (1994) Biotechnology 12, 899) and can be used to derive from a murine antibody a fully human antibody conserving the epitope and binding charateristics of the parental antibody.

For chimeric antibodies, humanisation typically involves modification of the framework regions of the variable region sequences.

Amino acid residues that are part of a CDR will typically not be altered in connection with humanisation, although in certain cases it may be desirable to alter individual CDR amino acid residues, for example to remove a glycosylation site, a deamidation site or an undesired cysteine residue. N-linked glycosylation occurs by attachment of an oligosaccharide chain to an asparagine residue in the tripeptide sequence Asn-X-Ser or Asn-X-Thr, where X may be any amino acid except Pro. Removal of an N-glycosylation site may be achieved by mutating either the Asn or the Ser/Thr residue to a different residue, for instance by way of conservative substitution. Deamidation of asparagine and glutamine residues can occur depending on factors such as pH and surface exposure. Asparagine residues are particularly susceptible to deamidation, primarily when present in the sequence Asn-Gly, and to a lesser extent in other dipeptide sequences such as Asn-Ala. When such a deamidation site, for instance Asn-Gly, is present in a CDR sequence, it may therefore be desirable to remove the site, typically by conservative substitution to remove one of the implicated residues. Substitution in a CDR sequence to remove one of the implicated residues is also intended to be encompassed by the present invention.

Taking the so-called “antibody MAb2” as an example, a humanised antibody or fragment thereof may comprise the following mutations in the variable heavy chain: P instead of G in position 9 ; and/or G instead of V in position 10 ; and/or S instead of K in position 19 ; and/or R instead of K in position 43 ; and/or G instead of R in position 44 ; and/or A instead of F in position 60 ; and/or S instead of D in position 62 ; and/or K instead of Q in position 65 ; and/or T instead of K in position 87 ; and/or V instead of

I in position 89 ; and/or S instead of A in position 113 ; the positions being given by reference to SEQ ID NO:33.

Still taking the so-called "antibody MAb2" as an example, a humanised antibody or fragment thereof may comprise the following mutations in the variable light chain: D instead of E in position 17 ; and/or R instead of T in position 18 ; and/or P instead of Q in position 40 ; and/or K instead of Q in position 45 ; and/or R instead of K in position 52 ; and/or D instead of Q in position 70 ; and/or T instead of K in position 74 ; and/or S instead of N in position 76 ; and/or A instead of G in position 84 ; and/or T instead of S in position 85 ; the positions being given by reference to SEQ ID NO:34.

In an embodiment, the antibody of the invention is a humanised antibody comprising, or consisting of, a heavy chain comprising the following mutations, the positions being given by reference to SEQ ID NO:33:

a) P instead of G in position 9 ; and G instead of V in position 10 ; and S instead of K in position 19 ; and R instead of K in position 43 ; and S instead of D in position 62 ; and K instead of Q in position 65 ; and T instead of K in position 87; or

b) P instead of G in position 9 ; and G instead of V in position 10 ; and S instead of K in position 19 ; and R instead of K in position 43 ; and G instead of R in position 44 ; and A instead of F in position 60 ; and S instead of D in position 62 ; and K instead of Q in position 65 ; and T instead of K in position 87 ; and V instead of I in position 89 ; and S instead of A in position 113; and/or

a humanised antibody comprising a light chain comprising the following mutations, the positions being given by reference to SEQ ID NO:34:

c) D instead of E in position 17 ; and P instead of Q in position 40 ; and K instead of Q in position 45 ; and T instead of K in position 74 ; and S instead of N in position 76 ; or

d) D instead of E in position 17 ; and R instead of T in position 18 ; and P instead of Q in position 40 ; and K instead of Q in position 45 ; and D instead of Q in position 70 ; and T instead of K in position 74 ; and S instead of N in position 76 ; and A instead of G in position 84 ; and T instead of S in position 85 ; or

e) D instead of E in position 17 ; and R instead of T in position 18 ; and P instead of Q in position 40 ; and K instead of Q in position 45 ; and R instead of K in position 52 ; and D instead of Q in position 70 ; and T instead of K in position 74 ; and S instead of N in position 76 ; and A instead of G in position 84 ; and T instead of S in position 85.

In an embodiment, the antibody of the invention is a humanized antibody obtained by grafting the CDRs of an antibody of the invention into alternative antibody framework regions, more specifically into human framework regions. Taking MAb2 as an example, the 6 CDRs of $MAb2_{K52R}$ have been grafted into a human framework consisting of IGHV3-23 and IGKV1D-39 genes, and three back-mutations were introduced corresponding to positions 34 and 53 in the VL (SEQ ID NO. 34) and position 50 in the VH (SEQ ID NO. 33) resulting in an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:74 and a variable domain of light chain of sequence SEQ ID NO:75.

In an embodiment, the antibody of the invention is a humanised antibody comprising, or consisting of, a heavy chain of sequence SEQ ID NO:51, SEQ ID NO:5, or SEQ ID NO: 74, or a sequence at least 85% identical thereto; and/or a light chain of sequence SEQ ID NO:17, SEQ ID NO:23, SEQ ID NO:29, SEQ ID NO:55 or SEQ ID NO: 75 or a sequence at least 85% identical thereto (humanised variable domains of heavy and light chains of MAb2).

In an embodiment, the antibody of the invention is a humanised antibody comprising a heavy chain of sequence SEQ ID NO:51 or a sequence at least 85% identical thereto and a light chain of sequence SEQ ID NO:17 or a sequence at least 85% identical thereto, or a heavy chain of sequence SEQ ID NO:5 or a sequence at least 85% identical thereto and a light chain of sequence SEQ ID NO:23 or a sequence at least 85% identical thereto, or heavy chain of sequence SEQ ID NO:5 or a sequence at least 85% identical thereto and a light chain of sequence SEQ ID NO:29 or a sequence at least 85% identical thereto, or heavy chain of sequence SEQ ID NO:51 or a sequence at least 85% identical thereto and a light chain of sequence SEQ ID NO:55 or a sequence at least 85% identical thereto, or a heavy chain of sequence SEQ ID NO: 74 or a sequence at least 85% identical thereto and a light chain of sequence SEQ ID NO: 75 or a sequence at least 85% identical thereto.

In said humanised antibody or fragment thereof, the variable domains of heavy and light chains may comprise human acceptor framework regions. The humanised antibody further comprises human constant heavy and light chain domains, where present.

In an embodiment, the antibody of the invention is antibody huMAb2-3 or a variant thereof, i.e. an isolated antibody which binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins and which comprises:

a) a heavy chain consisting of sequence SEQ ID NO:87 or a sequence at least 85% identical thereto; or

b) a light chain consisting of sequence SEQ ID NO:88 or a sequence at least 85% identical thereto or a heavy chain and a light chain.

In an embodiment, the antibody of the invention is antibody huMAb2-4 (MAb2_VL1d VH1-IgG1) or a variant thereof, i.e. an isolated antibody which binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins and which comprises:

c) a heavy chain consisting of sequence SEQ ID NO:89 or a sequence at least 85% identical thereto; and/or

d) a light chain consisting of sequence SEQ ID NO:90 or a sequence at least 85% identical thereto.

The antibody according to the invention may also be a single domain antibody or a fragment thereof. In an embodiment of the invention, a single domain antibody fragment may consist of a variable heavy chain (VHH) which comprises the CDR1-H, CDR2-H and CDR3-H of the antibodies as described above. The antibody may also be a heavy chain antibody, i.e. an antibody devoid of light chain, which may or may not contain a CH1 domain.

The single domain antibody or a fragment thereof may also comprise the framework regions of a camelid single domain antibody, and optionally the constant domain of a camelid single domain antibody.

The antibody according to the invention may also be an antibody fragment for instance a humanised antibody fragment, selected from the group consisting of Fv, Fab, F(ab')2, Fab', dsFv, (dsFv)2, scFv, sc(Fv)2, and diabodies.

The antibody may also be a bispecific or multispecific antibody formed from antibody fragments, at least one antibody fragment being an antibody fragment according to the invention. Multispecific antibodies are polyvalent protein complexes as described for instance in EP 2 050 764 A1 or US 2005/0003403 A1.

The bispecific or multispecific antibodies according to the invention can have specificity for (a) the A3-B3 epitope on human/ *Macaca fascicularis* CEACAM5 targeted by one of the so-called MAb1, MAb2, MAb3, MAb4 and MAb5 antibodies and (b) at least one other antigen. According to an embodiment the at least one other antigen is not a human or *Macaca fascicularis* CEACAM family member, and in an

embodiment not at least one or all of human and *Macaca fascicularis* CEACAM1, human and monkey CEACAM6, human and *Macaca fascicularis* CEACAM7, and human and *Macaca fascicularis* CEACAM8. According to another embodiment, the at least one other antigen may be an epitope on human *Macaca fascicularis* CEACAM5 other than said A3-B3 epitope targeted by one of the so-called MAb1, MAb2, MAb3, MAb4 and MAb5 antibodies.

Said antibodies can be produced by any technique well known in the art. In an embodiment said antibodies are produced by techniques as hereinafter described.

Antibodies and fragments thereof according to the invention can be used in an isolated (e.g., purified) from or contained in a vector, such as a membrane or lipid vesicle (e.g. a liposome).

Nucleic acids, vectors and recombinant host cells

A further object of the invention relates to a nucleic acid sequence comprising or consisting of a sequence encoding an antibody of the invention as defined above.

Typically, said nucleic acid is a DNA or RNA molecule, which may be included in any suitable vector, such as a plasmid, cosmid, episome, artificial chromosome, phage or a viral vector.

The terms "vector", "cloning vector" and "expression vector" mean the vehicle by which a DNA or RNA sequence (e.g. a foreign gene) can be introduced into a host cell, so as to transform the host and promote expression (e.g. transcription and translation) of the introduced sequence.

So, a further object of the invention relates to a vector comprising a nucleic acid of the invention.

Such vectors may comprise regulatory elements, such as a promoter, enhancer, terminator and the like, to cause or direct expression of said polypeptide upon administration to a subject. Examples of promoters and enhancers used in the expression vector for an animal cell include early promoter and enhancer of SV40 (Mizukami T. et al. 1987), LTR promoter and enhancer of Moloney mouse leukemia virus (Kuwana Y et al. 1987), promoter (Mason JO et al. 1985) and enhancer (Gillies SD et al. 1983) of immunoglobulin H chain and the like.

Any expression vector for animal cell can be used, so long as a gene encoding the human antibody C region can be inserted and expressed. Examples of suitable vectors include pAGE107 (Miyaji H et al. 1990), pAGE103 (Mizukami T et al. 1987),

pHSG274 (Brady G et al. 1984), pKCR (O'Hare K et al. 1981), pSG1 beta d2-4-(Miyaji H et al. 1990) and the like.

Other examples of plasmids include replicating plasmids comprising an origin of replication, or integrative plasmids, such as for instance pUC, pcDNA, pBR, and the like.

Other examples of viral vector include adenoviral, retroviral, herpes virus and AAV vectors. Such recombinant viruses may be produced by techniques known in the art, such as by transfecting packaging cells or by transient transfection with helper plasmids or viruses. Typical examples of virus packaging cells include PA317 cells, PsiCRIP cells, GPenv+ cells, 293 cells, etc. Detailed protocols for producing such replication-defective recombinant viruses may be found for instance in WO 95/14785, WO 96/22378, US 5,882,877, US 6,013,516, US 4,861,719, US 5,278,056 and WO 94/19478.

A further object of the present invention relates to a cell which has been transfected, infected or transformed by a nucleic acid and/or a vector according to the invention.

The term "transformation" means the introduction of a "foreign" (i.e. extrinsic) gene, DNA or RNA sequence to a host cell, so that the host cell will express the introduced gene or sequence to produce a desired substance, typically a protein or enzyme coded by the introduced gene or sequence. A host cell that receives and expresses introduced DNA or RNA bas been "transformed".

The nucleic acids of the invention may be used to produce a recombinant antibody of the invention in a suitable expression system. The term "expression system" means a host cell and compatible vector under suitable conditions, e.g. for the expression of a protein coded for by foreign DNA carried by the vector and introduced to the host cell.

Common expression systems include *E. coli* host cells and plasmid vectors, insect host cells and Baculovirus vectors, and mammalian host cells and vectors. Other examples of host cells include, without limitation, prokaryotic cells (such as bacteria) and eukaryotic cells (such as yeast cells, mammalian cells, insect cells, plant cells, etc.). Specific examples include *E. coli, Kluyveromyces* or *Saccharomyces* yeasts, mammalian cell lines (e.g., Vero cells, CHO cells, 3T3 cells, COS cells, etc.) as well as primary or established mammalian cell cultures (e.g., produced from lymphoblasts, fibroblasts, embryonic cells, epithelial cells, nervous cells, adipocytes,

etc.). Examples also include mouse SP2/0-Ag14 cell (ATCC CRL1581), mouse P3X63-Ag8.653 cell (ATCC CRL1580), CHO cell in which a dihydrofolate reductase gene (hereinafter referred to as "DHFR gene") is defective (Urlaub G et al; 1980), rat YB2/3HL.P2.G11.16Ag.20 cell (ATCC CRL1662, hereinafter referred to as "YB2/0 cell"), and the like. In an embodiment the YB2/0 cell is used, since ADCC activity of chimeric or humanised antibodies is enhanced when expressed in this cell.

, For expression of humanised antibody, the expression vector may be either of a type in which a gene encoding an antibody heavy chain and a gene encoding an antibody light chain exists on separate vectors or of a type in which both genes exist on the same vector (tandem type). In respect of easiness of construction of a humanised antibody expression vector, easiness of introduction into animal cells, and balance between the expression levels of antibody H and L chains in animal cells, the humanised antibody expression vector is of the tandem type Shitara K et al. J Immunol Methods. 1994 Jan. 3;167(1-2):271-8). Examples of tandem type humanised antibody expression vector include pKANTEX93 (WO 97/10354), pEE18 and the like.

The present invention also relates to a method of producing a recombinant host cell expressing an antibody according to the invention, said method comprising the steps consisting of : (i) introducing *in vitro* or *ex vivo* a recombinant nucleic acid or a vector as described above into a competent host cell, (ii) culturing *in vitro* or *ex vivo* the recombinant host cell obtained and (iii), optionally, selecting the cells which express and/or secrete said antibody.

Such recombinant host cells can be used for the production of antibodies of the invention.

Methods of producing antibodies of the invention

Antibodies of the invention may be produced by any technique known in the art, such as, without limitation, any chemical, biological, genetic or enzymatic technique, either alone or in combination.

Knowing the amino acid sequence of the desired sequence, one skilled in the art can readily produce said antibodies or immunoglobulin chains, by standard techniques for production of polypeptides. For instance, they can be synthesized using well-known solid phase method using a commercially available peptide synthesis apparatus (such as that made by Applied Biosystems, Foster City, California) and following the manufacturer's instructions. Alternatively, antibodies and

immunoglobulin chains of the invention can be synthesized by recombinant DNA techniques as is well-known in the art. For example, these fragments can be obtained as DNA expression products after incorporation of DNA sequences encoding the desired (poly)peptide into expression vectors and introduction of such vectors into suitable eukaryotic or prokaryotic hosts that will express the desired polypeptide, from which they can be later isolated using well-known techniques.

The invention further relates to a method of producing an antibody of the invention, which method comprises the steps consisting of: (i) culturing a transformed host cell according to the invention; (ii) expressing said antibody or polypeptide; and (iii) recovering the expressed antibody or polypeptide.

Antibodies of the invention are suitably separated from the culture medium by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

In an r embodiment, a humanised chimeric antibody of the present invention can be produced by obtaining nucleic sequences encoding humanised VL and VH domains as previously described, constructing a human chimeric antibody expression vector by inserting them into an expression vector for animal cell having genes encoding human antibody CH and human antibody CL, and expressing the coding sequence by introducing the expression vector into an animal cell.

As the CH domain of a human chimeric antibody, it may be any region which belongs to human immunoglobulin heavy chains, but those of IgG class are suitable and any one of subclasses belonging to IgG class, such as IgG1, IgG2, IgG3 and IgG4, can also be used. Also, as the CL of a human chimeric antibody, it may be any region which belongs to human immunoglobulin light chains, and those of kappa class or lambda class can be used.

Methods for producing humanised or chimeric antibodies involve conventional recombinant DNA and gene transfection techniques are well known in the art (See Morrison SL. et al. (1984) and patent documents US5,202,238; and US5,204, 244).

Methods for producing humanised antibodies based on conventional recombinant DNA and gene transfection techniques are well known in the art (See, e. g., Riechmann L. et al. 1988; Neuberger MS. et al. 1985). Antibodies can be humanised using a variety of techniques known in the art including, for example, the technique disclosed in the application WO2009/032661, CDR-grafting (EP 239,400;

PCT publication WO91/09967; U.S. Pat. Nos. 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan EA (1991); Studnicka GM et al. (1994); Roguska MA. et al. (1994)), and chain shuffling (U.S. Pat. No.5,565,332). The general recombinant DNA technology for preparation of such antibodies is also known (see European Patent Application EP 125023 and International Patent Application WO 96/02576).

The Fab of the present invention can be obtained by treating an antibody which specifically reacts with CEACAM5 with a protease, such as papaine. Also, the Fab can be produced by inserting DNA sequences encoding both chains of the Fab of the antibody into a vector for prokaryotic expression, or for eukaryotic expression, and introducing the vector into procaryotic or eukaryotic cells (as appropriate) to express the Fab.

The F(ab')2 of the present invention can be obtained treating an antibody which specifically reacts with CEACAM5 with a protease, pepsin. Also, the F(ab')2 can be produced by binding Fab' described below via a thioether bond or a disulfide bond.

The Fab' of the present invention can be obtained treating F(ab')2 which specifically reacts with CEACAM5 with a reducing agent, such as dithiothreitol. Also, the Fab' can be produced by inserting DNA sequences encoding Fab' chains of the antibody into a vector for prokaryotic expression, or a vector for eukaryotic expression, and introducing the vector into prokaryotic or eukaryotic cells (as appropriate) to perform its expression.

The scFv of the present invention can be produced by taking sequences of the CDRs or VH and VL domains as previously described, constructing a DNA encoding an scFv fragment, inserting the DNA into a prokaryotic or eukaryotic expression vector, and then introducing the expression vector into prokaryotic or eukaryotic cells (as appropriate) to express the scFv. To generate a humanised scFv fragment, a well known technology called CDR grafting may be used, which involves selecting the complementary determining regions (CDRs) according to the invention, and grafting them onto a human scFv fragment framework of known three dimensional structure (see, e. g., W098/45322; WO 87/02671; US5,859,205; US5,585,089; US4,816,567; EP0173494).

Modification of the antibodies of the invention

Amino acid sequence modification(s) of the antibodies described herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. It is known that when a humanised antibody is produced by simply grafting only CDRs in VH and VL of an antibody derived from a non-human animal in FRs of the VH and VL of a human antibody, the antigen binding activity may be reduced in comparison with that of the original antibody derived from a non-human animal. It is considered that several amino acid residues of the VH and VL of the non-human antibody, not only in CDRs but also in FRs, may be directly or indirectly associated with the antigen binding activity. Hence, substitution of these amino acid residues with different amino acid residues derived from FRs of the VH and VL of the human antibody would reduce the binding activity. In order to solve the problem, in human antibodies grafted with non-human CDRs, attempts have to be made to identify, among amino acid sequences of the FR of the VH and VL of human antibodies, an amino acid residue which is directly associated with binding of the antibody, or which interacts with an amino acid residue of a CDR, or which maintains the three-dimensional structure of the antibody and which is directly associated with binding to the antigen. The reduced antigen binding activity could be increased by replacing the identified amino acids with amino acid residues of the original antibody derived from a non-human animal.

In one embodiment of the present invention, the six CDRs of a murine antibody of the invention and three amino acids from its framework were grafted onto a human framework, resulting in a humanized antibody (MAb2_VLg5VHg2) having a heavy chain of sequence SEQ ID NO:74 and a light chain of sequence SEQ ID NO:75, which maintained the binding characteristics to human and cynomolgus CEACAM5.

Modifications and changes may be made in the structure of the antibodies of the present invention, and in the DNA sequences encoding them, and still result in a functional antibody or polypeptide with desirable characteristics.

In making the changes in the amino sequences of polypeptide, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art. It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes,

substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8) ; phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophane (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate -3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

A further object of the present invention also encompasses function-conservative variants of the polypeptides of the present invention.

For example, certain amino acids may be substituted by other amino acids in a protein structure without appreciable loss of activity. Since the interactive capacity and nature of a protein define its biological functional activity, certain amino acid substitutions can be made in a protein sequence, and of course in its DNA encoding sequence, while nevertheless obtaining a protein with like properties. It is thus contemplated that various changes may be made in the antibodies sequences of the invention, or corresponding DNA sequences which encode said polypeptides, without appreciable loss of their biological activity.

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e. still obtain a biological functionally equivalent protein. It is also possible to use well-established technologies, such as alanine-scanning approaches, to identify, in an antibody or polypeptide of the invention, all the amino acids that can be substituted without significant loss of binding to the antigen. Such residues can be qualified as neutral, since they are not involved in antigen binding or in maintaining the structure of the antibody. One or more of these neutral positions can be substituted by alanine or by another amino acid can without changing the main characteristics of the antibody or polypeptide of the invention.

This was illustrated in the current invention by an alanine-scanning approach made on the CDRs of $MAb2_{K52R,}$ showing that several positions of these CDRs appear as neutral, since an alanine could indeed be substituted without significant effect on the binding to human and cynomolgus CEACAM5. Antibody variants resulting from such neutral substitutions are therefore expected to remain functionally identical to the parental antibody. In the provided example 6.4, substitutions were done in a humanized variant of MAb2, but it is predictable that the same variations would also

maintain the biological function when introduced into any variant of MAb2, Mab4 or Mab5, since these related antibodies all carry the same set of 6 CDRs or very closely related ones. The neutral positions can be defined as residues 27, 28, 29, 31, 51, 52, 89, 90, 93, 94, 96, 97 in VL sequences of this antibody family (SEQ ID NO:34 or SEQ ID NO:38 or SEQ ID NO:40 or SEQ ID NO:17 or SEQ ID NO:23 or SEQ ID NO:29 or SEQ ID NO:55 or SEQ ID NO:75) and residues 26 to 31, 51 to 58, 97, 103, 104, 107, 109 in VH sequences of this antibody family (SEQ ID NO:33 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:5 or SEQ ID NO:51 or SEQ ID NO:74).

Neutral positions can be seen as positions where any amino acid substitution could be incorporated to Mab2, Mab4 or Mab5 CDRs. Indeed, in the principle of alanine-scanning, alanine is chosen since it this residue does not carry specific structural or chemical features. It is generally admitted that if an anlanine can be substituted for a specific amino acid without changing the properties of a protein, many other, if not all amino acid substitutions are likely to be also neutral. In the opposite case where alanine is the wild-type amino acid, if a specific substitution can be shown as neutral, it is likely that other substitutions would also be neutral.

In the provided example 6.4, four positions in the CDRs of Mab2, Mab4 or Mab5 are also identified, that were not found neutral in the context of the alanine-scanning, but where a conservative type of amino acid substitutions has a neutral effect (residues 30 and 92 in VL sequences and residues 98 and 100 in VH sequences of this antibody family)

It is also expected that two or more neutral mutations at different positions in any or in both of the two antibody chain sequences, when combined, would usually result in an antibody which essentially keeps the functional activities of the parental antibody. This has been illustrated for instance with the combined subsitutions LC_T51A and LC_T94A,, VL_S31A and VH_G54Y, or VL _T53I and VH _S53A in MAb2_VLg5VHg2.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions which take any of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

It may be also desirable to modify the antibody of the invention with respect to

effector function, e.g. so as to enhance antigen-dependent cell-mediated cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing inter-chain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and/or antibody-dependent cellular cytotoxicity (ADCC) (Caron PC. et al. 1992; and Shopes B. 1992).

Another type of amino acid modification of the antibody of the invention may be useful for altering the original glycosylation pattern of the antibody, i.e. by deleting one or more carbohydrate moieties found in the antibody, and/or adding one or more glycosylation sites that are not present in the antibody. The presence of either of the tripeptide sequences asparagine-X-serine, and asparagine-X-threonine, where X is any amino acid except proline, creates a potential glycosylation site. Addition or deletion of glycosylation sites to the antibody is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites).

Another type of modification involves the removal of sequences identified, either in silico or experimentally, as potentially resulting in degradation products or heterogeneity of antibody preparations. As examples, deamidation of asparagine and glutamine residues can occur depending on factors such as pH and surface exposure. Asparagine residues are particularly susceptible to deamidation, primarily when present in the sequence Asn-Gly, and to a lesser extent in other dipeptide sequences such as Asn-Ala. When such a deamidation site, in particular Asn-Gly, is present in an antibody or polypeptuide of the invention, it may therefore be desirable to remove the site, typically by conservative substitution to remove one of the implicated residues. Such substitutions in a sequence to remove one or more of the implicated residues are also intended to be encompassed by the present invention.

Another type of covalent modification involves chemically or enzymatically coupling glycosides to the antibody. These procedures are advantageous in that they do not require production of the antibody in a host cell that has glycosylation capabilities for N-or O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as

those of serine, threonine, orhydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. For example, such methods are described in WO87/05330.

Removal of any carbohydrate moieties present on the antibody may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the antibody to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the antibody intact. Chemical deglycosylation is described by Sojahr H. et al. (1987) and by Edge, AS. et al. (1981). Enzymatic cleavage of carbohydrate moieties on antibodies can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, NR. et al. (1987).

Another type of covalent modification of the antibody comprises linking the antibody to one of a variety of non proteinaceous polymers, eg. , polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in US Patent Nos. 4,640, 835; 4,496, 689; 4,301, 144; 4,670, 417; 4,791, 192 or 4,179,337.

Immunoconjugates

The present invention also includes cytotoxic conjugates, or immunoconjugates, or antibody-drug conjugates, or conjugates. As used herein, all these terms have the same meaning and are interchangeable.

The murine antibodies, MAb1, MAb2, MAb3, MAb4, and MAb5, have been conjugated to a maytansinoid (DM4) through a SPDB linker (N-succinimidyl pyridyldithiobutyrate). The resulting antibody-drug-conjugates (ADC) were found to have cytotoxic activity on MKN45 human gastric cancer cells, with IC_{50} values ≤ 1 nM.

Similarly, antibody-SPDB-DM4 conjugates were prepared based on a chimeric form of each of MAb1, MAb2, MAb4, and MAb5. The resulting chMAb1-SPDB-DM4, chMAb2-SPDB-DM4, chMAb3-SPDB-DM4, and chMAb4-SPDB-DM4 were evaluated at two doses against measurable primary colon CR-IGR-034P tumors implanted s.c. in female SCID mice. Analysis of changes in tumor volume for each treated and control and % of tumor regression indicated that chMAb2-SPDB-DM4, chMAb4-SPDB-DM4, and chMAb5-SPDB-DM4 were highly active, at least at the highest dose assayed, and that chMAb2-SPDB-DM4 was active at both assayed doses. Percentages of tumor regression up to 82% were notably obtained.

Antibody-SPDB-DM4 conjugates were also prepared using the humanised variants of MAb2 (huMAb2-1-SPDB-DM4, huMAb2-2-SPDB-DM4, and huMAb2-3-SPDB-DM4). ADC including the chimeric (chMAb2-SPDB-DM4) or humanised variants of MAb2 were compared with an irrelevant antibody-SPDB-DM4 for cytotoxic activity on MKN45 cells. All chimeric and humanised variants of MAb2 ADCs displayed IC_{50} values ≤ 1 nM, i.e. IC_{50} values 53 to 35 fold lower than the measured cytotoxic activity of the irrelevant DM4 conjugate, thereby indicating CEACAM5-mediated cytotoxic activities of the anti-CEACAM5 conjugates.

Anti-tumor activity of huMAb2-3-SPDB-DM4 and huMAb2-4-SPDB-DM4 was evaluated and compared to the chMAb2-SPDB-DM4 against measurable primary colon CR-IGR-034P tumors implanted s.c. in female CD-1 nude mice. All conjugates were highly active at the highest dose assayed (10 mg/kg).

Anti-tumor activity of huMAb2-3-SPDB-DM4 and huMAb2-3-sulfo-SPDB-DM4 was further evaluated against measurable primary colon CR-IGR-034P tumors implanted s.c. in female SCID mice. huMAb2-3-SPDB-DM4 was active at 5 and 2.5 mg/kg, huMAb2-3-sulfo-SPDB-DM4 was highly active at 5 mg/kg and active at 2.5 mg/kg.

Anti-tumor activity of huMAb2-3-SPDB-DM4 was further evaluated against measurable primary lung LUN-NIC-0014 tumors implanted s.c. in female SCID mice and was found to be was highly active at 10 and 5 mg/kg.

Each DM4 conjugate included a mean number of DM4 molecules (or “drug-to-antibody ratio” or “DAR”) ranging from 2 to 5.

Accordingly, the invention relates to “immunoconjugates” comprising an antibody of the invention linked or conjugated to at least one growth inhibitory agent , such as a cytotoxic agent or or a radioactive isotope.

A "growth inhibitory agent", or “anti-proliferative agent”, which can be used indifferently, refers to a compound or composition which inhibits growth of a cell, especially tumour cell, either *in vitro* or *in vivo*.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term "cytotoxic agent" is intended to include chemotherapeutic agents, enzymes, antibiotics, and 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. In some embodiments, the cytotoxic

agent is a taxoid, vincas, a maytansinoid or maytansinoid analog such as DM1 or DM4, a small drug, a tomaymycin or pyrrolobenzodiazepine derivative, a cryptophycin derivative, a leptomycin derivative, an auristatin or dolastatin analog, a prodrug, topoisomerase II inhibitors, a DNA alkylating agent, an anti-tubulin agent, a CC-1065 or CC-1065 analog.

As used herein "maytansinoids" denotes maytansinoids and maytansinoid analogs. Maytansinoids are drugs that inhibit microtubule formation and that are highly toxic to mammalian cells.

Examples of suitable maytansinoids include maytansinol and maytansinol analogs.

Examples of suitable maytansinol analogues include those having a modified aromatic ring and those having modifications at other positions. Such suitable maytansinoids are disclosed in U.S. Patent Nos. 4,424,219; 4,256,746; 4,294,757; 4,307,016; 4,313,946; 4,315,929; 4,331,598; 4,361,650; 4,362,663; 4,364,866; 4,450,254; 4,322,348; 4,371,533; 6,333,410; 5,475,092; 5,585,499; and 5,846,545.

Specific examples of suitable analogues of maytansinol having a modified aromatic ring include:

(1) C-19-dechloro (U.S. Pat. No. 4,256,746) (prepared by LAH reduction of ansamytocin P2);

(2) C-20-hydroxy (or C-20-demethyl) +/-C-19-dechloro (U.S. Pat. Nos. 4,361,650 and 4,307,016) (prepared by demethylation using *Streptomyces* or *Actinomyces* or dechlorination using LAH); and

(3) C-20-demethoxy, C-20-acyloxy (-OCOR), +/-dechloro (U.S. Pat. No 4,294,757) (prepared by acylation using acyl chlorides).

Specific examples of suitable analogues of maytansinol having modifications of other positions include:

(1) C-9-SH (U.S. Pat. No. 4,424,219) (prepared by the reaction of maytansinol with H_2S or P_2S_5);

(2) C-14-alkoxymethyl (demethoxy/CH_2OR) (U.S. Pat. No. 4,331,598);

(3) C-14-hydroxymethyl or acyloxymethyl (CH_2OH or CH_2OAc) (U.S. Pat. No. 4,450,254) (prepared from *Nocardia*);

(4) C-15-hydroxy/acyloxy (U.S. Pat. No. 4,364,866) (prepared by the conversion of maytansinol by *Streptomyces*);

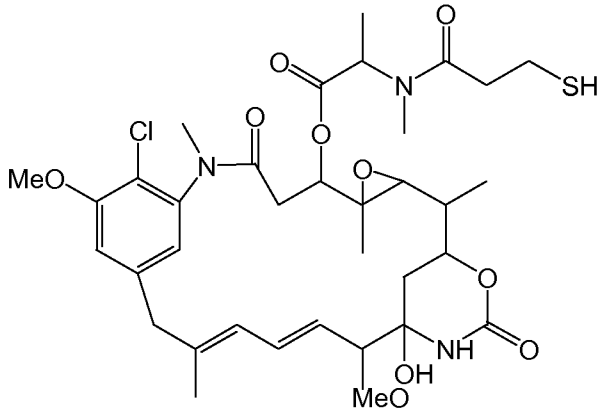
(5) C-15-methoxy (U.S. Pat. Nos. 4,313,946 and 4,315,929) (isolated from

Trewia nudiflora);

(6) C-18-*N*-demethyl (U.S. Pat. Nos. 4,362,663 and 4,322,348) (prepared by the demethylation of maytansinol by *Streptomyces*); and

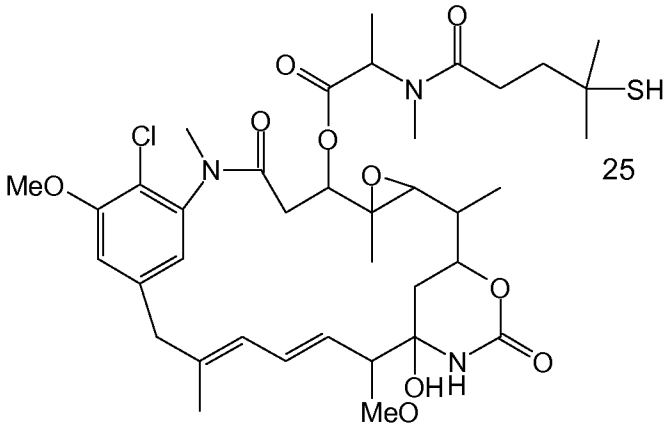
(7) 4,5-deoxy (U.S. Pat. No 4,371,533) (prepared by the titanium trichloride/LAH reduction of maytansinol).

In an embodiment of the invention , the cytotoxic conjugates of the present invention utilize the thiol-containing maytansinoid (DM1), formally termed $N^{2'}$-deacetyl-$N^{2'}$-(3-mercapto-1-oxopropyl)-maytansine, as the cytotoxic agent. DM1 is represented by the following structural formula (I):



(I).

In another embodiment, the cytotoxic conjugates of the present invention utilize the thiol-containing maytansinoid DM4, formally termed $N^{2'}$-deacetyl-N-$^{2'}$(4-methyl-4-mercapto-1-oxopentyl)-maytansine, as the cytotoxic agent. DM4 is represented by the following structural formula (II):



(II)

In further embodiments of the invention, other maytansines, including thiol and

disulfide-containing maytansinoids bearing a mono or di-alkyl substitution on the carbon atom bearing the sulfur atom, may be used. These include a maytansinoid having, at C-3, C-14 hydroxymethyl, C-15 hydroxy, or C–20 desmethyl, an acylated amino acid side chain with an acyl group bearing a hindered sulfhydryl group, wherein the carbon atom of the acyl group bearing the thiol functionality has one or two substituents, said substituents being CH_3, C_2H_5, linear or branched alkyl or alkenyl having from 1 to 10 reagents and any aggregate which may be present in the solution.

Examples of these cytotoxic agents and of methods of conjugation are further given in the application WO2008/010101 which is incorporated by reference.

The term "radioactive isotope" is intended to include radioactive isotopes suitable for treating cancer, such as At^{211}, Bi^{212}, Er^{169}, I^{131}, I^{125}, Y^{90}, In^{111}, P^{32}, Re^{186}, Re^{188}, Sm^{153}, Sr^{89}, and radioactive isotopes of Lu. Such radioisotopes generally emit mainly beta-radiation.In an embodiment the radioactive isotope is alpha-emitter isotope, more precisely Thorium 227 which emits alpha-radiation. The immunoconjugates according to the present invention can be prepared as described in the application WO2004/091668.

In some embodiments, the antibodies of the present invention are covalently attached, directly or via a cleavable or non-cleavable linker, to at least one growth inhibitory agent.

"Linker", as used herein, means a chemical moiety comprising a covalent bond or a chain of atoms that covalently attaches a polypeptide to a drug moiety.

The conjugates may be prepared by *in vitro* methods. In order to link a drug or prodrug to the antibody, a linking group is used. Suitable linking groups are well known in the art and include disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups and esterase labile groups. Conjugation of an antibody of the invention with cytotoxic agents or growth inhibitory agents may be made using a variety of bifunctional protein coupling agents including but not limited to N-succinimidyl pyridyldithiobutyrate (SPDB), butanoic acid 4-[(5-nitro-2-pyridinyl)dithio]-2,5-dioxo-1-pyrrolidinyl ester (nitro-SPDB), 4-(Pyridin-2-yldisulfanyl)-2-sulfo-butyric acid (sulfo-SPDB), N-succinimidyl (2-pyridyldithio) propionate (SPDP), succinimidyl (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 et al (1987). Carbon labeled 1-isothiocyanatobenzyl methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody (WO 94/11026).

The linker may be a "cleavable linker" facilitating release of the cytotoxic agent or growth inhibitory agent in the cell. For example, an acid-labile linker, a peptidase-sensitive linker, an esterase labile linker, a photolabile linker or a disulfide-containing linker (See e.g. U.S. Patent No. 5,208,020) may be used. The linker may be also a "non-cleavable linker" (for example SMCC linker) that might led to better tolerance in some cases.

Alternatively, a fusion protein comprising the antibody of the invention and a cytotoxic or growth inhibitory polypeptide may be made, by recombinant techniques or peptide synthesis. The length of DNA may comprise respective regions encoding the two portions of the conjugate either adjacent one another or separated by a region encoding a linker peptide which does not destroy the desired properties of the conjugate.

The antibodies of the present invention may also be used in Dependent Enzyme Mediated Prodrug Therapy by conjugating the polypeptide to a prodrug-activating enzyme which converts a prodrug (e.g. a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug (See, for example, WO 88/07378 and U.S. Patent No. 4,975,278). The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to convert it into its more active, cytotoxic form. Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic fluorocytosine into the anticancer drug, 5-fluorouracil; proteases, such as serratia protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as O-galactosidase and neuraminidase useful for converting glycosylated prodrugs into free

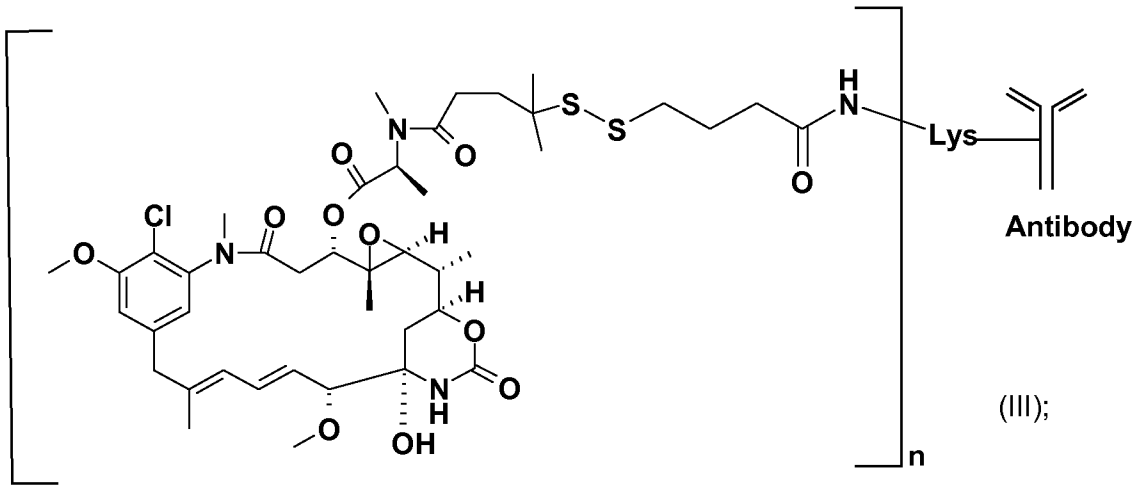
drugs; P-lactamase useful for converting drugs derivatized with P- lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. The enzymes can be covalently bound to the polypeptides of the invention by techniques well known in the art such as the use of the heterobifunctional crosslinking reagents discussed above.

According to an embodiment, in the conjugate of the invention, the growth inhibitory agent is a maytansinoid, in an embodiment DM1 or DM4.

In said conjugate, the antibody is conjugated to said at least one growth inhibitory agent by a linking group. In an embodiment said linking group is a cleavable or a non-cleavable linker, such as SPDB, sulfo-SPDB, or SMCC.

The conjugate may be selected from the group consisting of:

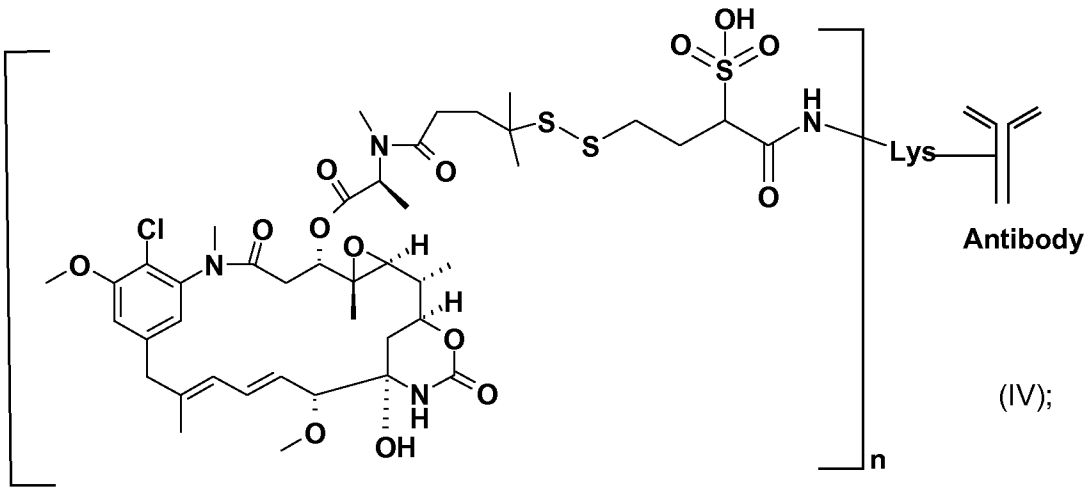
i) an antibody-SPDB-DM4 conjugate of fomula (III)



(III);

Ab-SPDB-DM4

ii) an antibody-sulfo-SPDB-DM4 conjugate of fomula (IV)

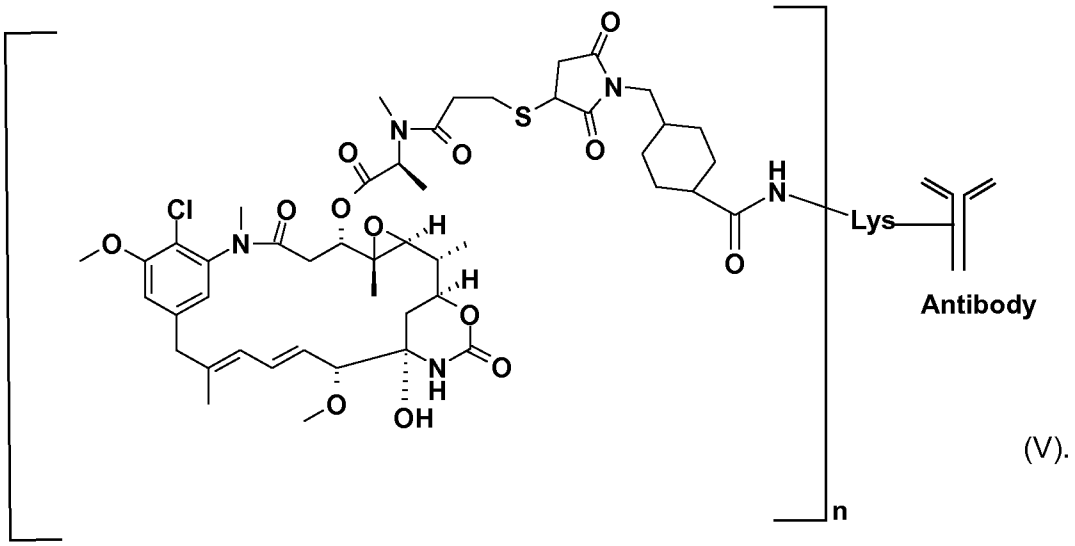


(IV);

Ab-SulfoSPDB-DM4

and

iii) an antibody-SMCC-DM1 conjugate of fomula (V)



(V).

Ab-SMCC-DM1

In said embodiment, the antibody included in the conjugate is selected from the group consisting of:

i) a humanised antibody comprising a heavy chain of sequence SEQ ID NO:51 and a light chain of sequence SEQ ID NO:17,

ii) a humanised antibody comprising a heavy chain of sequence SEQ ID NO:5 and a light chain of sequence SEQ ID NO:23,

iii) a humanised antibody comprising heavy chain of sequence SEQ ID NO:5 and a light chain of sequence SEQ ID NO:29, and

iv) a humanised antibody comprising heavy chain of sequence SEQ ID NO:51 and a light chain of sequence SEQ ID NO:55.

In an embodiment the conjugate is a conjugate of formula (III), (IV) or (V) as defined above, in which the antibody is a humanised antibody comprising heavy chain of sequence SEQ ID NO:5 and a light chain of sequence SEQ ID NO:29.

In general, the conjugate can be obtained by a process comprising the steps of:

(i) bringing into contact an optionally-buffered aqueous solution of a cell-binding agent (e.g. an antibody according to the invention) with solutions of a linker and a cytotoxic compound;

(ii) then optionally separating the conjugate which was formed in (i) from the

unreacted cell-binding agent.

The aqueous solution of cell-binding agent can be buffered with buffers such as, e.g. potassium phosphate, acetate, citrate or N-2-Hydroxyethylpiperazine-N'-2-ethanesulfonic acid (Hepes buffer). The buffer depends upon the nature of the cell-binding agent. The cytotoxic compound is in solution in an organic polar solvent, e.g. dimethyl sulfoxide (DMSO) or dimethylacetamide (DMA).

The reaction temperature is usually comprised between 20 and 40°C. The reaction time can vary from 1 to 24 hours. The reaction between the cell-binding agent and the cytotoxic agent can be monitored by size exclusion chromatography (SEC) with a refractometric and/or UV detector. If the conjugate yield is too low, the reaction time can be extended.

A number of different chromatography methods can be used by the person skilled in the art in order to perform the separation of step (ii): the conjugate can be purified e.g. by SEC, adsorption chromatography (such as ion exchange chromatography, IEC), hydrophobic interaction chromatograhy (HIC), affinity chromatography, mixed-support chromatography such as hydroxyapatite chromatography, or high performance liquid chromatography (HPLC). Purification by dialysis or diafiltration can also be used.

As used herein, the term "aggregates" means the associations which can be formed between two or more cell-binding agents, said agents being modified or not by conjugation. The aggregates can be formed under the influence of a great number of parameters, such as a high concentration of cell-binding agent in the solution, the pH of the solution, high shearing forces, the number of bonded dimers and their hydrophobic character, the temperature (see Wang & Gosh, 2008, *J. Membrane Sci.*, 318: 311-316, and references cited therein); note that the relative influence of some of these parameters is not clearly established. In the case of proteins and antibodies, the person skilled in the art will refer to Cromwell *et al.* (2006, *AAPS Jounal*, 8(3): E572-E579). The content in aggregates can be determined with techniques well known to the skilled person, such as SEC (see Walter *et al.*, 1993, *Anal. Biochem.*, 212(2): 469-480).

After step (i) or (ii), the conjugate-containing solution can be submitted to an additional step (iii) of chromatography, ultrafiltration and/or diafiltration.

The conjugate is recovered at the end of these steps in an aqueous solution.

According to an embodiment, the conjugate according to the invention is

characterised by a "drug-to-antibody ratio" (or "DAR") ranging from 1 to 10, for instance from 2 to 5, in particular from 3 to 4. This is generally the case of conjugates including maytansinoid molecules.

This DAR number can vary with the nature of the antibody and of the drug (i.e. the growth-inhibitory agent) used along with the experimental conditions used for the conjugation (like the ratio growth-inhibitory agent/antibody, the reaction time, the nature of the solvent and of the cosolvent if any). Thus the contact between the antibody and the growth-inhibitory agent leads to a mixture comprising several conjugates differing from one another by different drug-to-antibody ratios; optionally the naked antibody; optionally aggregates. The DAR that is determined is thus a mean value.

A method which can be used to determine the DAR consists in measuring spectrophotometrically the ratio of the absorbance at of a solution of substantially purified conjugate at λ_D and 280 nm. 280 nm is a wavelength generally used for measuring protein concentration, such as antibody concentration. The wavelength λ_D is selected so as to allow discriminating the drug from the antibody, i.e. as readily known to the skilled person, λ_D is a wavelength at which the drug has a high absorbance and λ_D is sufficiently remote from 280 nm to avoid substantial overlap in the absorbance peaks of the drug and antibody. λ_D may be selected as being 252 nm in the case of maytansinoid molecules. A method of DAR calculation may be derived from Antony S. Dimitrov (ed), LLC, 2009, Therapeutic Antibodies and Protocols, vol 525, 445, Springer Science:

The absorbances for the conjugate at λ_D ($A_{\lambda D}$) and at 280 nm (A_{280}) are measured either on the monomeric peak of the size exclusion chromatography (SEC) analysis (allowing to calculate the "DAR(SEC)" parameter) or using a classic spectrophotometer apparatus (allowing to calculate the "DAR(UV)" parameter). The absorbances can be expressed as follows:

$$A_{\lambda D} = (c_D \times \varepsilon_{D\lambda D}) + (c_A \times \varepsilon_{A\lambda D})$$

$$A_{280} = (c_D \times \varepsilon_{D280}) + (c_A \times \varepsilon_{A280})$$

wherein :

- c_D and c_A are respectively the concentrations in the solution of the drug and of the antibody
- $\varepsilon_{D\lambda D}$ and ε_{D280} are respectively the molar extinction coefficients of the drug at λ_D and 280 nm

- $\varepsilon_{A\lambda D}$ and ε_{A280} are respectively the molar extinction coefficients of the antibody at λ_D and 280 nm.

Resolution of these two equations with two unknowns leads to the following equations:

$$c_D = [(\varepsilon_{A280} \times A_{\lambda D}) - (\varepsilon_{A\lambda D} \times A_{280})] / [(\varepsilon_{D\lambda D} \times \varepsilon_{A280}) - (\varepsilon_{A\lambda D} \times \varepsilon_{D280})]$$

$$c_A = [A_{280} - (c_D \times \varepsilon_{D280})] / \varepsilon_{A280}$$

The average DAR is then calculated from the ratio of the drug concentration to that of the antibody: $DAR = c_D / c_A$.

Pharmaceutical compositions

The antibodies or immunoconjugates of the invention may be combined with pharmaceutically acceptable excipients, and optionally sustained-release matrices, such as biodegradable polymers, to form therapeutic compositions.

Thus, another object of the invention relates to a pharmaceutical composition comprising an antibody or an immunoconjugate of the invention and a pharmaceutically acceptable carrier or excipient.

The invention also relates to a polypeptide or an immunoconjugate according to the invention, for use as a medicament.

"Pharmaceutically" or "pharmaceutically acceptable" refers to molecular entities and compositions that do not produce an adverse, allergic or other untoward reaction when administered to a mammal, especially a human, as appropriate. A pharmaceutically acceptable carrier or excipient refers to a non-toxic solid, semi-solid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type.

As used herein, "pharmaceutically-acceptable carriers" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, and the like that are physiologically compatible. Examples of suitable carriers, diluents and/or excipients include one or more of water, amino acids, saline, phosphate buffered saline, buffer phosphate, acetate, citrate, succinate; amino acids and derivates such as histidine, arginine, glycine, proline, glycylglycine; inorganic salts NaCl, calcium chloride; sugars or polyalcohols such as dextrose, glycerol, ethanol, sucrose, trehalose, mannitol; surfactants such as Polysorbate 80, polysorbate 20, poloxamer 188; and the like, as well as combination thereof. In many cases, it will be preferable to include isotonic agents, such as sugars, polyalcohols, or sodium chloride in the composition, and formulation may also contain an antioxidant such as tryptamine and

a stabilizing agent such as Tween 20.

The form of the pharmaceutical compositions, the route of administration, the dosage and the regimen naturally depend upon the condition to be treated, the severity of the illness, the age, weight, and gender of the patient, etc.

The pharmaceutical compositions of the invention can be formulated for a topical, oral, parenteral, intranasal, intravenous, intramuscular, subcutaneous or intraocular administration and the like.

In an embodiment, the pharmaceutical compositions contain vehicles which are pharmaceutically acceptable for a formulation capable of being injected. These may be isotonic, sterile, saline solutions (monosodium or disodium phosphate, sodium, potassium, calcium or magnesium chloride and the like or mixtures of such salts), or dry, especially freeze-dried compositions which upon addition, depending on the case, of sterilized water or physiological saline, permit the constitution of injectable solutions.

The pharmaceutical composition can be administrated through drug combination devices.

The doses used for the administration can be adapted as a function of various parameters, and for instance as a function of the mode of administration used, of the relevant pathology, or alternatively of the desired duration of treatment.

To prepare pharmaceutical compositions, an effective amount of the antibody or immunoconjugate of the invention may be dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions; formulations including sesame oil, peanut oil or aqueous propylene glycol; and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases, the form must be sterile and injectable with the appropriate device or system for delivery without degradation. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi.

Solutions of the active compounds as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with a surfactant. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

A polypeptide, antibody or immunoconjugate of the invention can be formulated into a composition in a neutral or salt form. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, glycine, histidine, procaine and the like.

The carrier can also be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetables oils. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminium monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with any of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The preparation of more concentrated, or highly concentrated solutions for direct injection is also contemplated, where the use of DMSO as solvent is envisioned to result in extremely rapid penetration, delivering high concentrations of the active agents to a small tumor area.

Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms, such as the type of injectable solutions described above, but drug release capsules and the like can also be employed.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, sterile aqueous media which can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage could be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject.

The antibody or immunoconjugate of the invention may be formulated within a therapeutic mixture to comprise about 0.01 to 100 milligrams, per dose or so.

In addition to the antibody or immunoconjugate formulated for parenteral administration, such as intravenous or intramuscular injection, other pharmaceutically acceptable forms include, e.g. tablets or other solids for oral administration; time release capsules; and any other form currently used.

In certain embodiments, the use of liposomes and/or nanoparticles is contemplated for the introduction of polypeptides into host cells. The formation and use of liposomes and/or nanoparticles are known to those of skill in the art.

Nanocapsules can generally entrap compounds in a stable and reproducible way. To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) are generally designed using polymers able to be degraded in vivo. Biodegradable polyalkyl-cyanoacrylate nanoparticles, or biodegradable polylactide or polylactide co glycolide nanoparticules that meet these requirements are contemplated for use in the present invention, and such particles may be are easily made.

Liposomes are formed from phospholipids that are dispersed in an aqueous

medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)). MLVs generally have diameters of from 25 nm to 4 µm. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations.

Therapeutic methods and uses

The inventors have shown that the five antibodies they have produced are able to internalize the CEACAM5-antibody complex after binding. Furthermore, they have shown that these antibodies, combined with a cytotoxic maytansinoid (DM4), induce cytotoxic activity on human MKN45 tumor cells in vitro. They have also shown that these immunoconjugates induce a marked anti-tumor activity in vivo in a murine model of human primary colon tumor xenografts derived from patient, when used at a dose of 5 mg/kg and 2.5 mg/kg, with a single injection at day 14 post tumor implantation.

Thus, polypeptides, antibodies, immunoconjugates, or pharmaceutical compositions of the invention may be useful for treating cancer.

The cancer to be treated with antibodies, immunoconjugates, or pharmaceutical compositions of the invention is a cancer expressing CEACAM5, in particular overexpressing CEACAM5 as compared to normal (i.e. non tumoral) cells of the same tissular origin. Expression of CEACAM5 by cancer cells may be readily assayed for instance by using an antibody according to the invention, as described in the following section “Diagnostic uses”, and in particular by an immunohistochemical method for instance as described in Example 8.

In an embodiment, the cancer may be a colorectal, stomach, lung, uterus cervix, pancreas, oesophagus, ovary, thyroid, bladder, endometrium, breast, liver (for instance cholangiocarcinoma), prostate, or skin cancer. Screening of a panel of human tumors by immunohistochemistry using a mouse anti-human CEACAM5 antibody according to the invention indeed showed antibody staining in these types of cancers, as described in further details in Example 8.

The antibodies or immunoconjugates of the invention may be used alone or in combination with any suitable growth-inhibitory agent.

The antibodies of the invention may be conjugated or linked to a growth

inhibitory agent, cytotoxic agent, or a prodrug-activating enzyme as previously described. Antibodies of the invention may be indeed useful for targeting said growth inhibitory agent, cytotoxic agent, or a prodrug to the cancerous cells expressing or over-expressing CEACAM5 on their surface.

It is also well known that therapeutic monoclonal antibodies can lead to the depletion of cells bearing the antigen specifically recognized by the antibody. This depletion can be mediated through at least three mechanisms: antibody mediated cellular cytotoxicity (ADCC), complement dependent lysis, and direct anti-tumour inhibition of tumour growth through signals given via the antigen targeted by the antibody.

"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system to antibodies which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g. as described in Gazzano-Santoro et al. (1997) may be performed.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted antibodies bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g. Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell. To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed.

Thus, an object of the invention relates to a method for treating a cancer comprising administering a subject in need thereof with a therapeutically effective amount of a polypeptide, an antibody, an immunoconjugate or a pharmaceutical composition of the invention.

In the context of the invention, the term "treating" or "treatment", as used herein, means reversing, alleviating, inhibiting the progress of, or preventing the disorder or condition to which such term applies, or one or more symptoms of such disorder or condition. By the term "treating cancer" as used herein is meant the inhibition of the growth of malignant cells of a tumour and/or the progression of metastases from said tumor. Such treatment can also lead to the regression of tumor growth, i.e., the decrease in size of a measurable tumor. In particular, such treatment leads to the complete regression of the tumor or metastase.

According to the invention, the term "patient" or "patient in need thereof" is intended for a human or non-human mammal affected or likely to be affected with a malignant tumor. In particular, said patient may be a patient who has been determined to be susceptible to a therapeutic agent targeting CEACAM5, in particular to an antibody or immunoconjugate according to the invention, for instance according to a method as described herebelow.

By a "therapeutically effective amount" of the polypeptide of the invention is meant a sufficient amount of the polypeptide to treat said cancer disease, at a reasonable benefit/risk ratio applicable to any medical treatment. It will be understood, however, that the total daily usage of the polypeptides and compositions of the present invention will be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective dose level for any particular patient will depend upon a variety of factors including the disorder being treated and the severity of the disorder; activity of the specific polypeptide employed; the specific composition employed, the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific polypeptide employed; the duration of the treatment; drugs used in combination or coincidental with the specific polypeptide employed; and like factors well known in the medical arts. For example, it is well known within the skill of the art to start doses of the compound at levels lower than those required to achieve the desired therapeutic effect and to gradually increase the dosage until the desired effect is achieved.

Another object of the invention relates to a polypeptide, an antibody, an immunoconjugate or a pharmaceutical composition of the invention for use in the treatment of a malignant tumour.

The polypeptide, antibody, immunoconjugate or pharmaceutical composition may be used for inhibiting the progression of metastases of a malignant tumour.

Polypeptides of the invention may be used in combination with any other therapeutical strategy for treating malignant tumour (e.g. adjuvant therapy), and/or for reducing the growth of the metastatic tumour.

Efficacy of the treatment with an antibody or immunoconjugate according to the invention may be readily assayed in vivo, for instance on a mouse model of cancer and by measuring e.g. changes in tumor volume between treated and control groups, % tumor regression, partial regression and/or complete regression as defined in Example 5.3.

Diagnostic uses

CEACAM5 has been reported to be highly expressed on the surface of colorectal, gastric, lung, uterine tumor cells and weakly expressed in few normal epithelial cells such as colon and esophagus epithelial cells. Additionally, screening of a panel of human tumors by immunohistochemistry using a mouse anti-human CEACAM5 antibody according to the invention showed antibody staining in colorectal, stomach, lung, uterus cervix, pancreas, oesophagus, ovary, thyroid, bladder, endometrium, breast, liver (in particular cholangiocarcinoma), prostate, and skin cancers.

Therefore, CEACAM5 constitutes a cancer marker and, therefore, has the potential to be used to indicate the effectiveness of an anti-cancer therapy or detecting recurrence of the disease.

In an embodiment, the antibody of the invention is used as component of an assay in the context of a therapy targeting CEACAM5 expressing tumours, in order to determine susceptibility of the patient to the therapeutic agent, monitor the effectiveness of the anti-cancer therapy or detect recurrence of the disease after treatment. In particular, the same antibody of the invention is used both as component of the therapeutic agent and as component of the diagnostic assay.

Thus, a further object of the invention relates to an antibody according to the invention for use for *in vivo* detecting CEACAM5 expression in a subject, or for use for *ex vivo* detecting CEACAM5 expression in biological sample of a subject. Said detection may be intended in particular for

a) diagnosing the presence of a cancer in a subject, or

b) determining susceptibility of a patient having cancer to a therapeutic agent targeting CEACAM5, in particular an immunoconjugate according to the invention, or

c) monitoring effectiveness of anti-CEACAM5 cancer therapy or detecting cancer relapse after anti-CEACAM5 cancer therapy, in particular for therapy with an immunoconjugate according to the invention;

by detecting expression of the surface protein CEACAM5 on tumor cells.

In an embodiment, the antibody is intended for an *in vitro* or *ex vivo* use. For example, CEACAM5 may be detected *in vitro* or *ex vivo* in a biological sample obtained from a subject, using an antibody of the invention. The use according to the invention may also be an *in vivo* use. For example, an antibody according to the invention is administered to the subject and antibody-cells complexes are detected

and/or quantified, whereby the detection of said complexes is indicative of a cancer.

The invention further relates to an *in vitro* or *ex vivo* method of detecting the presence of a cancer in a subject, comprising the steps consisting of:

(a) contacting a biological sample of a subject with an antibody according to the invention, in particular in conditions sufficient for the antibody to form complexes with said biological sample;

(b) measuring the level of antibody bound to said biological sample,

(c) detecting the presence of a cancer by comparing the measured level of bound antibody with a control, an increased level of bound antibody compared to control being indicative of a cancer.

The invention also relates to an *in vitro* or *ex vivo* method of determining susceptibility of a patient having cancer to a therapeutic agent targeting CEACAM5, in particular to an immunoconjugate according to the invention, which method comprises the steps consisting of:

(a) contacting a biological sample of a patient having cancer with an antibody according to the invention, in particular in conditions sufficient for the antibody to form complexes with said biological sample;

(b) measuring the level of antibody bound to said biological sample sample,

(c) comparing the measured level of bound antibody to said biological sample sample with the level of antibody bound to a control;

wherein an increased level of bound antibody to said biological sample sample compared to control is indicative of a patient susceptible to a therapeutic agent targeting CEACAM5.

In the above methods, said control can be a normal, non cancerous, biological sample of the same type, or a reference value determined asrepresentative of the antibody binding level in normal biological sample of the same type.

In an embodiment, the antibodies of the invention are useful for diagnosing a CEACAM5 expressing cancer, such as a colorectal, stomach, lung, uterus cervix, pancreas, oesophagus, ovary, thyroid, bladder, endometrium, breast, liver (in particular cholangiocarcinoma), prostate, or skin cancer.

The invention further relates to an *in vitro* or *ex vivo* method of monitoring effectiveness of anti-CEACAM5 cancer therapy, comprising the steps consisting of:

(a) contacting a biological sample of a subject undergoing anti-CEACAM5 cancer therapy, with an antibody according to the invention, in particular in conditions sufficient for the antibody to form complexes with said biological sample;

(b) measuring the level of antibody bound to said biological sample,

(c) comparing the measured level of bound antibody with the level of antibody bound to a control;

wherein a decreased level of bound antibody to said biological sample compared to control is indicative of effectiveness of said anti-CEACAM5 cancer therapy.

In said method, an increased level of bound antibody to said biological sample compared to control is indicative of ineffectiveness of said anti-CEACAM5 cancer therapy.

In an embodiment said control is a biological sample of the same type as the biological sample submitted to analysis, but which was obtained from the subject previously in time, during the course of the anti-CEACAM5 cancer therapy.

The invention further relates to an *in vitro* or *ex vivo* method of detecting cancer relapse after anti-CEACAM5 cancer therapy, comprising the steps consisting of:

(a) contacting a biological sample of a subject having completed anti-CEACAM5 cancer therapy, with an antibody according to the invention, in particular in conditions sufficient for the antibody to form complexes with said biological sample;

(b) measuring the level of antibody bound to said biological sample,

(c) comparing the measured level of bound antibody with the level of antibody bound to a control;

wherein an increased level of bound antibody to said biological sample compared to control is indicative of cancer relapse after anti-CEACAM5 cancer therapy.

Said control is in particular a biological sample of the same type as the biological sample submitted to analysis, but which was obtained from the subject previously in time, upon or after completion of the anti-CEACAM5 cancer therapy.

Said anti-CEACAM5 cancer therapy is in particular a therapy using an antibody or immunoconjugate according to the invention. Said anti-CEACAM5 cancer therapy targets a CEACAM5 expressing cancer, in particular a colorectal, stomach, lung,

uterus cervix, pancreas, oesophagus, ovary, thyroid, bladder, endometrium, breast, liver (in particular cholangiocarcinoma), prostate, or skin cancer.

In an embodiment, antibodies of the invention may be labelled with a detectable molecule or substance, such as a fluorescent molecule, a radioactive molecule or any other labels known in the that provide (either directly or indirectly) a signal.

As used herein, the term "labeled", with regard to the antibody according to the invention, is intended to encompass direct labeling of the antibody by coupling (i.e., physically linking) a detectable substance, such as a radioactive agent or a fluorophore (e.g. fluorescein isothiocyanate (FITC) or phycoerythrin (PE) or Indocyanine (Cy5)) to the polypeptide, as well as indirect labeling of the polypeptide by reactivity with a detectable substance.

An antibody of the invention may be labelled with a radioactive molecule by any method known to the art. For example radioactive molecules include but are not limited radioactive atom for scintigraphic studies such as I^{123}, I^{124}, In^{111}, Re^{186}, Re^{188}, Tc^{99}. Polypeptides of the invention may be also labelled with a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, MRI), such as iodine-123, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

A "biological sample" encompasses a variety of sample types obtained from a subject and can be used in a diagnostic or monitoring assay. Biological samples include but are not limited to blood and other liquid samples of biological origin, solid tissue samples such as a biopsy specimen or tissue cultures or cells derived therefrom, and the progeny thereof. Therefore, biological samples encompass clinical samples, cells in culture, cell supernatants, cell lysates, serum, plasma, biological fluid, and tissue samples, in particular tumor sample.

In an embodiment, the biological sample may be formalin-fixed and paraffin embedded (FFPE) tissue sample. Indeed, antibodies according to the invention can advantageously be used on FFPE tissues which is the format used by most hospitals to collect and archive tissue samples.

The invention also relates to an *in vivo* method of detecting the presence of a cancer in a subject, comprising the steps consisting of:

a) administering an antibody according to the invention detectably labelled to a patient;

b) detecting localisation of said detectably labelled antibody in the patient

by imaging.

Antibodies of the invention may be useful for staging of cancer (e.g., in radioimaging). They may be used alone or in combination with other cancer markers.

The terms "detection" or "detected" as used herein includes qualitative and/or quantitative detection (measuring levels) with or without reference to a control.

In the content of the invention, the term "diagnosing", as used herein, means the determination of the nature of a medical condition intended to identify a pathology which affects the subject from a number of collected data.

In said method, the cancer is a CEACAM5 expressing cancer, in particular a colorectal, stomach, lung, uterus cervix, pancreas, oesophagus, ovary, thyroid, bladder, endometrium, breast, liver (in particular cholangiocarcinoma), prostate, or skin cancer.

Kits

Finally, the invention also provides kits comprising at least one antibody or immunoconjugate of the invention. Kits containing antibodies of the invention find use in detecting the surface protein CEACAM5, or in therapeutic or diagnostic assays. Kits of the invention can contain a polypeptide or antibody coupled to a solid support, e.g., a tissue culture plate or beads (e.g., sepharose beads). Kits can be provided which contain antibodies for detection and quantification of the surface protein CEACAM5 *in vitro*, e.g. in an ELISA or a Western blot. Such an antibody useful for detection may be provided with a label such as a fluorescent or radiolabel.

BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NO:1-4, and 6 show the sequences of the CDR1-H, CDR2-H, CDR3-H, CDR1-L and CDR3-L of the so-called "MAb1" antibody.

SEQ ID NO:5 shows the VH variant sequence VH1a of humanized MAb2 antibody.

SEQ ID NO:7-10, and 12 show the sequences of the CDR1-H, CDR2-H, CDR3-H, CDR1-L and CDR3-L of the so-called "MAb2" antibody.

SEQ ID NO:11 shows the sequence of human CEACAM1 as available from GenBank NP_001703.2.

SEQ ID NO:13-16, and 18 show the sequences of the CDR1-H, CDR2-H,

CDR3-H, CDR1-L and CDR3-L of the so-called “MAb3” antibody.

SEQ ID NO:17 shows the VL variant sequence VL1 of humanized MAb2 antibody.

SEQ ID NO:19-22, and 24 show the sequences of the CDR1-H, CDR2-H, CDR3-H, CDR1-L and CDR3-L of the so-called “MAb4” antibody.

SEQ ID NO:23 shows the VL variant sequences VL1a of humanized MAb2 antibody.

SEQ ID NO:25-28, and 30 show the sequences of the CDR1-H, CDR2-H, CDR3-H, CDR1-L and CDR3-L of the so-called “MAb5” antibody.

SEQ ID NO:29 shows the VL variant sequences VL1c of humanized MAb2 antibody.

SEQ ID NO:31 shows the VH sequence of the “MAb1” antibody.

SEQ ID NO:32 shows the VL sequence of the “MAb1” antibody.

SEQ ID NO:33 shows the VH sequence of the “MAb2” antibody.

SEQ ID NO:34 shows the VL sequence of the “MAb2” antibody.

SEQ ID NO:35 shows the VH sequence of the “MAb3” antibody.

SEQ ID NO:36 shows the VL sequence of the “MAb3” antibody.

SEQ ID NO:37 shows the VH sequence of the “MAb4” antibody.

SEQ ID NO:38 shows the VL sequence of the “MAb4” antibody.

SEQ ID NO:39 shows the VH sequence of the “MAb5” antibody.

SEQ ID NO:40 shows the VL sequence of the “MAb5” antibody.

SEQ ID NO:41 shows the heavy chain sequence of chMAb1 antibody.

SEQ ID NO:42 shows the light chain sequence of chMAb1 antibody.

SEQ ID NO:43 shows the heavy chain sequence of chMAb2 antibody.

SEQ ID NO:44 shows the light chain sequence chMAb2 antibody.

SEQ ID NO:45 shows the heavy chain sequence chMAb3 antibody.

SEQ ID NO:46 shows the light chain sequence chMAb3 antibody.

SEQ ID NO:47 shows the heavy chain sequence chMAb4 antibody.

SEQ ID NO:48 shows the light chain sequence of chMAb4 antibody

SEQ ID NO:49 shows the heavy chain sequence of chMAb5 antibody.

SEQ ID NO:50 shows the light chain sequence of chMAb5 antibody.

SEQ ID NO:51 shows the VH variant sequence VH1 of humanized MAb2 antibody.

SEQ ID NO:52 shows the sequence of full-length human CEACAM5 as available

from GenBank database under accession number AAA51967.1.

SEQ ID NO:53 shows the sequence of the extracellular domain of *Macaca fascicularis* CEACAM5.

SEQ ID NO:54 shows the sequence of the light chain of a chimeric antibody (derived from the "MAb2" antibody) comprising a K52 to R52 mutation.

SEQ ID NO: 55 shows the VL variant sequence VL1d of humanized MAb2 antibody.

SEQ ID NO:56 shows the sequence of hCEACAM1 extracellular domain (positions 35-428 of full length hCEACAM1 (NP_001703.2), followed by a 24 amino acid extension containing a His-Tag).

SEQ ID NO:57 shows the sequence of cCEACAM1 extracellular domain followed by a 24 amino acid extension containing a His-Tag.

SEQ ID NO:58 shows the sequence of hCEACAM5 extracellular domain (positions 35-685 of full length hCEACAM5 (AAA51967.1) followed by a 24 amino acid extension containing a His-Tag).

SEQ ID NO:59 shows the sequence of cCEACAM5 extracellular domain followed by a 24 amino acid extension containing a His-Tag.

SEQ ID NO:60 shows the sequence of hCEACAM6 extracellular domain (positions 35-327 of full length hCEACAM6 (NP_002474.3), followed by a 24 amino acid extension containing a His-Tag).

SEQ ID NO:61 shows the sequence of cCEACAM6 extracellular domain followed by a 24 amino acid extension containing a His-Tag.

SEQ ID NO:62 shows the sequence of hCEACAM8 extracellular domain (positions 35-332 of full length hCEACAM8 (NP_001807.2), followed by a 24 amino acid extension containing a His-Tag.

SEQ ID NO:63 shows the sequence of cCEACAM8 extracellular domain, followed by 24 amino acid extension containing a His-Tag.

SEQ ID NO:64 shows the sequence of hCEACAM7 extracellular domain (positions 36-248 of full length hCEACAM7 (NP_008821.1), followed by 24 amino acid extension containing a His-Tag).

SEQ ID NO:65 shows the sequence of hCEACAM5 N-A1-B1 (positions 35-320 of full length hCEACAM5 (AAA51967.1.)) followed by 6 amino acid His-Tag.

SEQ ID NO:66 shows the sequence of hCEACAM5- A2-B2 (positions 321-498 of full length hCEACAM5 (AAA51967.1.)) followed by 6 amino acid His-Tag.

SEQ ID NO:67 shows the sequence of hCEACAM5 A3-B3 (positions 499-685 of full length hCEACAM5 (AAA51967.1.)) followed by 6 amino acid His-Tag-.

SEQ ID NO:68 shows the sequence of cCEACAM5 N-A1-B1, followed by 24 amino acid extension containing a His-Tag.

SEQ ID NO:69 shows the sequence of cCEACAM5 A2-B2, followed by 24 amino acid extension containing a His-Tag.

SEQ ID NO:70 shows the sequence of cCEACAM5 A3-B3, followed by 24 amino acid extension containing a His-Tag.

SEQ ID NO:71 shows the sequence of human CEACAM6 full-length protein as available from GenBank NP_002474.3.

SEQ ID NO:72 shows the sequence of human CEACAM7 full-length protein as available from GenBank NP_008821.1.

SEQ ID NO:73 shows the sequence of human CEACAM8 full-length protein as available in GenBank NP_001807.2.

SEQ ID NO: 74 shows the VH sequence of the variant humanized MAb2_VLg5VHg2.

SEQ ID NO: 75 shows the VL sequence of the variant humanized MAb2_VLg5VHg2.

SEQ ID NO: 76 shows the sequence of amino acids at positions 109-115 of human CEACAM5 A3-B3.

SEQ ID NO: 77 shows the sequence of amino acids at positions 131-143 of human CEACAM5 A3-B3.

SEQ ID NO: 78 shows a consensus sequence for CDR1-H of MAb2/MAb4/MAb5 antibody family based on sequence comparisons.

SEQ ID NO: 79 shows a consensus sequence for CDR2-H of MAb2/MAb4/MAb5 antibody family based on sequence comparisons.

SEQ ID NO: 80 shows a consensus sequence for CDR3-H of MAb2/MAb4/MAb5 antibody family based on sequence comparisons.

SEQ ID NO: 81 shows a consensus sequence for CDR1-H of MAb1/MAb3 antibody family.

SEQ ID NO: 82 shows a consensus sequence for CDR2-H of MAb1/MAb3 antibody family.

SEQ ID NO:83 shows a consensus sequence for CDR1-H of MAb2/MAb4/MAb5 antibody family based on residues identified as neutral in the binding of human and

Macaca fascicularis CEACAM5 extracellulair domains.

SEQ ID NO:84 shows a consensus sequence for CDR3-H of MAb2/MAb4/MAb5 antibody family based on residues identified as neutral in the binding of human and *Macaca fascicularis* CEACAM5 extracellulair domains.

SEQ ID NO:85 shows a consensus sequence for CDR1-L of MAb2/MAb4/MAb5 antibody family based on residues identified as neutral in the binding of human and *Macaca fascicularis* CEACAM5 extracellulair domains.

SEQ ID NO:86 shows a consensus sequence for CDR3-L of MAb2/MAb4/MAb5 antibody family based on residues identified as neutral in the binding of human and *Macaca fascicularis* CEACAM5 extracellulair domains.

SEQ ID NO:87 shows the heavy chain sequence of huMAb2-3 (MAb2_VL1cVH1a-IgG1).

SEQ ID NO:88 shows the light chain sequence of huMAb2-3 (MAb2_VL1cVH1a-IgG1).

SEQ ID NO:89 shows the heavy chain sequence of huMAb2-4 (MAb2_VL1d VH1-IgG1).

SEQ ID NO:90 shows the light chain sequence of huMAb2-4 (MAb2_VL1d VH1-IgG1).

DESCRIPTION OF THE FIGURES

Figure 1: Evaluation of the selectivity of the anti-CEACAM5 antibodies.

Figure 2: Domain mapping of the anti-CEACAM5 antibodies on human CEACAM5.

Figure 3: Domain mapping of the anti-CEACAM5 antibodies on cynomolgus CEACAM5.

Figure 4: Evaluation of the anti-tumor activity of chMAb4-SPDB-DM4, chMAb1-SPDB-DM4, chMAb5-SPDB-DM4, and chMAb2-SPDB-DM4 conjugates against primary human colon adenocarcinoma CR-IGR-034P in SCID female mice.

Figure 5: Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4, huMAb2-4-SPDB-DM4 and chMAb2-SPDB-DM4 conjugates against primary human colon adenocarcinoma CR-IGR-034P in SCID female mice.

Figure 6: Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 conjugate against primary human stomach adenocarcinoma STO-IND-006 in SCID

female mice.

Figure 7: Sequence alignments of the VH and VL regions of the MAb1, MAb2, MAb3, MAb4 and MAb5 antibodies.

Figure 8: HRMS analysis of chMAb1-SPDB-DM4 conjugate.

Figure 9: HRMS analysis of chMAb2-SPDB-DM4 conjugate.

Figure 10: HRMS analysis of chMAb4-SPDB-DM4 conjugate.

Figure 11: HRMS analysis of chMAb5-SPDB-DM4 conjugate.

Figure 12: HRMS analysis of huMAb2-2-SPDB-DM4 conjugate.

Figure 13: HRMS analysis of huMAb2-1-SPDB-DM4 conjugate.

Figure 14: HRMS analysis of huMAb2-3-SPDB-DM4 conjugate.

Figure 15: HRMS analysis of huMAb2-4-SPDB-DM4 conjugate.

Figure 16: Binding activity of humanized variants of MAb2 to human and monkey CEACAM5 extracellular domain.

Figure 17: Stability of binding of humanized variants of MAb2 to human and monkey CEACAM5 extracellular domain.

Figure 18: Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 conjugate against primary human lung adenocarcinoma LUN-NIC-0014 in SCID female mice.

Figure 19: Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 and huMAb2-3-sulfo-SPDB-DM4 conjugates against primary human colon adenocarcinoma CR-IGR-034P in CD1 nude female mice.

Figure 20: HRMS analysis of huMAb2-3-sulfoSPDB-DM4.

Figure 21: HRMS analysis of huMAb2-3-SMCC-DM1.

Figure 22: Heavy Chain variable domain alignment of MAb2, MAb4, MAb5, humanized VH1a, humanized VH1 and humanized VHg2.

Figure 23: Light Chain variable domain alignment of MAb2, MAb4, MAb5, humanized VL1, humanized VL1a, humanized VL1c, humanized VL1d and humanized VLg5.

EXAMPLES

The present invention is further illustrated by the folloing examples which should not be construed as further limiting.

The contents of the Sequence Listing, figures and all references, patens andpublished patent applications cited throughout this application are expressly incorporated herein by reference in ther entirety.

Example 1: Preparation of recombinant extracellular domains of CEACAM proteins

In this example, the extracellular protein domains (ECD) of CEACAM from human (h) or cynomolgus monkey (c) origin have been prepared by transient expression in human embryonic kidney HEK293 cells with plasmids allowing expression of the respective cDNA as outlined on Table 1.

Each expression plasmid was complexed with 293fectin™ (Life Technologies) and added to suspension-cultivated 293-F cells (derived from HEK293 cells). Eight days post-transfection, the culture supernatants were collected and the corresponding soluble protein was purified by IMAC (GE Healthcare) to generate a protein batch (see Table 1).

Table 1: Description of the recombinant extracellular domains of CEACAM proteins

Protein name	Protein desription	cDNA sequence origin	Sequence identifier
hCEACAM1	human CEACAM1 ECD (35-428)	NP_001703.2	SEQ ID NO:56
cCEACAM1	*M.fascicularis* CEACAM1 ECD (35-428)	cloned internally	SEQ ID NO:57
hCEACAM5	human CEACAM5 ECD (35-685)	AAA51967.1	SEQ ID NO:58
cCEACAM5	*M.fascicularis* CEACAM5 ECD (35-688)	cloned internally	SEQ ID NO:59
hCEACAM6	human CEACAM6 ECD (35-327)	NP_002474.3	SEQ ID NO:60
cCEACAM6	*M.fascicularis* CEACAM6 ECD (35-327)	cloned internally	SEQ ID NO:61
hCEACAM8	human CEACAM8 ECD (35-332)	NP_001807.2	SEQ ID NO:62
cCEACAM8	*M.fascicularis* CEACAM8 ECD (35-332)	cloned internally	SEQ ID NO:63
hCEACAM7	human CEACAM7 ECD (36-248)	NP_008821.1	SEQ ID NO:64
hCEACAM5 NA1B1	human CEACAM5 N-A1-B1 domain (35-320)	AAA51967.1	SEQ ID NO:65
hCEACAM5 A2B2	human CEACAM5 A2-B2 domain (321-498)	AAA51967.1	SEQ ID NO:66
hCEACAM5 A3B3	human CEACAM5 A3-B3 domain (499-685)	AAA51967.1	SEQ ID NO:67
cCEACAM5 NA1B1	*M.fascicularis* CEACAM5 N-A1-B1 domain (35-320)	cloned internally	SEQ ID NO:68
cCEACAM5 A2B2	*M.fascicularis* CEACAM5 A2-B2 domain (321-498)	cloned internally	SEQ ID NO:69
cCEACAM5 A3B3	*M.fascicularis* CEACAM5 A3-B3 domain (499-688)	cloned internally	SEQ ID NO:70

Example 2: Generation of monoclonal mouse anti-CEACAM5 antibodies

In this example, monoclonal antibodies have been generated following mice immunization according to a protocol that led to the generation of antiCEACAM5 mAb.

Example 2.1: Immunization & Hybridoma generation

Immunizations, fusion and screening were performed using P3X63-Ag8.653 myeloma cells with either the extracellular domain of human CEACAM5, the extracellular domain of cynomolgus CEACAM5 or with human tumoral UMC11 cells as described in Wennerberg A.E et al., 1993. Am. J. Pathol., 143(4), 1050-1054 and Kilpatrick et al. 1997. Hybridoma 16: 381389.

Using the RIMMS method as described by Kilpatrick et al. (1997. Hybridoma 16:

381389), 6-8 weeks old female BALB/c mice (S082342; Charles River Labs, Bar Harbor, ME) each received four rounds of immunization over a course of 14 days at intervals of 3-4 days. Antigens emulsified in Titermax's adjuvant (TierMax Gold Adjuvant; Sigma #T2684) was administered subcutaneously to six sites proximal to draining lymph nodes, along the back of the mice and to six juxtaposed sites along abdomen. Four days after the last injection, mice were sacrified. Bilateral popliteal, superficial inguinal, axillary and branchial lymph nodes were isolated aseptically and washed with fresh RPMI medium.

Using the classical method as described by Wennerberg A.E et al. (1993. Am. J. Pathol., 143(4), 1050-1054), 6-8 weeks old female BALB/c mice (S082342; Charles River Labs, Bar Harbor, ME) each received three rounds of immunization over a course of 41 days. Antigens were administered intraperitonealy to ventral site of mice. Three days after the last injection, mice were sacrified and spleens were isolated aseptically and washed with fresh RPMI medium.

Lymphocytes were released from the lymph nodes or from the spleens and single-cell suspension was washed twice with RPMI medium before being fused with P3X63-AG8.653 myeloma cells using polyethylene glycol. After fusion, the cell mixture was incubated in an incubator at 37° C for 16-24 hours. The resulting cells preparation was transferred into selective semi-solid medium and aseptically plated out into 100 mm Petri plates and incubated at 37°C. Ten days after initiation of selection, the plates were examined for hybridoma growth, and visible colonies were picked-up and placed into 96-well plates containing 200 µL of growth medium. The 96-well plates were kept in an incubator at 37°C for 2 to 4 days.

Example 2.2: Screening and in vitro characterization of murine anti-CEACAM5 antibodies

Primary screening for anti-CEACAM5 IgG production was performed by Enzyme-linked immunosorbent assay (ELISA) using human CEACAM5 protein (prepared as described in Example 1) as capturing antigen and by FACS using several human tumoral cells (H460, MKN45, SW1463, SKMEL28 and UMC11). For ELISA assay, plates were coated with human CEACAM5 protein at 0.25 µg/well in PBS and 100 µL/well of anti-CEACAM5 antibodies were added to the plate. The plate was incubated at 37°C for 1h and washed five times with PBS containing 0.05% Tween-20 (PBS-T). Then, 100 µL of a 1:50,000 dilution of rabbit anti-mouse IgG

conjugated with horseradish peroxidase (Sigma; #A9044) was added to each well. Following incubation at 37°C for 1h in darkness, plates were washed with PBS-T five times. Antibody binding was visualized by adding TMB-H2O2 buffer and read at a wavelength of 450 nm. For FACS assay, human tumoral cells were coated at 40,000 cells/well on 96-well High Bind plate (MSD L15XB-3) and 100 µL/well of anti-CEACAM5 antibodies were added for 45 min at 4°C and washed three times with PBS 1% BSA. 100 µL/well of goat anti-mouse IgG conjugated with Alexa647 (Invitrogen; # A2135) was added for 45 min at 4°C and washed three times with PBS 1% BSA. Antibody binding was evaluated after centrifugation and resuspension of cells by adding 200 µl/well PBS 1% BSA and read using Guava® easyCyte™ 8HT Flow Cytometry System.

For evaluating specificity to CEACAM5 of anti-CEACAM5 antibodies, 96-well plates were coated with recombinant human CEACAM1, CEACAM6, CEACAM7 and CEACAM8 proteins (prepared as described in Example 1) using the same coating conditions described previously. Anti-CEACAM5 antibodies were added to the plates and detected by using rabbit anti-mouse IgG conjugated with horseradish peroxidase (Sigma; #A9044). Antibody binding was visualized by adding TMB-H2O2 buffer and read at a wavelength of 450 nm. The results presented on Figure 1 show that the anti-CEACAM5 antibodies are selective for human CEACAM5 *v.* human CEACAM1, CEACAM6, CEACAM7 and CEACAM8.

Example 2.3: mAb binding characterization

The apparent affinity of anti-CEACAM5 antibodies to hCEACAM5 expressed on the surface of human MKN45 (DSMZ, ACC 409) tumoral cells were determined by Guava® easyCyte™ 8HT Flow Cytometry System. MKN45 tumoral cells were coated at 40,000 cells/well on 96-well High Bind plate (MSD L15XB-3) and 100 µL/well of anti-CEACAM5 antibodies were added in 2-fold serial dilutions starting at 20 µg/ml up to 12 dilutions in assay diluant for 45 min at 4°C and and washed three times with PBS 1% BSA. 100 µL/well of goat anti-mouse IgG conjugated with Alexa647 (Invitrogen; # A2135) was added for 45 min at 4°C and washed three times with PBS 1% BSA. The antibody binding was evaluated after centrifugation and resuspension of cells by adding 200 µl/well PBS 1% BSA and read using Guava® easyCyte™ 8HT Flow Cytometry System. Apparent KD and EC50 values were estimated using BIOST@T-BINDING and BIOST@T-SPEED softwares, respectively.

Table 2: EC50 values obtained on MKN45 cells

Antibodies	MAb1	MAb2	MAb3	MAb4	MAb5
EC50 values	16 nM	3.4 nM	6.2 nM	4.9 nM	0.73 nM

Domain mapping of anti-CEACAM5 antibodies to human CEACAM5 and cynomolgus CEACAM5 proteins was determined by ELISA. 96-well plates were coated with recombinant human A1 (143-237), A1-B1 (143-320), A2-B2 (321-498) and A3-B3 (499-685) domains of CEACAM5 protein (prepared as described in Example 1) and with recombinant cynomolgus N-A1-B1 (1-320), A1-B1 (143-320), A2-B2 (321-498) and A3-B3 (499-688) domains of CEACAM5 protein (prepared as described in Example 1) using the same coating conditions described previously. Purified antibodies were added to the plates and detected by using rabbit anti-mouse IgG conjugated with horseradish peroxidase (Sigma; #A9044). Antibody binding was visualized by adding TMB-H2O2 buffer and read at a wavelength of 450 nm. The results are presented on Figure 2 and 3 and show that the anti-CEACAM5 antibodies bind to the A3-B3 domain of human and cynomolgus CEACAM5 proteins.

Isotypes of individual mAbs were determined using a mouse IgG isotyping kit according to the manufacturer's instructions (SEROTEC ref. MMT1). The five CEACAM5-specific mAbs were of the IgG1, k isotype.

Example 3: Characterization of murine anti-CEACAM5 antibodies

Example 3.1: In vitro characterization of murine anti-CEACAM5 antibodies

Mouse hybridoma expressing CEACAM5-specific Abs were produced into T500 flask and conditioned media collected after 7 days of growth. CEACAM5-specific Abs were purified by passing the conditioned media through a Protein-G column, washed and eluted with Glycine/HCl 100mM pH 2.7 buffer. The eluate was dialyzed against PBS before sterile filtration and stored at 4°C.

All CEACAM5-specific mAbs were assessed for their ability to bind human and primate CEACAM5 protein by ELISA. Plates were coated with human or primate CEACAM5 protein, anti-hCEACAM5 mAbs were added to the plate and detected with rabbit anti-mouse IgG conjugated with horseradish peroxidase (Sigma; #A9044). The antibody binding was visualized by adding TMB-H2O2 buffer and read at a wavelength of 450 nm.

Table 3: EC50 values corresponding to binding ability of CEACAM5-specific

mAbs to primate CEACAM5 proteins

Antibodies	MAb1	MAb2	MAb3	MAb4	MAb5
EC50 (nM) hCEACAM5	0.53	0.14	0.36	0.08	0.40
EC50 (nM) cCEACAM5	1.18	0.07	3.72	0.05	0.45
Ratio c/h	2.2	0.5	10	0.6	1.1

Example 3.2: Apparent affinity and antibody binding capacity of anti-CEACAM5 antibodies to advanced human primary colon tumor cells CR-IGR-034P by Flow Cytometry

Advanced human primary colon tumor CR-IGR-034P (Julien et al., *Clin Cancer Res* October 1, **2012** 18:5314-5328) was obtained from Patient-derived xenograft in mice. Tumor CR-IGR-034P was enzymatically dissociated using collagenase Type IV (Invitrogen; #17104-019) and deoxyribonuclease I (Invitrogen; #18047-019) for 1h at 4°C. Cell viability was estimated by Viacount application using Guava® easyCyte™ 8HT Flow Cytometry System. For apparent affinity estimation, CR-IGR-034P tumoral cells were coated at 40,000 cells/well on 96-well High Bind plate (MSD L15XB-3) and 100 µL/well of anti-CEACAM5 antibodies were added in 2-fold serial dilutions starting at 20 µg/ml up to 12 dilutions in assay diluant for 45 min at 4°C and washed three times with PBS 1% BSA. 100 µL/well of goat anti-mouse IgG conjugated with Alexa647 (Invitrogen; # A2135) or goat anti-human IgG conjugated with Alexa488 (Invitrogen; # A11013) was added for 45 min at 4°C and washed three times with PBS 1% BSA. The antibody binding was evaluated after centrifugation and resuspension of cells by adding 200 µl/well PBS 1% BSA and read using Guava® easyCyte™ 8HT Flow Cytometry System. Apparent KD and EC50 values were estimated using BIOST@T-BINDING and BIOST@T-SPEED softwares, respectively.

Antibody binding capacity of anti-CEACAM5 antibodies was determined using Mouse IgG Calibrator kit (Biocytex #7208) or Human IgG Calibrator Kit (Biocytex #CP010) according to the manufacturer's instructions.

Table 4: KD and EC50 values obtained on advanced human primary colon tumor cells CR-IGR-034P

Antibodies	MAb1	MAb2	MAb3	MAb4	MAb5
KD value	1.92 nM	0.38 nM	1.01 nM	0.16 nM	0.5 nM
EC50 value	1 nM	0.53 nM	2.8 nM	0.2 nM	1.4 nM

Example 3.3: Internalization activity of murine CEACAM5-specific antibodies

To evaluate the internalization of the anti-CEACAM5 antibodies MAb1, MAb2, MAb3, MAb4 and MAb5, viable MKN45 cells were incubated for 24 h at 37°C/5% CO2 (or 4°C on ice for negative control) with 10 µg/ml of AlexaFluor488-pre-labeled anti-CEACAM5 antibodies. Then, one part of the wells were rinced with culture medium and the extracellular AF-labeled antibodies bound to the cells were quenched by incubating the cells with anti-AlexaFluor 488 antibody (50 µg/mL) on ice for 30 min (intracellular fluorescence level). The other part of the wells was only incubated with culture medium in the same time condition (total fluorescence level).

The cells were then detached and washed, and collected in culture medium before flow cytometry analysis using a MACSQUANT Vyb analyzer. The cellular-associated fluorescence of 1×10^4 cells was measured, and the mean fluorescent intensity of gated viable cells was quantified. The internalization ratio (%) is defined by dividing the quenched cell-associated fluorescence by the total cell-associated fluorescence multiplicated by 100. Data are expressed as the mean ± standard deviation (SD)

Table 5: Anti-CEACAM5 murine antibody internalization at 24 hrs in MKN45 cell line

Antibody	Internalization 24hrs, 37°C/5%CO2 % ± StD
MAb1	49.9 ± 5.1
MAb2	45.0 ± 5.5
MAb3	51.1 ± 3.5
MAb4	42.5 ± 6.7
MAb5	51.7 ± 3.1

The five CEACAM5-specific antibodies undergo internalization after binding of CEACAM5 expressed at the cell surface membrane, supporting their use in the field

of antibody immunoconjugates to specifically address cytotoxic to cancer cells. The anti-CEACAM5 antibodies MAb1, MAb2, MAb3, MAb4 and MAb5 showed internalization in MKN45 human cancer cell line of 49.9 %, 45 %, 51.1 %, 42.5 %, 51.7 %, respectively, after 24 hours of incubation.

Example 3.4 : Cytotoxic activity of the corresponding murine ADCs on MKN45 cell line

The murine antibodies were conjugated in order to define their *in vitro* cytotoxic activity. In a 15 ml tube, at room temperature (23°C), mAb, Buffer A /HEPES (4%), DMA (dimethylacetamide, 20% v/v), then 6 equivalent of SPDB linker are successively introduced under magnetic stirring. After one night at room temperature, DM4 (maytansinoid, 9.6 equivalent) in 15 mM DMA solution is added, and reacted 5 hours. Crude conjugation mixture is purified on Superdex 200pg 16/60 or G25 26/10 columns (PBS-Na pH7.4 / 5% NMP), concentrated on Amicon 15 @ 5000g and filtered on Millex 0.22µm.

The effect of the anti-CEACAM5 maytansinoid conjugates were then tested on tumor cell viability using the Cell Titer-Glo kit (Promega). To do so, MKN45 human gastric cancer cells were plated in 96-well plates and allowed to adhere during 4 hours in 37°C/5%CO2 atmosphere. Different concentrations of anti-CEACAM5 conjugates were added to the seeded cells. The cells were then incubated for 96 hours in the same atmosphere. Cell Titer-Glo reagent was then added to the wells for 10 min at room temperature and the luminescent signal was measured using an EnVision plate counter (Perkin-Elmer).

Table 6: Cytotoxic activities of the CEACAM5-specific murine ADCs on CEACAM5+ MKN45 cell line

Antibody Drug Conjugate	Cytotoxic activity IC_{50} (nM)
MAb1-SPDB-DM4	0.89 ± 0.23
MAb2-SPDB-DM4	0.14 ± 0.01
MAb3-SPDB-DM4	0.53 ± 0.15
MAb4-SPDB-DM4	0.96 ± 0.02
MAb5-SPDB-DM4	0.24 ± 0.04

The anti-CEACAM5 antibodies conjugated to maytansinoid (DM4) MAb1-SPDB-DM4, MAb2-SPDB-DM4, MAb3-SPDB-DM4, MAb4-SPDB-DM4 and MAb5-SPDB-DM4 showed *in vitro* cytotoxic activities with an IC50 of 0.89, 0.14, 0.53, 0.96 and 0.24 nM, respectively.

Example 4: Sequence determination of heavy and light chains of the anti-CEACAM5 mAbs

The sequences of the variable domains of the mAb were retrieved from the hybridoma and cloned into an expression vector to ensure that the cloned mAbs had the same characteristics as the initial murine mAbs.

The derived amino acid sequences provided information in agreement with the data obtained on purified mAbs derived from the hybridoma by N-terminal sequencing and mass spectrometry (LC/MS) of the heavy and light chains (LC, HC) (see Table 7).

Table 7: Mass spectrometry analysis of anti-CEACAM5 mAbs from hybridoma

		Mass (Da)	
Clone ID	Chain	by LC/MS from batch	*in silico* value retrieved sequence
MAb1	LC	23837	23836
	HC (G0F)	50328	50330
MAb2i*	LC	23467	23467
	HC (G0F)	50288	50286
MAb3	LC	23907	23907
	HC (G0F)	50372	50373
MAb4	LC	23731	23731
	HC (G0F)	50370	50370
MAb5	LC	23659	23659
	HC (G0F)	50329	50330

* : MAb2i is the antibody produced by one of the cloned hybridoma and from which the so-called "MAb2" has been derived by introducing canonical residues in the framework regions of VL and VH, as explained in example 5.

Example 5: Antibody Drug Conjugate (ADC) (chimer)

Example 5.1: Naked chimer mAb

The nucleic acid sequences of the variable domains VH, VL were cloned into expression vectors in fusion with the human IgG1 or the human Ckappa constant domain coding sequences respectively to then generate batches of chimer mAbs by transient expression in HEK293 as described in Example 1. Affinities to human and cynomolgus CEACAM5 remained similar for murine and chimer mAbs. On Table 8, affinities are illustrated by the EC50 obtained by ELISA with human or cynomolgus CEACAM5.

Table 8: EC50 obtained with CEACAM5 for murine hybridoma and corresponding chimer mAbs

EC50 obtained for murine hybridoma mAbs			EC50 obtained for chimeric mAbs		
clone ID	hCEACAM5	cCEACAM5	clone ID	hCEACAM5	cCEACAM5
MAb1	0.53	1.18	chMAb1	0.51	1.57
MAb2i	0.14	0.07	chMAb2 (lot 1)	0.16	0.13
			chMAb2 (lot 2)	0.14	0.17
			$chMab2_{K52R}$	0.11	0.15
MAb3	0.36	3.72	chMAb3	Not done	Not done
MAb4	0.08	0.05	chMAb4	0.14	0.12
MAb5	0.4	0.45	chMAb5	0.18	0.13

The sequences for the CDR regions were deduced from the protein sequence

using the IMGT nomenclature. They correspond to SEQ ID NO: 1-4, 6, 7-10, 12, 13-16, 18, 19-22, 24, 25-28, 30.

Of note, compared to the antibody produced by the cloned hybridoma (MAb2i) , canonical residues have been introduced into clone MAb2 at positions 41G, 42K, and 45Q on VL, and at positions 5Q and 7S on VH.

In addition, lysine at position 52 on the VL of clone MAb2 CEA-4 is located in the CDR2, has been replaced by arginine in clone $Mab2_{K52R}$. A batch was generated in the same conditions as that corresponding to clone MAb2 and led to similar affinity to human and cynomolgus CEACAM5 extracellular domain as shown on Table 7. It highlighted that this point mutation in the CDR can be made without any impact on binding.

The LC and HC sequences of the chimer mAb for clone MAb2and clone $Mab2_{K52R}$correspond to SEQ ID NO:43, 44, 54.

chMAb2 was constructed as described in example 4. It is a chimer mAb derived from clone MAb2 with a human IgG1, Ck isotype. The sequences correspond to SEQ ID NO:43, and 44. A batch was prepared at 300 mg scale by transient expression in HEK293 followed by protein An affinity chromatography purification, see Table 7 for the binding data. It was the naked mAb used for the production of the ADC.

Example 5.2: Production and Characterisation of ADC

In this example, immunoconjugates were prepared from naked chimer mAb. *in vivo* efficacy were then assessed.

DAR Calculation:

A conjugate comprises generally from 1 to 10 molecule(s) of the maytansinoid attached covalently to the antibody (so called, “drug-to-antibody ratio” or “DAR”). This number can vary with the nature of the antibody and of the maytansinoid used along with the experimental conditions used for the conjugation (like the ratio maytansinoid/antibody, the reaction time, the nature of the solvent and of the cosolvent if any). Thus the contact between the antibody and the maytansinoid leads to a mixture comprising several conjugates differing from one another by different drug-to-antibody ratios; optionally the naked antibody; optionally aggregates. The DAR that is determined is thus a mean value.

The method used herein to determine the DAR consists in measuring spectrophotometrically the ratio of the absorbance at 252 nm and 280 nm of a solution

of the substantially purified conjugate. In particular, said DAR can be determined spectrophotometrically using the measured extinction coefficients at respectively 280 and 252 nm for the antibody and for the maytansinoid (ε_{D280} = 5,180 $M^{-1}cm^{-1}$ and ε_{D252} = 26,159 $M^{-1}cm^{-1}$). The method of calculation is derived from Antony S. Dimitrov (ed), LLC, 2009, Therapeutic Antibodies and Protocols, vol 525, 445, Springer Science and is described in more details below :

The absorbances for the conjugate at 252 nm (A252) and at 280 nm (A280) are measured either on the monomeric peak of the size exclusion chromatography (SEC) analysis (allowing to calculate the "DAR(SEC)" parameter) or using a classic spectrophotometer apparatus (allowing to calculate the "DAR(UV)" parameter). The absorbances can be expressed as follows :

$$A_{252} = (c_D \times \varepsilon_{D252}) + (c_A \times \varepsilon_{A252})$$

$$A_{280} = (c_D \times \varepsilon_{D280}) + (c_A \times \varepsilon_{A280})$$

wherein :

- c_D and c_A are respectively the concentrations in the solution of the maytansinoid and of the antibody
- ε_{D252} and ε_{D280} are respectively the molar extinction coefficients of the maytansinoid at 252 nm and 280 nm
- ε_{A252} and ε_{A280} are respectively the molar extinction coefficients of the antibody at 252 nm and 280 nm.

Resolution of these two equations with two unknowns leads to the following equations :

$$c_D = [(\varepsilon_{A280} \times A_{252}) - (\varepsilon_{A252} \times A_{280})] / [(\varepsilon_{D252} \times \varepsilon_{A280}) - (\varepsilon_{A252} \times \varepsilon_{D280})]$$

$$c_A = [A_{280} - (c_D \times \varepsilon_{D280})] / \varepsilon_{A280}$$

The average DAR is then calculated from the ratio of the drug concentration to that of the antibody: $DAR = c_D / c_A$

<u>Deglycosylation and High Resolution Mass Spectrometry of conjugates (HRMS)</u>

Deglycosylation is a technique of enzymatic digestion by means of glycosidase. The deglycosylation is made from 500 µl of conjugated + 100 µl of Tris buffer HCl 50 mM + 10 µl of glycanase-F enzyme (100 units of freeze-dried enzyme/ 100 µl of water). The medium is vortexed and maintained one night at 37°C. The deglycosylated sample is then ready to be analyzed in HRMS. Mass spectra were obtained on a Waters Q-Tof-2 system in electrospray positive mode (ES+).

Chromatographic conditions are the following : column : 4 µm BioSuite 250 URH SEC 4,6x300 mm (Waters) ; solvents : A : ammonium formate 25 mM +1% formic acid : B : CH3CN ; column temperature : 30°C ; flow rate 0,4 ml/min ; isocratic elution 70% A + 30% B (15 min).

Analytical Size Exclusion Chromatography (SEC)

- Column: TSKgel G3000 SWXL 5µm column, 7.8 mm x 30 cm, TOSOH BIOSCIENCE, LLC Part # 08541 + guard column TSK-GEL SWXL 7 µM, 40 mm x 6mm, TOSOH BIOSCIENCE, LLC Part # 08543
- Mobile Phase: KCl (0.2M), KH2PO4 (0.052 M), K2HPO4 (0.107 M), iPrOH (20% in volume)
- Analysis Conditions: isocratic elution at 0.5 ml/min for 30 min
- Analysis performed on a Lachrom Elite HPLC system (Merck) using a L2455 DAD spectrophotometer detector.

Buffers contents

- Buffer A (pH 6.5) : NaCl (50 mM), Potassium Phosphate buffer (50 mM), EDTA (2 mM)
- Buffer HGS (pH 5.5) : histidine (10 mM), glycine (130 mM), sucrose 5% (w/v), HCl (8 mM)

Abreviations used

CV: Column Volume ; DAR : Drug Antibody Ratio ; DMA : dimethylacetamide ; HEPES : 4-(2-hydroxyethyl)-1-piperazine-ethanesulfonic acid ; HRMS : High Resolution Mass Spectroscopy ; NHS : N-hydroxysuccinimide ; Nitro-SPDB : butanoic acid, 4-[(5-nitro-2-pyridinyl)dithio]-, 2,5-dioxo-1-pyrrolidinyl ester (could be prepared as described in WO2004016801 patent) ; NMP : N-methylpyrrolidinone ; RT : room temperature ; SEC : Size Exclusion Chromatography

ADC (chimers):

chMAb1-SPDB-DM4

Analytical data:

MW(Ab) = 148438 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm}(Ab) = 213320 ; ε_{252nm}(Ab) = 73473

ε_{280nm}(DM4) = 5180 et ε_{252nm}(DM4) = 26159

Under stirring, at RT, 3.59 ml of chMAb1 (C = 5.72 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.312 ml of DMA and 0.046 ml of nitro-SPDB linker solution (5.0 Eq – 15mM solution in DMA). Solution is vortexed for 30 sec

and then slowly stirred at RT for 3 hours. Under magnetic stirring, 3.8 ml of PBS pH7.5 buffer, 0.389 ml of DMA and 0.074 ml of DM4 solution (15 mM solution in DMA) were sucessively added. After 2.5 hours at RT, crude reaction mixture is purified on HiLoad 26/60 desalting column (Superdex 200 pg ; GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of PBS pH7.4 buffer containg 5% of NMP in volume. Conjugate is eluted with PBS pH7.4 buffer containg 5% of NMP, and monomeric conjugate fractions are pooled, concentrated on Amicon Ultra-15 (Ultracel 10 k, Millipore) and filtered on 0.22µm filter.

7.6 ml of chMAb1-SPDB-DM4 conjugate (c=2.19 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity : DAR (UV)= 3.38 ; DAR (SEC)= 3.34 ; RT= 17.54 min ; monomeric purity= 99.8%.

The result of HRMS analysis is shown on Figure 8.

chMAb2-SPDB-DM4

Analytical data:

MW(Ab) = 147900 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm}(Ab) = 201400 ; ε_{252nm}(Ab) = 70889

ε_{280nm}(DM4) = 5180 et ε_{252nm}(DM4) = 26159

Under stirring, at RT, 3.8 ml of chMAb2 (C = 5.08 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.337 ml of DMA and 0.0433 ml of nitro-SPDB linker solution (5.0 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 3 hours. Under magnetic stirring, 3.12 ml of PBS pH7.5 buffer, 0.319 ml of DMA and 0.069 ml of DM4 solution (15 mM solution in DMA) were sucessively added. After 2 hours at RT, crude reaction mixture is filtered on 0.45 µm filter and purified on HiLoad 26/60 desalting column (Superdex 200 pg ; GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of PBS pH7.4 buffer containg 5% of NMP in volume. Conjugate is eluted with PBS pH7.4 buffer containg 5% of NMP, and monomeric conjugate fractions are pooled, concentrated on Amicon Ultra-15 (Ultracel 10 k, Millipore) and filtered on 0.22µm filter.

7.5 ml of chMAb2-SPDB-DM4 conjugate (c=1.8 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity : DAR (UV)= 4.10 ; DAR (SEC)= 4.05 ; RT= 17.52 min ; monomeric purity= 99.9%.

The result of HRMS analysis is shown on Figure 9.

chMAb4-SPDB-DM4

Analytical data:

MW(Ab) = 148124 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm} 280nm(Ab) = 204380 ; ε_{280nm} 252nm(Ab) = 73142

ε_{280nm} 280nm(DM4) = 5180 et ε_{280nm} 252nm(DM4) = 26159

Under stirring, at RT, 3.63 ml of chMAb4 (C = 5.69 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.316 ml of DMA and 0.0465 ml of nitro-SPDB linker solution (5.0 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 3 hours. Under magnetic stirring, 3.8 ml of PBS pH7.5 buffer, 0.389 ml of DMA and 0.074 ml of DM4 solution (15 mM solution in DMA) were sucessively added. After 2 hours at RT, crude reaction mixture is purified on HiLoad 26/60 desalting column (Superdex 200 pg ; GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of PBS pH7.4 buffer containg 5% of NMP in volume. Conjugate is eluted with PBS pH7.4 buffer containg 5% of NMP, and monomeric conjugate fractions are pooled, concentrated on Amicon Ultra-15 (Ultracel 10 k, Millipore) and filtered on 0.22µm filter.

6.5 ml of chMAb4-SPDB-DM4 conjugate (c=2.20 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity : DAR (UV)= 3.87 ; DAR (SEC)= 3.85 ; RT= 17.52 min ; monomeric purity= 99.8%.

The result of HRMS analysis is shown on Figure 10.

chMAb5-SPDB-DM4

Analytical data:

MW(Ab) = 148040 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm} 280nm(Ab) = 207360 ; ε_{280nm} 252nm(Ab) = 72288

ε_{280nm} 280nm(DM4) = 5180 et ε_{280nm} 252nm(DM4) = 26159

Under stirring, at RT, 3.15 ml of chMAb5 (C = 6.38 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.269 ml of DMA and 0.0453 ml of nitro-SPDB linker solution (5.0 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 3 hours. Under magnetic stirring, 4.1 ml of PBS pH7.5 buffer, 0.317 ml of DMA and 0.072 ml of DM4 solution (15 mM solution in DMA) were sucessively added. After 2 hours at RT, crude reaction mixture is filtered on 0.45 µm filter and purified on HiLoad 26/60 desalting column (Superdex 200 pg ; GE

Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of PBS pH7.4 buffer containg 5% of NMP in volume. Conjugate is eluted with PBS pH7.4 buffer containg 5% of NMP, and monomeric conjugate fractions are pooled, concentrated on Amicon Ultra-15 (Ultracel 10 k, Millipore) and filtered on 0.22µm filter.

7.5 ml of AntiCEACAM5_hyb_1917CEA4_VH5Q7S_VL41G42K45Q_IgG1-SPDB-DM4 conjugate (c=3.4 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity : DAR (UV)= 3.4 ; DAR (SEC)= 3.4 ; RT= 17.49 min ; monomeric purity= 99.8%.

The result of HRMS analysis is shown on Figure 11.

Example 5.3: In vivo efficacy

Four chimeric conjugates (chMAb4-SPDB-DM4, chMAb1-SPDB-DM4, chMAb5-SPDB-DM4 and chMAb2-SPDB-DM4) were evaluated at 2 doses against measurable primary colon CR-IGR-034P tumors implanted s.c. in female SCID mice. Control groups were left untreated. The doses conjugates were given in mg/kg. They were administered at 5 and 2.5 by an intravenous (IV) bolus injection, on day 14 after tumor implantation.

For the evaluation of anti-tumor activity of conjugates, animals were weighed daily and tumors were measured 2 times weekly by caliper. A dosage producing a 20% weight loss at nadir (mean of group) or 10% or more drug deaths, was considered an excessively toxic dosage. Animal body weights included the tumor weights. Tumor volume were calculated using the formula mass (mm^3) = [length (mm) × width (mm)2]/2. The primary efficacy end points are ΔT/ΔC, percent median regression, partial and complete regressions (PR and CR).

Changes in tumor volume for each treated (T) and control (C) are calculated for each tumor by subtracting the tumor volume on the day of first treatment (staging day) from the tumor volume on the specified observation day. The median ΔT is calculated for the treated group and the median ΔC is calculated for the control group. Then the ratio ΔT/ΔC is calculated and expressed as a percentage: ΔT/ΔC = (delta T/delta C) x 100.

The dose is considered as therapeutically active when ΔT/ ΔC is lower than 40% and very active when ΔT/ ΔC is lower than 10%. If ΔT/ ΔC is lower than 0, the dose is considered as highly active and the percentage of regression is dated (Plowman J, Dykes DJ, Hollingshead M, Simpson-Herren L and Alley MC. Human tumor xenograft

models in NCI drug development. *In:* Feibig HH BA, editor. Basel: Karger.; 1999 p 101-125):

% tumor regression is defined as the % of tumor volume decrease in the treated group at a specified observation day compared to its volume on the first day of first treatment.

At a specific time point and for each animal, % regression is calculated. The median % regression is then calculated for the group:

$$\% \text{ regression (at t)} = \frac{\text{volume}_{t0} - \text{volume}_{t}}{\text{volume}_{t0}} \times 100$$

Partial regression (PR): Regressions are defined as partial if the tumor volume decreases to 50 % of the tumor volume at the start of treatment.

Complete regression (CR): Complete regression is achieved when tumor volume = 0 mm^3 (CR is considered when tumor volume cannot be recorded).

Results:

The results are presented on Figure 4 and Table 9 (below). Using a single administration schedule at 2.5 and 5 mg/kg, all conjugates tested in this study did not induce toxicity.

chMAb1-SPDB-DM4 was very active at 5 and 2.5 mg/kg with a $\Delta T/\Delta C$ of 0 and 7 % ($p < 0.0001$ and $p = 0.0170$ vs control), respectively. chMAb4-SPDB-DM4 and chMAb5-SPDB-DM4 were highly active at 5 mg/kg with $\Delta T/\Delta C$ of -5 and -7% ($p < 0.0001$ vs control), respectively and tumor regression of 25 and 65%, respectively. They were very active at 2.5 mg/kg with $\Delta T/\Delta C$ of 7 and 2% ($p = 0.0152$ and $p = 0.0020$ vs control), respectively. chMAb2-SPDB-DM4 was highly active at 5 and 2.5 mg/kg with $\Delta T/\Delta C$ of -10 and -8% ($p < 0.0001$ vs control), respectively, tumor regression of 82 and 39%, respectively and 3 and 1 CR/6, respectively.

From these results, all chimeric conjugates chMAb4-SPDB-DM4, chMAb1-SPDB-DM4, chMAb5-SPDB-DM4 and chMAb2-SPDB-DM4 were usable to develop a therapeutic ADC.

Table 9: Evaluation of the anti-tumor activity of chMAb1-SPDB-DM4, chMAb2-SPDB-DM4, chMAb4-SPDB-DM4, and chMAb5-SPDB-DM4 conjugates against primary human colon adenocarcinoma CR-IGR-034P in SCID female mice.

Agent[1]	Route/ Dosage in mL/kg	Dosage in mg/kg per injection	Schedule in days	Drug death (Day)	Average body weight change in % per mouse at nadir (day of nadir)	Median ΔT/ΔC in % (day)	Median % of regression (day)	Regressions		Biostatistic p value[2]	Comments
								Partial	Com-plete		
chMAb1-SPDB-DM4	IV (10mL/Kg)	5	14	0/6	-0.3 (D23)	0 (D33)	-	2/6	0/6	< 0.0001	Very active
		2.5	14	0/6	-1.2 (D22)	7 (D21)	-	0/6	0/6	= 0.0170	Very active
chMAb2-SPDB-DM4	IV (10mL/Kg)	5	14	0/6	-1.1 (D29)	-10 (D33)	82 (D33)	6/6	3/6	< 0.0001	Highly active
		2.5	14	0/6	-1.3 (D57)	-8 (D28)	39 (D28)	2/6	1/6	< 0.0001	Highly active
chMAb4-SPDB-DM4	IV (10mL/Kg)	5	14	0/6	-1.9 (D22)	-5 (D28)	25 (D28)	2/6	0/6	< 0.0001	Highly active
		2.5	14	0/6	-1.8 (D21)	7 (D25)	-	0/6	0/6	= 0.0152	Very active
chMAb5-SPDB-DM4	IV (10mL/Kg)	5	14	0/6	-1.8 (D29)	-7 (D33)	65 (D33)	4/6	0/6	< 0.0001	Highly active
		2.5	14	0/6	-0.8 (D23)	2 (D21)	-	0/6	0/6	= 0.0020	Very active
Control	-	-	14	-	-3.6 (D29)	-	-	-	-	-	-

[1] drug formulation: HGS(10 mM Histidine, 130 mM Glycine, 5% v/v Sucrose, 0.01 % Tween 80) pH 7.4

[2] p-value: Dunett's test versus control after 2-way Anova with repeated measures on rank transformed changes of tumour volume from baseline.

Example 6: Humanization of the anti-CEACAM5_MAb2 mAb

In this example, humanized variants of parental murine IgG MAb2 have been designed *in silico*. The resulting mAbs were produced and provided similar characteristics as the chimeric IgG ch-MAb2.

Example 6.1: 4D-Humanization protocol

a) Humanization Based on Molecular Dynamic Trajectories

The VL & VH sequences of the murine MAb2 clone were compared against the protein data base (PDB) (Berman et al., Nucleic Acids Research, 2000, 28:235-242). The following templates were used: light and heavy chain framework – 3EHB (90.9% Framework light chain identity and 90.8% Framework heavy chain identity), L1 – 1I8M, L2 – 1F6L, L3 – 1P7K, H1 – 2QHR, H2 – 1IGT and H3 – 1P4B to build a homology model of anti-CEACAM5 LC and HC using Molecular Operating Environment (MOE) (v. 2011.10 - Chemical Computing Group, Quebec, Canada). The homology model was subsequently energy minimized using the standard procedures implemented in MOE.

A molecular dynamics (MD) simulation of the minimized 3D homology model of the murine MAb2 was subsequently performed, with constraints on the protein backbone at 500 K temperature for 1.1 nanoseconds (ns) in Generalized Born implicit solvent. 10 diverse conformations were extracted from this first MD run every 100 picoseconds (ps) for the last 1 ns. These diverse conformations were then each submitted to a MD simulation, with no constraints on the protein backbone and at 300 K temperature, for 2.3 ns. For each of the 10 MD runs, the last 2,000 snapshots, one every ps, from the MD trajectory were then used to calculate, for each murine MAb2 amino acid, its root mean square deviations (rmsd) compared to a reference medoid position. By comparing the average rmsd on the 10 separate MD runs of a given amino acid to the overall average rmsd of all MAb2 murine amino acids, one decides if the amino acid is flexible enough, as seen during the MD to be considered as likely to interact with T-cell receptors and responsible for activation of the immune response. 32 amino acids were identified as flexible in the murine MAb2 antibody, excluding the CDR and its immediate 5 Å vicinity.

The motion of the 60 most flexible murine MAb2 amino acids, during the 20 ns (10 x 2 ns) of molecular dynamic simulation, were then compared to the motion of the corresponding flexible amino acids of 49 human 3D homology models, for each of

which were run the same MD simulations. These 49 human germline models have been built by systematically combining a representative pannel of 7 human light chains (namely vk1, vk2, vk3, vk4, vlambda1, vlambda2, vlambda3) with a representative pannel of 7 human heavy chains (namely vh1a, vh1b, vh2, vh3, vh4, vh5, vh6) (Nucleic Acid Research, 2005, Vol. 33, Database issue D593-D597).

The vk1-vh6 combination showed the highest (72.6%) 4D similarity of its flexible amino acids compared to the flexible amino acids of the murine MAb2 antibody; this model was therefore used to humanize the MAb2 antibody focusing on the flexible amino acids. For the pairwise amino acid association between the murine MAb2 and vk1-vh6 amino acids, the 2 sequences were aligned based on the optimal 3D superposition of the alpha carbons f the 2 corresponding homology models.

b) Stabilizing Mutations

To improve the stability of VL and VH regions of the anti-CEACAM5 antibody, the amino acids of the light and heavy chains with low frequency of occurrence vs. their respective canonical sequences, excluding the CDRs, are originally proposed to be mutated into the most frequently found amino acids ($\Delta\Delta Gth > 0.5$ kcal/mol; (Monsellier *et al.* J. Mol. Biol. 2006, 362,580-593). A first list of consensus mutations for the LC and for the HC has been restricted to the amino acids found in the closest human model (*i.e* vk1-vh6). None of these mutations are located in the "Vernier" zone (Foote *et al.,* J. Mol. Biol. 1992, 224, 487-499). Other criteria are taken into account to consider these consensus mutations for potentially stabilizing the anti-CECAM5 MAb2 antibody. These criteria are a favourable change of hydropathy at the surface or a molecular mechanics based predicted stabilization of the mutant. Stabilizing mutations reported to be successful in the literature (Bedouelle, H. J. Mol. Biol. 2006, 362,580-593; Steipe B. J. Mol. Biol. 1994, 240, 188-192) were considered.

c) Removal of Unwanted Sequence Motifs

The following motifs of sequences were considered: Asp-Pro (acide labile bond), Asn-X-Ser/Thr (glycosylation, X=any amino acid but Pro), Asp-Gly/Ser/Thr (succinimide/iso-asp formation in flexible areas), Asn-Gly/His/Ser/Ala/Cys (exposed deamidation sites), Met (oxidation in exposed area). The resulting humanized sequences were blasted for sequence similarity against the Immune Epitope Data Base (IEDB) database ((PLos Biol (2005) 3(3)e91) http://www.immuneepitope.org) to ensure that none of the sequences contain any known B- or T-cell epitope listed in.

d) Humanized VH and VL Regions

Three versions for the light chain (VL1, VL1a, and VL1c) and three versions for the heavy chain are proposed (VH1, VH1a and VH1b). The particular combination of amino acid residues altered in each humanized MAb2 VL and VH variant are set forth in Table 10 and Table 11, respectively. The complete amino acid sequences of the humanized VH and VL domains are set forth in Table 12.

The VL1 variant displays 5 mutations which derive from the direct comparison between the non-CDR most flexible amino acids of the anti-CEACAM5 MAb2 light chain and the vk1 human light chain sequence.

The VL1a variant derives from VL1 and includes 4 new mutations that are consensus (vk1 sequence) and potentially stabilizing. Moreover, 1 of these mutations addresses a potentially problematic deamidation site ($D_{17}T_{18}$).

The VL1c variant derives from VL1a with the introduction of 1 mutation R instead of K at position 52. Indeed, this K52 is located in the CDR L2 and could be a "target" for the conjugation process.

The VH1 variant displays 7 mutations which derive from the direct comparison between the non-CDR most flexible amino acids of the anti-CEACAM5 heavy chain and the vh6 human heavy chain sequence.

The VH1a variant derives from VH1 and includes 4 new mutations that are consensus (vh6 sequence) and potentially stabilizing.

The humanized anti-CEACAM5 MAb2 antibody VL and VH domains were combined as follows: VL1 and VH1; VL1a and VH1a; VL1c and VH1a; VL1a and VH1b

Table 10: Mutations of the VL variants of the anti-CEACAM5 MAb2 antibody

Mouse MAb2 VL	VL1	VL1d	VL1a	VL1c
E17	D	D	D	D
T18			R	R
Q40	P	P	P	P
Q45	K	K	K	K
K52		R		R
Q70			D	D
K74	T	T	T	T
N76	S	S	S	S
G84			A	A
S85			T	T

Table 11: Mutations of the VH variants of the anti-CEACAM5 MAb2 antibody

Mouse MAb2 VH	VH1	VH1a
G9	P	P
V10	G	G
K19	S	S
K43	R	R
R44		G
F60		A
D62	S	S
Q65	K	K
N84		
K87	T	T
I89		V
A113		S

Table 12: VH and VL amino acid sequences of exemplary humanized anti-CEACAM5 antibodies.

VH or VL variant	Sequence	SEQ ID NO.
clone MAb2 VH1	EVQLQESGPGLVKPGGSLSLSCAASGFVFS SYDMSWVRQTPERRLEWVAYISSGGGITYF PSTVKGRFTVSRDNAKNTLYLQMNSLTSED TAIYYCAAHYFGSSGPFAYWGQGTLVTVSA	SEQ ID NO:51
clone MAb2 VH1a	EVQLQESGPGLVKPGGSLSLSCAASGFVFS SYDMSWVRQTPERGLEWVAYISSGGGITYA PSTVKGRFTVSRDNAKNTLYLQMNSLTSED TAVYYCAAHYFGSSGPFAYWGQGTLVTVSS	SEQ ID NO:5
clone MAb2 VL1	DIQMTQSPASLSASVGDTVTITCRASENIF SYLAWYQQKPGKSPKLLVYNTKTLAEGVPS	SEQ ID NO:17

	RFSGSGSGTQFSLTISSLQPEDFGSYYCQH HYGTPFTFGSGTKLEIK	
clone MAb2 VL1a	DIQMTQSPASLSASVGDRVTITCRASENIF SYLAWYQQKPGKSPKLLVYNTKTLAEGVPS RFSGSGSGTDFSLTISSLQPEDFATYYCQH HYGTPFTFGSGTKLEIK	SEQ ID NO:23
clone MAb2 VL1c	DIQMTQSPASLSASVGDRVTITCRASENIF SYLAWYQQKPGKSPKLLVYNTRTLAEGVPS RFSGSGSGTDFSLTISSLQPEDFATYYCQH HYGTPFTFGSGTKLEIK	SEQ ID NO:29
clone MAb2 VL1d	DIQMTQSPASLSASVGDTVTITCRASENIF SYLAWYQQKPGKSPKLLVYNTRTLAEGVPS RFSGSGSGTQFSLTISSLQPEDFGSYYCQH HYGTPFTFGSGTKLEIK	SEQ ID NO:55

Example 6.2: Sequence of humanized anti CEACAM5 mAb

From the amino acid sequences of *in silico* VL and VH variants, the nucleic acid sequences were derived and synthesized by Geneart. The sequences were cloned into expression vectors in fusion with the human IgG1 or the human Ckappa constant domain coding sequences respectively.

Example 6.3: Production and in vitro characterization

Batches of humanized mAbs were produced by transient expression in HEK293 and purified by protein A affinity chromatography. Structure and identity were confirmed by SDS-PAGE analysis, Size Exclusion Chromatography and Mass Spectrometry.

Affinity to human and cynomolgus CEACAM5 was verified by ELISA, EC50 are provided on Table 13.

Table 13: Affinity of humanized anti-CEACAM5 mAb to human and cynomolgus CEACAM5

		Human CEACAM5		Cynomolgus CEACAM5	
code	**mAb**	EC50 (nM)	CV	EC50 (nM)	CV
huMAb2-1	MAb2VL1VH1-IgG1	0.22	4.7 %	0.20	7.9 %
huMAb2-2	MAb2_VL1aVH1a-IgG1	0.20	9.2 %	0.17	5.0 %
huMAb2-3	MAb2_VL1cVH1a-IgG1	0.18	11 %	0.19	4.3 %
huMAb2-4	MAb2_VL1d VH1-IgG1	0.22	4.3 %	0.17	5.0 %
chMAb2	MAb2-IgG1	0.16	9.9 %	0.17	3.0 %

Specificity to human CEACAM5 versus human CEACAM1, CEACAM6, CEACAM7 and CEACAM8 was verified by ELISA. It was reported as the percentage of binding compared to full binding with human CEACAM5, see Table 14.

Table 14: Percentage of binding of humanized anti-CEACAM5 mAb to human CEACAMs

		hCEA				
code	**mAb**	CAM5	CAM1	CAM6	CAM7	CAM8
huMAb2-1	MAb2_VL1VH1-IgG1	100 %	0.3 %	0.2 %	0.3 %	0.9 %
huMAb2-2	MAb2_VL1aVH1a-IgG1	100 %	0.3 %	0.3 %	0.3 %	0.5 %
huMAb2-3	MAb2_VL1cVH1a-IgG1	100 %	0.2 %	0.3 %	0.3 %	0.6 %
huMAb2-4	MAb2_VL1d VH1-IgG1	100 %	0.3 %	0.3 %	0.3 %	1.4 %
chMAb2	MAb2-IgG1	100 %	0.3 %	0.3 %	0.3 %	0.6 %

Epitope binding domain was verified by ELISA and showed that humanized variants recognized the A3-B3 domain specifically. It was reported as the percentage of binding compared to full binding with human CEACAM5 on Table 15.

Table 15: Percentage of binding of humanized anti-CEACAM5 mAb to human CEACAM5 domains

		hCEACAM5		
code	**mAb**	N-ter-A1-B1	A2-B2	A3-B3
huMAb2-1	MAb2_VL1VH1-IgG1	0.4 %	0.3 %	100 %
huMAb2-2	MAb2_VL1aVH1a-IgG1	0.4 %	0.3 %	100 %
huMAb2-3	MAb2_VL1cVH1a-IgG1	0.4 %	0.4 %	100 %
huMAb2-4	MAb2_VL1d VH1-IgG1	0.3 %	0.3 %	100 %
chMAb2	MAb2-IgG1	0.5 %	0.3 %	100 %

The binding kinetics of humanized anti-CEACAM5_MAb2 variants, compared with chimeric MAb2, to recombinant human CEACAM5 (hCEACAM5) and cynomolgus monkey CEACAM5 (cCEACAM5) were determined by surface plasmon resonance assay using a BIAcore 2000 (BIAcore Inc., Uppsala, NJ).

Briefly, a CM5 BIAcore biosensor chip was docked into the instrument and activated with 70 µL of 1:1 NHS/EDC at room temperature. A mouse anti-αhuman Fc

IgG1 (BIAcore #BR-1008-39) (50 µg/mL in 1M acetate buffer, pH5) were immobilized on the activated chips in all flow cells. The immobilization was carried out at a flow rate of 10 µL/min up to saturation. The chip was then blocked by injection of 70 µL of ethanolamine-HCl, pH8.5, followed by one wash with 3M MgCl2. To measure the binding of anti-CEACAM5 mAbs to the human CEACAM5 protein or cynomolgus CEACAM5 protein, antibodies were used at 1-5 µg/mL in BIAcore running buffer (HBS-EP). Antigens (human CEACAM5 or cynomolgus CEACAM5) were injected from 1 to 500 nM. Following completion of the injection phase, dissociation was monitored in a BIAcore running buffer at the same flow rate for 600 sec. The surface was regenerated between injections using 2 x 5 µL MgCl2 3M (2 x 30s). Individual sensorgrams were analyzed using BIAevaluation software.

Table 16: binding of humanized anti-CEACAM5 mAb to human and monkey CEACAM5

	Human CEACAM5	Cynomolgus CEACAM5
mAb	KD (nM)	KD (nM)
huMAb2-1	9.8	41.7
huMAb2-2	24.5	96.0
huMAb2-3	11.7	73.5
huMAb2-4	6.9	38.6
chMAb2	9.9	52.3

Specificity of humanized anti-CEACAM5_MAb2 variants, compared with chimeric MAb2, to cynomolgus CEACAM5 versus cynomolgus CEACAM1, CEACAM6 and CEACAM8 was verified by ELISA. It was reported as the percentage of binding compared to full binding with CEACAM5 or binding at the EC_{50}, see Table 17 below

Table 17: Percentage of binding of humanized anti-CEACAM5 mAb to cynomolgus CEACAMs

		Cynomolgus CEA			
code	mAb	CAM5	CAM1	CAM6	CAM8
huMAb2-1	MAb2_VL1VH1-IgG1	100 %	0.3 %	0.3 %	3.6 %
huMAb2-2	MAb2_VL1aVH1a-IgG1	100 %	0.3 %	0.3 %	0.9 %
huMAb2-3	MAb2_VL1cVH1a-IgG1	100 %	0.3 %	0.4 %	1.2 %
huMAb2-4	MAb2_VL1d VH1-IgG1	100 %	0.3 %	0.3 %	3.2 %
chMAb2	MAb2-IgG1	100 %	0.2 %	0.3 %	1.2 %

Example 6.4: Characterization of humanized variants of Mab2 obtained by grafting to human germline frameworks

In this example, humanized variants of Mab2 were obtained by a CRD-grafting approach. Further, the CDRs of the humanized antibody were submitted to an alanine-scanning approach to show that several positions could be substituted without affecting the binding to human and *Macaca fascicularis* CEACAM5.

The sequence of a humanized version of Mab2 was generated first in silico by selecting human germline frameworks on the basis of structural homology with the murine antibody Mab2. For the light chain, the selected human frameworks are defined by genes IGKV1D-39*01 and IGKJ2*02 and for the heavy chain, by genes IGHV3-23*04 and IGHJ4*01. The six CDRs of $Mab2_{K52R}$ were grafted into these human frameworks. Three back-mutations were introduced, corresponding to positions 34 and 53 in the VL (SEQ ID NO. 34) (FR2-L and FR3-L regions, respectively) and position 50 in the VH (SEQ ID NO. 33) (FR2-H region), resulting in the following sequence, defined as MAb2_VLg5VHg2.

Table 18: VH and VL sequences of MAb2_VLg5VHg2

VH or VL variant	Sequence	SEQ ID NO.
MAb2_VHg2	EVQLVESGGGLVQPGGSLRLSCAASGFVFSSYDMSWVR QAPGKGLEWVSYISSGGGITYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCAAHYFGSSGPFAYWGQGTLVT VSS	SEQ ID NO:74
MAb2_VLg5	DIQMTQSPSSLSASVGDRVTITCRASENIFSYLAWYQQKP GKAPKLLIYNTRTLQSGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQHHYGTPFTFGQGTKLEIK	SEQ ID NO:75

Several variants of MAb2_VLg5VHg2 were obtained by the single replacement of each amino acid of the six CDRs, preferentially by an alanine. When alanine is already found in MAb2_VLg5VHg2 CDRs, which occurs in H-CDR3, another amino acid was substituted (Val at residue 97, Arg at residue 98 and Asp at residue 108 of SEQ ID NO:74) .

From the in silico amino acid sequences of VL and VH variants, the nucleic acid sequences were derived and generated by gene synthesis. The sequences were cloned into a mammalian expression vector in fusion with the human IgG1 or the human Ckappa constant domain coding sequences respectively. Humanized

MAb2_VLg5VHg2, single variants differing from it by one position, and a limited number of combination mutants, were produced by transient expression in HEK293 cells. Cell supernatants containing the secreted IgGs (20 to 70 µg /ml) were diluted to 1 µg/ml for use in binding assays to human CEACAM5 ECD, *Macaca fascicularis* ECD and A3-B3 domain of human CEACAM5.

To evaluate impact of these modifications, IgGs binding was determined by measuring SPR signals with a Biacore T200 unit (GE Healthcare). Anti-human Fc antibodies were coupled to a Series S CM5 chip via amine coupling kit to reach a level of 10,000 response units (RU). Approximately 300 to 600 RU of each variant were captured by injecting supernatants at 1 µg/mL with a contact time of 60 seconds and a flow rate of 10 µL/min. All experiments were performed at 25°C with HBS-EP+ (10 mM Hepes, 150 mM NaCl, 3 mM EDTA, 0.05% surfactant P20) as the running buffer. In a screening mode, the human CEACAM5 / cynomolgus CEACAM5 / human A3B3 domain was injected at 50 nM over the captured IgG variants at a flow rate of 30 µL/min for 1 minute. A dissociation phase of 60 seconds was held before the surface was regenerated with 1 pulse injection of 3 M $MgCl_2$ at a flow rate of 10 µL/minute and a contact time of 30 seconds.

For each experiment, response data were processed using a reference surface, thereby allowing correction for bulk refractive index changes and any non-specific binding. Data were double referenced using response from blank injections. According to the screening method described in an application note from GE Healthcare (Application note 28-9777-72 AA), two parameters were considered to rank the variants with respect to binding characteristics. First, the binding activity is estimated by the proportion of the theoretical maximum signal measured (percentage of Rmax, see Figure 16). Second, the percentage of remaining signal is calculated using dissociation report points (the first one 10 seconds after the end of the injection and the second one 50 seconds after the end of injection) and reflects the stability of binding (see Figure 17).

Single alanine variants at the following positions demonstrated equivalent binding parameters, as compared to the original antibody, suggesting that the CDR amino acids at these positions are neutral for the binding : LC residues 27, 28, 29, 31, 51,52, 89, 90, 93, 94, 96, 97 and HC residues 26 to 31, 51 to 58, 97, 103, 104, 107, 109. Behaviors of these variants are similar with human and monkey CEACAM5, thus

maintaining their cross-reactivity. Binding to A3-B3 domain of CEACAM5 was also found unaffected. Some combinations of twoneutral substitutions were also generated and were found to result in unaltered binding parameters, as illustrated with association of LC_T51A with LC_T94A, LC_S31A with HC_G54Y, or LC_T53I with HC_S53A.

Conversely, at all the other CDR positions, substitution of alanine for the original amino acid was found to induce a complete loss of binding or dramatically altered binding parameters. Position 101 of the heavy chain or positions 32 and 91 of the light chain are examples shown on Figures 16 and 17), A second set of variants consisted in testing more conservative mutations at some such positions. Doing that, we found that the following conservative substitution were neutral for antigen binding : Tyr for Phe at residue 30 of MAb2_VLg5, Phe for Tyr at residue 92 of the MAb2_VLg5, Ser for Ala at residue 98 of MAb2_VHg2 and Phe for Tyr at residue 100 of MAb2_VHg2 (shown on figures)

Example 7: humanized variants of MAb2 drug conjugates

Example 7.1: Production and Characterisation

huMAb2-2-SPDB-DM4

Analytical data:

MW(Ab) = 147360 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm} (Ab) = 201400 ; ε_{280nm} (Ab) = 71693

ε_{280nm} (DM4) = 5180 ; ε_{280nm} (DM4) = 26159

Under stirring, at RT, 19.4 mg of huMAb2-2 (C = 5.1 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.375 ml of DMA and 0.0439 ml of nitro-SPDB linker solution (5.0 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 2 hours. An extra volume of 0.0044 ml of nitro-SPDB linker solution (5.0 Eq – 15 mM solution in DMA) is added. After 2 hours at RT under magnetic stirring, 2 ml of PBS pH=7.5 buffer and 0.0702 ml of DM4 solution (15 mM solution in DMA) were successively added. After 2 hours at RT, crude reaction mixture is filtered on 0.45 µm filter and purified on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer.

Conjugate is eluted with histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer, and monomeric conjugate fractions are pooled and filtered on 0.22µm filter.

10.3 ml of huMAb2-2-SPDB-DM4 conjugate (c=1.35 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity: DAR (UV)= 3.7 ; DAR (SEC)= 3.6 ; RT= 17.29 min ; monomeric purity= 97.9%.

Result of HRMS analysis is shown on Figure 12.

huMAb2-1-SPDB-DM4

Analytical data:

MW(Ab) = 147563 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm}(Ab) = 201400 ; ε_{252nm}(Ab) = 69669

ε_{280nm}(DM4) = 5180 ; ε_{252nm}(DM4) = 26159

Under stirring, at RT, 3.8 ml of a solution of huMAb2-1 (C = 5.08 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.341 ml of DMA and 0.0392 ml of nitro-SPDB linker solution (4.5 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 3 hours. An extra volume of 0.0087 ml of nitro-SPDB linker solution (1.0 Eq – 15 mM solution in DMA) is added. After 2 hours at RT under magnetic stirring, 2.62 ml of PBS pH7.5 buffer, 0.254 ml of DMA and 0.076 ml of DM4 solution (15 mM solution in DMA) were successively added. After 1 hour at RT, crude reaction mixture is filtered on 0.45 µm filter and purified on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer. Conjugate is eluted with histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer, and monomeric conjugate fractions are pooled and filtered on 0.22µm filter.

9.5 ml of huMAb2-1-SPDB-DM4 conjugate (c=1.35 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity: DAR (UV)= 4.1 ; DAR (SEC)= 4.0 ; RT= 17.39 min ; monomeric purity= 96.7%.

Result of HRMS analysis is shown on Figure 13.

huMAb2-3-SPDB-DM4

Analytical data:

MW(Ab) = 147417 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm}(Ab) = 201400 ; ε_{252nm}(Ab) = 71451

ε_{280nm}(DM4) = 5180 ; ε_{252nm}(DM4) = 26159

Under stirring, at RT, 3.8 ml of a solution of huMAb2-3 (C = 5.09 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.336 ml of DMA and 0.0437 ml of nitro-SPDB linker solution (5 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 3 hours. An extra volume of 0.0035 ml of nitro-SPDB linker solution (0.4 Eq – 15 mM solution in DMA) is added. After 1 hour at RT under magnetic stirring, 2.60 ml of PBS pH7.5 buffer, 0.248 ml of DMA and 0.074 ml of DM4 solution (15 mM solution in DMA) were successively added. After 1 hour at RT, crude reaction mixture is filtered on 0.45 µm filter and purified on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer. Conjugate is eluted with histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer, and monomeric conjugate fractions are pooled and filtered on 0.22µm filter.

11 ml of huMAb2-3-SPDB-DM4 conjugate (c=1.08 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity: DAR (UV)= 3.9 ; DAR (SEC)= 3.8 ; RT= 17.44 min ; monomeric purity= 98.4%.

Result of HRMS analysis is shown on Figure 14.

huMAb2-4-SPDB-DM4

Analytical data:

MW(Ab) = 147628 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm}(Ab) = 201400 ; ε_{252nm}(Ab) = 70628

ε_{280nm}(DM4) = 5180 ; ε_{252nm}(DM4) = 26159

Under stirring, at RT, 3.8 ml of a solution of huMAb2-4 (C = 5.09 mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 0.345 ml of DMA and 0.0448 ml of nitro-SPDB linker solution (5 Eq – 15 mM solution in DMA). Solution is vortexed for 30 sec and then slowly stirred at RT for 3 hours. An extra volume of 0.0027 ml of nitro-SPDB linker solution (0.3 Eq – 15 mM solution in DMA) is added. After 1 hour at RT under magnetic stirring, 2.70 ml of PBS pH7.5 buffer, 0.263 ml of DMA and 0.075 ml of DM4 solution (15 mM solution in DMA) were successively added. After 1 hour at

RT, crude reaction mixture is filtered on 0.45 µm filter and purified on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-conditioned with 1CV of NaOH 1M, 2 CV of water and 2 CV of histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer. Conjugate is eluted with histidine (10mM), glycine (130mM), sucrose (5%), pH=5.5 buffer, and monomeric conjugate fractions are pooled and filtered on 0.22µm filter.

11 ml of huMAb2-4-SPDB-DM4 conjugate (c=1.23 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity: DAR (UV)= 3.8 ; DAR (SEC)= 3.8 ; RT= 17.53 min ; monomeric purity= 99.3%.

Result of HRMS analysis is shown on Figure 15.

Example 7.2: In vitro cytotoxicity

Material and methods:

The effect of the anti-CEACAM5 maytansinoid conjugates on tumor cell viability was assessed as described in example 3.4.

Results:

Table 19: Cytotoxic activities of the CEACAM5-specific humanized ADCs on CEACAM5+ MKN45 cell line

ADC	Cytotoxic activity IC_{50} (nM) ± StD
chMAb2-SPDB-DM4	0.24 ± 0.02
huMAb2-1-SPDB-DM4	0.18 ± 0.01
huMAb2-2-SPDB-DM4	0.23 ± 0.02
huMAb2-3-SPDB-DM4	0.16 ± 0.01
Irrelevant ADC	8.52 ± 2.07

These chMAb2-SPDB-DM4, huMAb2-1-SPDB-DM4, huMAb2-2-SPDB-DM4, and huMAb2-3-SPDB-DM4 conjugates and the DM4 irrelevant conjugate showed in vitro cytotoxic activities on MKN45 cells in culture with an IC50 of 0.24, 0.18, 0.23, 0.16, and 8.52 nM respectively. The cytotoxic activities of the anti-CEACAM5 conjugates was 53 to 35 fold lower than the measured activity of the irrelevant DM4 conjugate indicating CEACAM5-mediated cytotoxic activities of the anti-CEACAM5 conjugates.

Example 7.3: In vivo efficacy against primary colon CR-IGR-034P tumors implanted s.c. in female CD-1 nude mice

Material and method

Two humanized sequences as conjugates huMAb2-3-SPDB-DM4 and huMAb2-4-SPDB-DM4 were evaluated at 4-dose levels compared to the chMAb2-SPDB-DM4, against measurable primary colon CR-IGR-034P tumors implanted s.c. in female CD-1 nude mice. Control groups were left untreated. The doses conjugates were given in mg/kg. They were administered at 10, 5, 2.5 and 1.25 mg/kg by an intravenous (IV) bolus injection, on day 19 after tumor implantation.

Toxicity and efficacy evaluation were performed as reported in example 5.

Results:

The results are presented in Figure 5 and Table 20 (below).

Using a single administration schedule at 1.25, 2.5, 5 and 10 mg/kg, all conjugates tested in this study did not induce toxicity.

huMAb2-4-SPDB-DM4 and chMAb2-SPDB-DM4 were highly active at 10 mg/kg with $\Delta T/\Delta C$ of -4 % ($p < 0.0001$ vs control) and tumor regression of 21 and 19%, respectively, active at 5 mg/kg with $\Delta T/\Delta C$ of 12 ($p = 0.0105$ vs control) and 17 % ($p = 0.0417$ vs control), respectively and marginally active at 2.5 mg/kg with $\Delta T/\Delta C$ of 36 and 37% (ns vs control), respectively, and inactive at 1.25 mg/kg. huMAb2-3-SPDB-DM4 was highly active at 10 mg/kg with $\Delta T/\Delta C$ of -6 % ($p < 0.0001$ vs control) and tumor regression of 31%, very active at 5 mg/kg with $\Delta T/\Delta C$ of 4 % ($p < 0.0001$ vs control), active at 2.5 mg/kg with $\Delta T/\Delta C$ of 12 ($p = 0.0322$ vs control) and marginally active at 1.25 mg/kg $\Delta T/\Delta C$ of 34% (ns vs control).

From these results, both humanized sequences huMAb2-3-SPDB-DM4 and huMAb2-4-SPDB-DM4 were usable to develop a therapeutic ADC. huMAb2-3-SPDB-DM4 was the best of the both sequence.

Table 20: Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 and huMAb2-4-SPDB-DM4 and chMAb2-SPDB-DM4 conjugates against primary human colon adenocarcinoma CR-IGR-034P in CD-1 female mice.

Agent[1]	Route/ Dosage in mL/kg	Dosage in mg/kg per injection	Schedule in days	Drug death (Day)	Average body weight change in % per mouse at nadir (day of nadir)	Median △T/△C in % (day)	Median % of regression (day)	Regressions		Biostatistic p value[2]	Comments
								Partial	Complete		
chMAb2-SPDB-DM4	IV (10mL/Kg)	10	19	0/6	-7.3 (D20)	-4 (D32)	19 (D32)	2/6	0/6	< 0.0001	Highly active
		5	19	0/6	-4.5 (D45)	12 (D32)	-	0/6	0/6	= 0.0105	Active
		2.5	19	0/6	-4.2 (D20)	36 (D32)	-	0/6	0/6	ns	Marginally active
		1.25	19	0/6	-4.1 (D20)	42 (D32)	-	0/6	0/6	ns	Inactive
huMAb2-3-SPDB-DM4	IV (10mL/Kg)	10	19	0/6	-4.3 (D27)	-6 (D35)	31 (D35)	2/6	0/6	< 0.0001	Highly active
		5	19	0/6	-3.3 (D20)	4 (D38)	-	0/6	0/6	< 0.0001	Very active
		2.5	19	0/6	-5.4 (D45)	12 (D38)	-	0/6	0/6	= 0.0322	Active
		1.25	19	0/6	-3.0 (D27)	34 (D38)	-	0/6	0/6	ns	Marginally active
huMAb2-4-SPDB-DM4	IV (10mL/Kg)	10	19	0/6	-3.7 (D22)	-4 (D32)	21 (D32)	2/6	0/6	< 0.0001	Very active
		5	19	0/6	-3.2 (D27)	17 (D32)	-	0/6	0/6	= 0.0417	Very active
		2.5	19	0/6	-3.4 (D20)	37 (D32)	-	0/6	0/6	ns	Marginally active
		1.25	19	0/6	-2.8 (D27)	50 (D32)	-	0/6	0/6	ns	Inactive
Control	-	-	19	-	- 3.9 (D24)	-	-	-	-	-	-

[1]: drug formulation: HGS (10mM Histidine, 130mM Glycine, 5% v/v Sucrose, 0.01% Tween80) pH7.4;
[2]: p-value : Dunnett's test versus control after 2-way Anova with repeated measures on rank transformed changes of tumour volume from baseline ; ns: no significant

Example 7.4: In vivo efficacy against primary stomach STO-IND-006 tumors implanted s.c. in female SCID mice

Material and method

The humanized conjugate huMAb2-3-SPDB-DM4 was evaluated at 3-dose levels against measurable primary stomach STO-IND-006 tumors implanted s.c. in female SCID mice. Control groups were left untreated. The doses conjugates were given in mg/kg. They were administered at 10, 5 and 2.5 mg/kg by an intravenous (IV) bolus injection, on day 27 after tumor implantation.

Toxicity and efficacy evaluation were performed as reported in example 5.

Results:

Using a single administration schedule at 2.5, 5 and 10 mg/kg, huMAb2-3-SPDB-DM4 did not induce toxicity.

As shown on Figure 6 and in Table 21, huMAb2-3-SPDB-DM4 was very active at 10 mg/kg with $\Delta T/\Delta C$ of 7 % ($p < 0.0001$ vs control), active at 5 mg/kg with $\Delta T/\Delta C$ of 36 % ($p = 0.0281$ vs control) and inactive at 2.5 mg/kg.

Table 21: Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 conjugates against primary human stomach adenocarcinoma STO-IND-006 in SCID female mice

Agent[1]	Route/ Dosage in mL/kg	Dosage in mg/kg per injection	Schedule in days	Drug death (Day)	Average body weight change in % per mouse at nadir (day of nadir)	Median △T/△C in % (day)	Median % of regression (day)	Regressions Partial	Regressions Com-plete	Biosta-tistic p value[2]	Comments
huMAb2-3-SPDB-DM4	IV (10mL/Kg)	10	27	0/6	-10.5 (D45)	7 (D34)	-	0/6	0/6	< 0.0001	Very active
		5	27	0/6	-8.4 (D45)	36 (D45)	-	0/6	0/6	= 0.0281	Active
		2.5	27	0/6	-5.8 (D45)	50 (D38)	-	0/6	0/6	ns	Inactive
Control	-	-	27	-	- 2.5 (D38)	-	-	-	-	-	-

[1]: drug formulation: HGS (10mM Histidine, 130mM Glycine, 5% v/v Sucrose, 0.01% Tween80) pH7.4;

[2]: p-value : Dunnett's test versus control after 2-way Anova with repeated measures on rank transformed changes of tumour volume from baseline ; ns: no significant

Example 7.5: In vivo efficacy against primary lung LUN-NIC-0014 tumors implanted s.c. in female SCID mice

Material and method

The humanized conjugate huMAb2-3-SPDB-DM4 was evaluated at 3-dose levels against measurable primary lung LUN-NIC-0014 tumors implanted s.c. in female SCID mice. Control groups were left untreated. The doses conjugates were given in mg/kg. It was administered at 10, 5 and 2.5 mg/kg by an intravenous (IV) bolus injection, on day 29 after tumor implantation.

Toxicity and efficacy evaluation were performed as reported in example 5.

Results

Using a single administration schedule at 2.5, 5 and 10 mg/kg, huMAb2-3-SPDB-DM4 did not induce toxicity.

As shown on Figure 18 and in Table 22, huMAb2-3-SPDB-DM4 was highly active at 10 and 5 mg/kg with $\Delta T/\Delta C$ inferior to 0 % ($p < 0.0001$ vs control) and tumor regression of 67 and 57% respectively and active at 2.5 mg/kg with $\Delta T/\Delta C$ of 12% ($p = 0.0363$ vs control).

Table 22 : Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 conjugate against primary human lung adenocarcinoma LUN-NIC-0014 in SCID female mice

Agent[1]	Route/ Dosage in mL/kg	Dosage in mg/kg per injection	Schedule in days	Drug death (Day)	Average body weight change in % per mouse at nadir (day of nadir)	Median △T/△C in % (day 42)	Median % of regression (day42)	Regressions		Biostatistic p value[2]	Comments
								Partial	Complete		
huMAb2-3-SPDB-DM4	IV (10 mL/kg)	10	29	0/6	+1.7 (D32)	< 0	67	5/6	1/6	< 0.0001	Highly active
		5	29	0/6	-1.1 (D36)	< 0	57	4/6	0/6	< 0.0001	Highly active
		2.5	29	0/6	+0.5 (D32)	12 (D39)	-	0/6	0/6	0.0363 (D39)	Active
Control	-	-	-	-	+0.1 (D34)	-	-	-	-	-	-

[1]: drug formulation: HGS (10mM Histidine, 130mM Glycine, 5% v/v Sucrose, 0.01% Tween80) pH7.4; [2]: p-value : Dunnett's test versus control after 2-way Anova with repeated measures on rank transformed changes of tumour volume from baseline .

Example 7.6: In vivo efficacy against primary colon CR-IGR-034P tumors implanted s.c. in female SCID mice

Material and method

Three conjugates, constituted by the humanized huMAb2-3 conjugated to the DM4 through two different linkers (SPDB and sulfo-SPDB), were evaluated at 2-dose levels against measurable primary colon CR-IGR-034P tumors implanted s.c. in female SCID mice. Control groups were left untreated. The doses conjugates were given in mg/kg. They were administered at 5 and 2.5 mg/kg by an intravenous (IV) bolus injection, on day 19 after tumor implantation.

Toxicity and efficacy evaluation were performed as reported in example 5.

Results

Using a single administration schedule at 2.5 and 5 mg/kg, huMAb2-3-SPDB-DM4 and huMAb2-3-sulfo-SPDB-DM4 did not induce toxicity.

As shown on Figure 19 and in Table 23, huMAb2-3-SPDB-DM4 was active at 5 and 2.5 mg/kg with $\Delta T/\Delta C$ of12% and 40%, respectively ($p < 0.0001$ vs control), huMAb2-3-sulfo-SPDB-DM4 was highly active at 5 mg/kg with $\Delta T/\Delta C$ inferior to 0% ($p < 0.0001$ vs control) and a tumor regression of 12% and active at 2.5 mg/kg with $\Delta T/\Delta C$ of 1 % ($p < 0.0001$ vs control).

Table 23 : Evaluation of the anti-tumor activity of huMAb2-3-SPDB-DM4 and huMAb2-3-sulfo-SPDB-DM4 conjugates against primary human colon adenocarcinoma CR-IGR-034P in SCID female mice

Agent[1]	Route/ Dosage in mL/kg	Dosage in mg/kg per injection	Schedule in days	Drug death (Day)	Average body weight change in % per mouse at nadir (day of nadir)	Median △T/△C in % (day 34)	Median % of regression (day34)	Regressions		Biostatistic p value[2]	Comments
								Partial	Complete		
huMAb2-3-SPDB-DM4	IV (10 mL/kg)	5	19	0/6	+1.6 (D20)	12	-	0/6	0/6	< 0.0001	Active
		2.5	19	0/6	-1.5 (D38)	40	-	0/6	0/6	< 0.0001	Marginally active
huMAb2-3-sulfo-SPDB-DM4	IV (10 mL/kg)	5	19	0/6	+0.1 (D20)	< 0	12	0/6	0/6	< 0.0001	Highly active
		2.5	19	0/6	+0.7 (D20)	11	-	0/6	0/6	< 0.0001	Active
		2.5	19	0/6	+2.5 (D20)	66	-	0/6	0/6	0.0306	Inactive
Control	-	-	-	-	+0.5 (D34)	-	-	-	-	-	-

[1]: drug formulation: HGS (10mM Histidine, 130mM Glycine, 5% v/v Sucrose, 0.01% Tween80) pH7.4; [2]: p-value : Dunnett's test versus control after 2-way Anova with repeated measures on rank transformed changes of tumour volume from baseline .

Example 8: Development of an immunohistochemistry (IHC) protocol dedicated to the detection of human and monkey CEACAM5 protein in formalin-fixed and paraffin embedded (FFPE) tissues.

Materials and methods

Tissues

FFPE tissue microarrays (TMA, Table 24) were used as source of human (tumor and non tumor) as well as cynomolgus monkey (normal) tissues.

Table 24: formalin-fixed and paraffin embedded tissue micro-arrays used as tissue sources

Reference	Provider	Description
ASM221	Pantomics	Cyno monkey, 22 organs, 22 samples
CyFDA	US Biomax	Cyno monkey normal tissue microarray, 33 organs, taken from 6 normal individual (99 cases)
COC1501	Pantomics	Colon cancer tissue array ,150 cores from normal/benign (5 cases) and cancer (70 cases) tissues
COC1502	Pantomics	Colon cancer tissue array ,150 cores from normal/benign (5 cases) and cancer (70 cases) tissues
COC1503	Pantomics	Colon cancer tissue array ,150 cores from normal/benign (5 cases) and cancer (70 cases) tissues
MTU951	Pantomics	40 types of tumors covering benign, malignant and metastatic entities of 27 anatomic sites
LUC1501	Pantomics	Lung cancer tissue array, 150 cores from normal/benign (5 cases) and cancer (70 cases) tissues
LUC1502	Pantomics	Lung cancer tissue array, 150 cores from normal/benign (5 cases) and cancer (70 cases) tissues
LUC1503	Pantomics	Lung cancer tissue array, 150 cores from normal/benign (5 cases) and cancer (70 cases) tissues
MNO961	Pantomics	35 types of normal tissues based on the FDA recommendation for antibody cross-reactivity testing.
MNO661	Pantomics	33 types of normal tissues based on the FDA recommendation for antibody cross-reactivity testing.
MNO341	Pantomics	33 types of normal tissues based on the FDA recommendation for antibody cross-reactivity testing.
PAC481	Pantomics	Pancreatic cancer tissue array contains 20 cases of cancers and 4 cases of normal and non-malignant pancreatic tissues
CC4	Superbiochips	59 cores array including 59 cases of lung cancer
A218(III)	Accumax	Esophagus cancer tissue array contains 40 cases of tumors and 8 non-neoplastic
A219(II)	Accumax	Head&Neck cancer tissue array contains 45 cases of tumors and 8 non-neoplastic
A213(II)	Accumax	Ovary cancer tissue array contains 43 cases of tumors and 8 non-neoplastic

Reference	Provider	Description
A301(IV)	Accumax	Various cancer tissues array with corresponding normal tissues (30 cancer cases, 30 non-neoplastic cases)
A103(V)	Accumax	Various normal tissues array in duplicate (45 cases)
MAN2	Superbiochips	59 cores array including 9 or 10 normal cases of stomach, esophagus, lung, colorectal, thyroid and kidney
MA2	Superbiochips	59 cores array including 9 or 10 cases of stomach, esophagus, lung, colorectal, thyroid and kidney cancers
MBN4	Superbiochips	59 cores array including 9 or 10 normal cases of breast, liver, urinary bladder, ovary, pancreas, prostate
MB4	Superbiochips	59 cores array including 9 or 10 cases of breast, liver, urinary bladder, ovary, pancreas, prostate cancers
MCN4	Superbiochips	59 cores array including 9 or 10 normal cases of endometrium, gallbladder, larynx, uterine cervix, skin
MC4	Superbiochips	59 cores array including 9 or 10 cases of endometrium, gallbladder, larynx, cervix, lymphoma, melanoma cancers
CJ1	Superbiochips	59 cores array including 59 cases of ovary cancer
CDN3	Superbiochips	59 cores array including 59 cases of normal colon and rectum
CCN2	Superbiochips	59 cores array including 59 cases of normal lung (matching CC4)
BB5	Superbiochips	60 cores, 30 human various cancer types
AA9	Superbiochips	59 cores array including 59 cases of normal organs
TMAhu3a	Asterand	Various cancer tissues array (76 cases)
STC1501	Pantomics	Stomach cancer tissue array, 150 cores including 75 cases of normal, reactive and canceroustissues of the stomach
STC1502	Pantomics	Stomach cancer tissue array, 150 cores including 75 cases of normal, reactive and canceroustissues of the stomach
STC1503	Pantomics	Stomach cancer tissue array, 150 cores including 75 cases of normal, reactive and canceroustissues of the stomach
STC481	Pantomics	Stomach cancer tissue array, 16 cases, 48 cores, one normal paired with two tumor tissue cores from each patient

Antibodies

MAb2 was used as primary mouse anti-human CEACAM5 monoclonal antibody. A biotin-conjugated goat anti-mouse IgG1 (γ1 chain specific) (reference 1070-08, batch L4309-X761, Southern Biotech, USA) was used as secondary antibody.

Immunostaining

Antigen retrieval procedure was applied with Cell Conditioning 1 (CC1) buffer at 95°C for 8 min and then at 100°C for 28 min. After endogen biotins blocking step,

slides were incubated with the primary anti-antibody diluted in phosphate buffer saline (PBS) at 5 µg/mL for 2 hours at 24°C. The secondary antibody biotin-conjugated goat anti-mouse was incubated at 24°C for 32 minutes at 0.5 µg/mL. Immunostaining was done with 3,3-diaminobenzidine tetrahydrochloride (DAB) from DABMap™ chromogenic detection kit (760-124, Ventana Medical Systems, Inc, USA) according to manufacturer's recommendations. A couterstaining step was done with hematoxylin (760-2037, Ventana Medical Systems, Inc, USA) and bluing reagent was applied (760-2037, Ventana Medical Systems, Inc, USA). Stained slides were dehydrated and coverslipped with cytoseal XYL (8312-4, Richard-Allan Scientific, USA).

IHC scoring

Immunostained slides were scanned using the ScanScope XT system (Aperio Technologies, Vista, CA). Digitized images were captured using the ImageScope software (version 10.2.2.2319, Aperio Technologies) at x20 magnification.

Staining evaluation included the histologic site of reactivity, main type of reactive cell, staining intensity and cell staining frequency. The negative samples were scored as 0+. The positive samples were scored with a scale of intensity from 1+ to 4+. Ranges of intensities were described as weak]0;2+[, moderate [2+;3+[and strong [3+;4+]. Cell frequency was the percentage of immunostained cells and was estimated by the histologist observation as a median by sample. The cell frequency was ordered in 5 categories of proportion score: 1 (0-5%), 2 (6-25%), 3 (26-50%), 4 (51-75%) and 5 (76-100%).

For tumors, a global expression score was adapted from the Allred score (AS) (Mohsin S, Weiss H, Havighurst T, Clark GM, Berardo M, Roanh LD, et al. Progesterone receptor by immunohistochemistry and clinical outcome in breast cancer: a validation study.Mod.Pathol.2004;17:1545–1554). This AS was obtained by adding the intensity and the proportion scores to obtain a total score that ranged from 0–9. The AS was reported as a percent of the maximum global score and ranged in 5 categories: very low (0-25%), weak (26-50%), moderate (51-75%), and high (76-100%). The prevalence was defined as the percent of positive cases for the indication

Descriptive statistical analysis

Descriptive statistics were calculated with Microsoft Excel 2003 software. For each indication, number of cases, positive cases number, prevalence, intensity score median, frequency median, Allred score mean, intensity range, frequency range and Allred score range were described.

Example 8.1: Use of an anti-CEACAM5 monoclonal antibody for evaluation of CEACAM5 protein in FFPE human tumors by immunohistochemistry (IHC)

Large panel of human tumors were studied using commercial tissue array slides (FFPE format). Expression of CEACAM5 protein was located in membrane +/- cytoplasm of tumor cells (Figure 1C, D). Some membrane staining was polarized at apical pole of cells in the more differentiated tumors. CEACAM5 protein was found to be expressed in:

- 89% of colon adenocarcinoma cases (194/219, intensity 2-2.5+, frequency 53-59%, AS 60-66%)
- 49% of stomach adenocarcinoma cases (95/195, intensity 2.5+, frequency 53%, AS 62%)
- 41% of lung adenocarcinoma cases (24/58, intensity 1.8-2+, frequency 50-53%, AS 54-58%)
- 79% of uterus cervix squamous carcinoma cases (11/14, intensity 2+, frequency 22%, AS 46%)
- 53% of pancreas adenocarcinoma cases (18/34, intensity 2+, frequency 23%, AS 42%)
- 37% of esophagus squamous cell carcinoma cases (23/62, intensity 2+, frequency 16%, AS 38%)
- 4% of ovary carcinoma cases (3/77, intensity 2+, frequency 43%, AS 54%)
- 11% of thyroid carcinoma cases (2/18, intensity 1.5+, frequency 63%, AS 56%)
- 25% of bladder carcinoma cases (5/20, intensity 1.5+, frequency 61%, AS 56%)
- 7% of endometrium adenocarcinoma cases (1/14, intensity 2+, frequency 50%, AS 56%)
- 11% of breast ductal carcinoma cases (2/18, intensity 1.5+, frequency 53%, AS 50%)
- 53% of cholangiocarcinoma cases (2/6, intensity 1.5+, frequency 75%, AS 50%)
- 53% of lung squamous cell carcinoma cases (31/148, intensity 1.5+, frequency 22%, AS 39%)
- 8% of prostate adenocarcinoma cases (1/13, intensity 2+, frequency 50%, AS

44%)

- 25% of skin squamous carcinoma cases (2/8, intensity 1.5+, frequency 23%, AS 39%)

Example 8.2: Tissue cross-reactivity of an anti-CEACAM5 monoclonal antibody in Cynomolgus monkey (Macaca fascicularis) and comparison with human expression pattern

The extracellular protein domain of CEACAM5 from human (h) or cynomolgus monkey (c) origin have been prepared by transient expression in human embryonic kidney HEK293 cells with CEACAM5 cDNA plasmid (example 1, Table 1). Cell pellets were fixed in 10% formalin (Sigma Aldrich, USA) for 16 hours, and embedded in paraffin as a piece of tissue according to standard histological procedure.

Commercial TMA were used as human and monkey normal tissues source (Table 21).

Crossreactivity of Mab2 was shown by immunostaining in both human and monkey CEACAM5 transfected cells (membrane and cytoplasm localization).

In cynomolgus normal tissues, CEACAM5 protein expression was found in columnar absorptive epithelial cells (2/3 positive cases, median intensity 1.5+, mean frequency 55%).

In human non tumor tissues, CEACAM5 expression was also observed in columnar absorptive epithelial cells (62/64 positive cases, median intensity 2+, mean frequency 90%). In human tissues, CEACAM5 expression was observed in less extent in esophagus epithelial cells, head&neck epithelial cells, stomach gastric pit epithelial cells and uterus cervix epithelial cells.

Example 9: Antibody drug conjugate (variant)

AntiCEACAM5 huMAb2-3-sulfoSPDB-DM4

Analytical data:

MW(Ab) = 147417 g/mol ; MW(DM4) = 780.38 g/mol

ε_{280nm}(Ab) = 201400 ; ε_{252nm}(Ab) = 71451

ε_{280nm}(DM4) = 5180 ; ε_{252nm}(DM4) = 26159

Under stirring, at RT, 7.0 ml of a solution of antiCEACAM5 huMAb2-3 (C = 5.32

mg / ml in PBS pH = 7.4 buffer) are introduced in a vessel, followed by 1.6 ml of DMA and 168.4 µl of nitro-sulfoSPDB linker (described in WO2009134977) solution (10 Eq – 15 mM solution in DMA). Solution is slowly stirred at RT for 3 hours. An extra volume of 3.4 µl of nitro-sulfoSPDB linker solution (2.0 Eq – 15 mM solution in DMA) is added. After 2 hours at RT under magnetic stirring, 2.90 ml of PBS pH 7.4 buffer, 0.407 ml of DMA and 0.322 ml of DM4 solution (15 mM solution in DMA) were sucessively added. After 1 hour at RT, and 16 hous at 5°C, crude reaction mixture is purified on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-condtionned with 1CV of NaOH 1M, 2 CV of water and 2 CV of histidine (10mM), glycine (130mM), sucrose (5%), pH=5,5 buffer. Conjugate is eluted with histidine (10mM), glycine (130mM), sucrose (5%), pH=5,5 buffer, and monomeric conjugate fractions are pooled and filtered on 0.22µm filter.

19 ml of antiCEACAM5 huMAb2-3-sulfoSPDB-DM4 conjugate (c=1.51 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity : DAR (UV)= 3.4 ; DAR (SEC)= 3.3 ; monomeric purity= 99.8% ; HRMS data : see Figure 20.

AntiCEACAM5 huMAb2-3-SMCC-DM1

Analytical data:

MW(Ab) = 147417 g/mol ; MW(DM1) = 738 g/mol

ε_{280nm}(Ab) = 201400 ; ε_{252nm}(Ab) = 71451

ε_{280nm}(DM1) = 5180 ; ε_{252nm}(DM1) = 26159

Under stirring, at RT, 11.3 ml of a solution of antiCEACAM5 huMAb2-3 (C = 3.47 mg / ml in buffer A pH = 6.5) are introduced in a vessel, followed by 0.387 ml of DMA and 178 µl of SMCC linker solution (10 Eq – 15 mM solution in DMA). Solution is slowly stirred at RT for 2 hours. Crude reaction mixture is buffer exchanged on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-condtionned with 2CV of NaOH 0.2M, 5 CV of water and 5 CV of citrate buffer (pH 5.5). Conjugate is eluted with citrate buffer (pH 5.5) and monomeric conjugate fractions are pooled and filtered on 0.22µm filter. To this solution are sucessively added, under stirring, at RT, 0.476 ml of DMA and 0.124 ml of DM1 solution (15 mM solution in DMA). After 2 hours at RT, crude reaction mixture is purified twice on HiPrep 26/10 desalting column (Sephadex G25, GE Healthcare), pre-condtionned with 2CV of NaOH 0.2M, 5 CV of

water and 5 CV of histidine (10mM), glycine (130mM), sucrose (5%), pH=5,5 buffer. Conjugate is eluted with histidine (10mM), glycine (130mM), sucrose (5%), pH=5,5 buffer, and monomeric conjugate fractions are pooled, filtered on 0.22µm filter.

9.5 ml of antiCEACAM5 huMAb2-3-SMCC-DM1 (c=1.73 mg/ml) was thus obtained as a colorless clear solution. The conjugate is then analyzed for final drug load and monomeric purity: DAR (UV)= 2.7 ; DAR (SEC)= 2.9 ; monomeric purity= 99.6% ; HRMS data : see Figure 21.

Example 10: Characterization of the epitope and of the paratope of CEACAM5-A3B3 in complex with MAb2 VH1aVL1c Fab using hydrogen-deuterium exchange associated with mass spectrometry (HDX MS)

Example 10.1 : Principle of HDX MS

Amide hydrogen-deuterium exchange (HDX) associated with mass spectrometry (MS) enables identification of regions of proteins implied in conformational changes or interactions. This technique enables more specifically to identify the regions of an antigen showing, after incubation in a deuterated buffer and proteolysis, a decrease of deuterium incorporation in its form bound to an antibody compared to its free form.

The epitope belongs to these regions, the exchange of which is slowed down by the binding to the antibody. A recent article describes in detail the different steps to characterize epitopes using this approach (Zhang, Q., Willison, L. N., Tripathi, P., Sathe, S. K., Roux, K. H., Emmett, M. R., Blakney, G. T., Zhang, H. M. & Marshall, A. G. (2011). *Analytical Chemistry* **83**, 7129-7136.).

Example 10.2: Materials

The variable domain coding sequences of MAb2_VH1aVL1c (SEQ ID NO:5 and SEQ ID NO:29) were cloned into a mammalian expression vector in fusion with the coding sequences of human CH1 domain (as found in papain cleaved IgG1 derived Fabs), followed by an hexa-Histidine tag or with the human Ckappa constant domain, respectively. A batch of MAb2_VH1aVL1c Fab was produced in suspension-cultivated HEK293-FS™ cells by transient transfection of two expression plasmids, encoding the two chains, complexed with 293fectin™ (Invitrogen). Culture supernatant containing the secreted protein was harvested seven days post-transfection, centrifuged and filtered on 0.22 µm membrane. The Fab was purified by affinity chromatography on IMAC (HisTrap, GE Healthcare) using imidazole gradient in PBS. Then, the pool of

fractions containing the Fab was purified by size exclusion chromatography (Superdex 200, GE Healthcare) equilibrated with PBS.

His-tagged hCEACAM5-A3B3 domain (SEQ ID NO:67) was produced with HEK293-FS™ cells cultivated in flask by transient transfection of expression plasmid. Kifunensine (inhibitor of trimming glycosylation process) was added each day. Culture supernatant containing the secreted protein was harvested seven days post-transfection, centrifuged and filtered on 0.22 µm membrane. EndoH was added into supernatant up to 625 u/ml then incubated 3 h at 37°C. Deglycosylated hCEACAM5-A3B3 was purified by affinity chromatography on IMAC (HisTrap, GE Healthcare) using imidazole gradient in PBS. Then, the pool of fractions containing deglycosylated hCEACAM5-A3B3 was purified by size exclusion chromatography (Superdex 200, GE Healthcare) equilibrated with PBS. Mass spectrometry analysis of deglycosylated hCEACAM5-A3B3 showed two species (22 485 and 22 278 Da), indicating that the protein carries 7 or 8 N-acetylglucosamine residues (GlcNAc).

To build a complex, both proteins, were pooled with an excess of 1.5 moles of deglycosylated hCEACAM5-A3B3 for one mole of Fab. This excess was removed by size exclusion chromatography on superdex 200 equilibrated with phosphate buffer saline. Fractions corresponding to complex Fab with the antigen were used for deuterium exchange study.

Example 10.3: Methods

Hydrogen/deuterium exchange (HDX) experiments were fully automated using a PAL autosampler (CTC Analytics). It enabled exchange start and quench, control of proteolysis temperature (4°C), injection of the deuterated peptides, management of the injection and washing valves and triggering acquisition of the mass spectrometer and HPLC pumps. A Peltier-cooled box (4°C) contained two Rheodyne automated valves (6-port for injection and 10-port for washing), a desalting cartridge (peptide Micro Trap from Bruker-Michrom) and a HPLC column (Poroshell 120 EC-C18, 1x 50 mm, 2.7 µM from Agilent Technologies). Deuteration was initiated by a 5-fold dilution of CEACAM5, mAb or complex with PBS in D_2O. 2M GndHCl, 0.8 M TCEP, 1 M glycine was used to quench back-exchange and reduce the disulfide bridges for 2 min at 4°C.

The proteins were digested with pepsin and nepenthesin proteases and the peptides were desalted using an Agilent Technologies HPLC pump with TFA 0.03 % in

water at 100 µL/min. The peptides were then separated using another Agilent Technologies HPLC pump with a 15-100 % B gradient in 20 min (A: TFA 0.03 % in water; B: acetonitrile 90 %, TFA 0.03 % in water). The peptides masses were measured using an electrospray-TOF mass spectrometer (Agilent 6210).

The peptides were identified by tandem MS (MSMS), using a Bruker APEX-Q FTMS (9.4 T) and a Bruker 12 T SolariX.

Data Analysis (Bruker) and Mass Hunter (Agilent Technologies) softwares were used for data acquisitions. Data Analysis and Mascot (Matrix Science) were used to process the MSMS data. Mass Hunter and HD Examiner (Sierra Analytics) softwares were used for HDX data processing.

The HDX experiments were repeated at least three times.

Example 10.4: Results

Identification and selection of the peptides

The disulfide bridges remained intact during the deuteration to keep the structural information related to them. To favor proteolysis and peptides identification the bridges were reduced with TCEP after the quench step at low pH and low temperature. Using MSMS after digestion of the CEACAM5-Fab complex it was possible to identify a large number of peptides arising from the three protein chains. After the HDX experiments only the ones giving good quality signals were selected: 25, 30 and 20 peptides from the CEACAM5-A3-B3 antigen, MAb2_VH1aVL1c Fab heavy chain and MAb2_VH1aVL1c light chain, respectively. These peptides cover 89%, 77% and 68% of CEACAM5-A3-B3 antigen, MAb2_VH1aVL1c Fab heavy chain and MAb2_VH1aVL1c light chain sequences, respectively (Table 25). The uncovered regions of the Fab chains are mainly in their C-terminal parts.

Table 25: sequence coverage with deuterated peptides

Peptides	Sequence coverage
CEACAM5-A3-B3	1-18; 1-22; 1-23; 1-19; 23-35; 36-51; 35-49; 50-70; 36-43; 44-51; 36-51; 36-49; 50-67; 37-49; 44-49; 59-67; 71-89; 93-107; 108-115; 128-143; 128-142; 143-157; 130-143; 130-142; 140-143; 163-186
MAb2_VH1aVL1c Fab heavy chain	1-6; 1-20; 1-19; 1-17; 1-18; 4-18; 5-20; 5-18; 24-29; 27-32; 27-29; 34-46; 47-68; 48-68; 50-68; 69-86; 84-93; 88-98; 92-

	104; 100-109; 110-115; 116-136; 111-128; 149-158; 151-158; 159-177; 162-177; 167-177; 187-206
MAb2_VH1aVL1c light chain	1-11; 5-11; 22-46; 47-54; 55-70; 55-71; 72-82; 87-104; 105-115; 117-132; 124-131; 127-145; 133-144; 136-145; 136-143; 136-144; 143-161; 144-151; 146-151

All the 8 asparagine residues that are potential sites of glycosylations were identified within several peptides with an GlcNAc remaining from the endo H deglycosylation. In particular, N114 was found in peptide 108-115. In first experiments (not used for HDX), N166 was found in both forms (with and without GlcNAc). It might explain the heterogeneity observed in the mass spectrum of CEACAM5-A3B3 after deglycosylation, corresponding to 7 and 8 GlcNAc.

Epitope and paratope identification

The free antigen, the free Fab and their complex were deuterated during 2 min or 20 min at 4°C or 20 min at room temperature (26°C). Considering the exchange kinetics of amide hydrogens with temperature (about 3-fold exchange increase with 10°C) the last condition is equivalent to 200 min deuteration at 4°C.

Epitope

The kinetics of deuterium incorporation for the 25 selected peptides of CEACAM5-A3B3 were compared when the antigen was deuterated in the free form and when it was in complex with the Fab. Several peptides did not show any significant HDX difference (ΔHDX) between both states. In contrast some of them (108-115 and 128-143), showed significant ΔHDX. The second region was covered with 5 different peptides: 128-142, 128-143, 130-142, 130-143 and 140-143 showing 13-15 ± 2 % (up to 1.6 ± 0.2 D) ΔHDX after 2 min deuteration.

Comparing 128-142 with 130-142 and 128-143 with 130-143, we did not measure any significant ΔHDX change in each case (1.3-1.4 D for the first two peptides and 1.6 for the last two, after 2 min deuteration), meaning that the amides W129 and R130 are likely not involved in the epitope. In contrast, comparing 128-142 with 128-143 and 130-142 with 130-143, we measured a small ΔHDX change (about 0.2 D), meaning that the amide F143 is involved. The ΔHDX in peptide 140-143 (about 0.3 D) indicates that amides V141or L142 might be also involved. Within the 9

amides from I131 to Q140, several of them are involved in the epitope (about 1 ΔHDX shared on average).

These differences of deuterium incorporation indicate that the epitope belongs in particular to regions (amides), i.e. peptides of sequences SGANLNL (SEQ ID NO: 76) and INGIPQQHTQVLF (SEQ ID NO: 77).

Paratope

The kinetics of deuterium incorporation for the 30 selected peptides of the Fab heavy chain were compared when the Fab was deuterated in the free form and when it was in complex with the antigen. Almost all peptides did not show any significant ΔHDX between both states. Only one peptide (100-109) presented a ΔHDX after 200 min deuteration: 11 ± 2% (0.7 ± 0.2 D). The region (amides) 101-109 of MAb2_VH1aVL1c Fab heavy chain is implied in the paratope.

The kinetics of deuterium incorporation for the 20 selected peptides of the Fab light chain were compared when the Fab was deuterated in the free form and when it was in complex with the antigen. Almost all peptides did not show any significant ΔHDX between both states. Only two peptides (47-54 and 87-104) presented a difference. After 20 min deuteration, it was 10 ± 2 % (0.6 ± 0.2 D) for the first one and 5 ± 2 % (0.9 ± 0.2 D) for the second one, respectively. The regions 48-54 and 88-104 of MAb2_VH1aVL1c light chain are involved in the paratope.

CLAIMS

1. An isolated antibody which:

a) binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins; and

b) does not significantly cross-react with human CEACAM1, human CEACAM6, human CEACAM7, human CEACAM8, *Macaca fascicularis* CEACAM1, *Macaca fascicularis* CEACAM6, and *Macaca fascicularis* CEACAM8.

2. An isolated antibody which competes for binding to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins with an antibody comprising the variable heavy and light chains of an antibody selected from the group consisting of

a) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:31 and a variable domain of light chain of sequence of sequence SEQ ID NO:32;

b) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:33 and a variable domain of light chain of sequence of sequence SEQ ID NO:34;

c) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:33 and a variable domain of light chain of sequence of sequence SEQ ID NO:34 in which K at position 52 has been replaced by R;

d) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:35 and a variable domain of light chain of sequence of sequence SEQ ID NO:36;

e) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:37 and a variable domain of light chain of sequence of sequence SEQ ID NO:38; and

f) an antibody comprising a variable domain of heavy chain of sequence SEQ ID NO:39 and a variable domain of light chain of sequence of sequence SEQ ID NO:40.

3. The antibody according to claim 2, wherein said antibody does not significantly cross-react with human CEACAM1, human CEACAM6, human CEACAM7, human CEACAM8, *Macaca fascicularis* CEACAM1, *Macaca fascicularis* CEACAM6 and *Macaca fascicularis* CEACAM8.

4. An antibody according to any one of claims 1 to 3, which binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5:

a) with a ratio of affinity for human CEACAM5 on to the affinity for *Macaca fascicularis* CEACAM5 which is ≤12; or

b) with an affinity for human CEACAM5 and/or *Macaca fascicularis* CEACAM5 which is ≤10nM,or

c) both a and b.

5. The antibody according to any one of claims 1 to 4, wherein said antibody binds to two regions of the A3-B3 domain of human CEACAM5 protein that comprise sequences SEQ ID NO:76 and SEQ ID NO:77, respectively.

6. An antibody according to any one of claims 1 to 5, which comprises:

a) a CDR1-H consisting of sequence $X_1X_2X_3X_4X_5X_6YD$ (SEQ ID NO:83) wherein each of X_1, X_2, X_3, X_4, X_5 and X_6 is any amino acid; and

a CDR2-H consisting of a 6 to 10 amino acid-long sequence, in which any amino acid may be present at any position; and

a CDR3-H consisting of sequence $X_1X_2HX_3FGX_4X_5GPX_6AX_7$ (SEQ ID NO:84) wherein each of X_1, X_4, X_5, X_6, and X_7 is any amino acid, X_2 is A or S, and X_3 is Y, F or W; or

b) a CDR1-L consisting of sequence $X_1X_2X_3X_4X_5Y$ (SEQ ID NO:85) wherein each of X_1, X_2, X_3 and X_5 is any amino acid, and X_4 is Y, F or W; and

a CDR2-L consisting of sequence NX_1X_2 wherein each of X_1 and X_2 is any amino acid; and

a CDR3-L consisting of sequence $X_1X_2HX_3X_4X_5PX_6X_7$ (SEQ ID NO:86) wherein each of X_1, X_2, X_4, X_5, X_6 and X_7 is any amino acid, X_3 is Y, F or W, or

c) both a and b.

7. An antibody according to any one of claims 1 to 6, which comprises:

a) a CDR1-H consisting of sequence GFX_1FSSYD (SEQ ID NO:78) wherein X_1 is T, A or V; and

a CDR2-H consisting of sequence $IX_1SX_2GGX_3T$ (SEQ ID NO:79) wherein X_1 is S or N, X_2 is Y or G, X_3 is R or I; and

a CDR3-H consisting of sequence X_1AHYFGX_2SGPFAY (SEQ ID NO:80) wherein X_1 is A or T, and X_2 is T or S; or

b) a CDR1-L consisting of sequence ENIFSY (SEQ ID NO:10) or ENIYSY (SEQ ID NO:22); and

a CDR2-L consisting of sequence NX_1X_2 wherein X_1 is A or T, and X_2 is K or R; and

a CDR3-L consisting of sequence QHHYGTPFT (SEQ ID NO:12) or QHHYGIPFT (SEQ ID NO:24), or

c) both a and b.

8. An antibody according to any one of claims 1 to 4, which comprises:

a) a CDR1-H consisting of sequence GFTFSX_1YX_2 (SEQ ID NO:81) wherein X_1 is R or S, and X_2 is A or D; and

a CDR2-H consisting of sequence ISSGG$X_1X_2X_3$ (SEQ ID NO:82) wherein X_1 is absent, S or G, X_2 is D, Y or I, and X_3 is T or I; and

a CDR3-H consisting of sequence ARPAYYGNPAMDY (SEQ ID NO:3) or ARVNYYDSSFLDW (SEQ ID NO:15); or

b) a CDR1-L consisting of sequence QNVGTN (SEQ ID NO:4); and

a CDR2-L consisting of sequence SAS; and

a CDR3-L consisting of sequence QQYNSYPLYT (SEQ ID NO:6) or QQYNNYPLYT (SEQ ID NO:18) , or

c) both a and b.

9. An antibody according to any one of claims 1 to 4 which comprises:

a) a CDR1-H of sequence SEQ ID NO:1 or a sequence differing from SEQ ID NO:1 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:2 or a sequence differing from SEQ ID NO:2 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:3 or a sequence differing from SEQ ID NO:3 by one amino acid substitution; CDR1-L of sequence SEQ ID NO:4 or a sequence differing from SEQ ID NO:4 by one amino acid substitution; CDR2-L of sequence SAS or a sequence differing from SAS by one amino acid substitution and CDR3-L of sequence SEQ ID NO:6 or a

sequence differing from SEQ ID NO:6 by one amino acid substitution; or

b) a CDR1-H of sequence SEQ ID NO:7 or a sequence differing from SEQ ID NO:7 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:8 or a sequence differing from SEQ ID NO:8 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:9 or a sequence differing from SEQ ID NO:9 by one or more amino acid substitutions; CDR1-L of sequence SEQ ID NO:10 or a sequence differing from SEQ ID NO:10 by one amino acid substitution; CDR2-L of sequence NTK or NTR or a sequence differing from NTK or NTR by one amino acid substitution and CDR3-L of sequence SEQ ID NO:12 or a sequence differing from SEQ ID NO:12 by one amino acid substitution; or

c) a CDR1-H of sequence SEQ ID NO:13 or a sequence differing from SEQ ID NO:13 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:14 or a sequence differing from SEQ ID NO:14 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:15 or a sequence differing from SEQ ID NO:15 by one amino acid substitution; CDR1-L of sequence SEQ ID NO:16 or a sequence differing from SEQ ID NO:16 by one amino acid substitution; CDR2-L of sequence SAS or a sequence differing from SAS by one amino acid substitution and CDR3-L of sequence SEQ ID NO:18 or a sequence differing from SEQ ID NO:18 by one amino acid substitution; or

d) a CDR1-H of sequence SEQ ID NO:19 or a sequence differing from SEQ ID NO:19 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:20 or a sequence differing from SEQ ID NO:20 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:21 or a sequence differing from SEQ ID NO:21 by one or more amino acid substitutiosn; CDR1-L of sequence SEQ ID NO:22 or a sequence differing from SEQ ID NO:22 by one amino acid substitution; CDR2-L of sequence NAK or a sequence differing from NAK by one or more amino acid substitutions and CDR3-L of sequence SEQ ID NO:24 or a sequence differing from SEQ ID NO:24 by one amino acid substitution; or

e) a CDR1-H of sequence SEQ ID NO:25 or a sequence differing from SEQ ID NO:25 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:26 or a sequence differing from SEQ ID NO:26 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:27 or a sequence differing

from SEQ ID NO:27 by one or more amino acid substitutions; CDR1-L of sequence SEQ ID NO:28 or a sequence differing from SEQ ID NO:28 by one amino acid substitution; CDR2-L of sequence NAK or a sequence differing from NAK by one or more amino acid substitutions and CDR3-L of sequence SEQ ID NO:30 or a sequence differing from SEQ ID NO:30 by one amino acid substitution.

10. An isolated antibody which binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins and which comprises:

a) a CDR1-H consisting of sequence $X_1X_2X_3X_4X_5X_6YD$ (SEQ ID NO:83) wherein each of X_1, X_2, X_3, X_4, X_5 and X_6 is any amino acid; and

a CDR2-H consisting of a 6 to 10 amino acid-long sequence, in which any amino acid may be present at any position; and

a CDR3-H consisting of sequence $X_1X_2HX_3FGX_4X_5GPX_6AX_7$ (SEQ ID NO:84) wherein each of X_1, X_4, X_5, X_6, and X_7 is any amino acid, X_2 is A or S, and X_3 is Y, F or W; or

b) a CDR1-L consisting of sequence $X_1X_2X_3X_4X_5Y$ (SEQ ID NO:85) wherein each of X_1, X_2, X_3 and X_5 is any amino acid, and X_4 is Y, F or W; and

a CDR2-L consisting of sequence NX_1X_2 wherein each of X_1 and X_2 is any amino acid; and

a CDR3-L consisting of sequence $X_1X_2HX_3X_4X_5PX_6X_7$ (SEQ ID NO:86) wherein each of X_1, X_2, X_4, X_5, X_6 and X_7 is any amino acid, X_3 is Y, F or W, or

c) both a and b.

11. An isolated antibody which binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins and which comprises:

a) a CDR1-H of sequence SEQ ID NO:1 or a sequence differing from SEQ ID NO:1 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:2 or a sequence differing from SEQ ID NO:2 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:3 or a sequence differing from SEQ ID NO:3 by one amino acid substitution; CDR1-L of sequence SEQ ID NO:4 or a sequence differing from SEQ ID NO:4 by one amino acid substitution; CDR2-L of sequence SAS or a sequence differing from SAS by one amino acid substitution and CDR3-L of sequence SEQ ID NO:6 or a

sequence differing from SEQ ID NO:6 by one amino acid substitution; or

b) a CDR1-H of sequence SEQ ID NO:7 or a sequence differing from SEQ ID NO:7 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:8 or a sequence differing from SEQ ID NO:8 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:9 or a sequence differing from SEQ ID NO:9 by one amino or more acid substitutions; CDR1-L of sequence SEQ ID NO:10 or a sequence differing from SEQ ID NO:10 by one amino acid substitution; CDR2-L of sequence NTK or NTR or a sequence differing from NTK or NTR by one amino acid substitution and CDR3-L of sequence SEQ ID NO:12 or a sequence differing from SEQ ID NO:12 by one amino acid substitution; or

c) a CDR1-H of sequence SEQ ID NO:13 or a sequence differing from SEQ ID NO:13 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:14 or a sequence differing from SEQ ID NO:14 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:15 or a sequence differing from SEQ ID NO:15 by one amino acid substitution; CDR1-L of sequence SEQ ID NO:16 or a sequence differing from SEQ ID NO:16 by one amino acid substitution; CDR2-L of sequence SAS or a sequence differing from SAS by one amino acid substitution and CDR3-L of sequence SEQ ID NO:18 or a sequence differing from SEQ ID NO:18 by one amino acid substitution; or

d) a CDR1-H of sequence SEQ ID NO:19 or a sequence differing from SEQ ID NO:19 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:20 or a sequence differing from SEQ ID NO:20 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:21 or a sequence differing from SEQ ID NO:21 by one or more amino acid substitutions; CDR1-L of sequence SEQ ID NO:22 or a sequence differing from SEQ ID NO:22 by one amino acid substitution; CDR2-L of sequence NAK or a sequence differing from NAK by one or more amino acid substitutions and CDR3-L of sequence SEQ ID NO:24 or a sequence differing from SEQ ID NO:24 by one amino acid substitution; or

e) a CDR1-H of sequence SEQ ID NO:25 or a sequence differing from SEQ ID NO:25 by one amino acid substitution; CDR2-H of sequence SEQ ID NO:26 or a sequence differing from SEQ ID NO:26 by one or more amino acid substitutions; CDR3-H of sequence SEQ ID NO:27 or a sequence differing

from SEQ ID NO:27 by one or more amino acid substitutions; CDR1-L of sequence SEQ ID NO:28 or a sequence differing from SEQ ID NO:28 by one amino acid substitution; CDR2-L of sequence NAK or a sequence differing from NAK by one or more amino acid substitutions and CDR3-L of sequence SEQ ID NO:30 or a sequence differing from SEQ ID NO:30 by one amino acid substitution.

12. An antibody according to claim 9 or 11, wherein said amino acid substitution is a conservative amino acid substitution.

13. The antibody according to any one of claims 1 to 12, which comprises:

a) a variable domain of heavy chain of sequence SEQ ID NO:31 or a sequence at least 85% identical thereto and/or a variable domain of light chain of sequence of sequence SEQ ID NO:32, or a sequence at least 85% identical thereto; or

b) a variable domain of heavy chain of sequence SEQ ID NO:33, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:34, or a sequence at least 85% identical thereto; or

c) a variable domain of heavy chain of sequence SEQ ID NO:35, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:36, or a sequence at least 85% identical thereto; or

d) a variable domain of heavy chain of sequence SEQ ID NO:37, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:38, or a sequence at least 85% identical thereto; or

e) a variable domain of heavy chain of sequence SEQ ID NO:39, or a sequence at least 85% identical thereto, and/or a variable domain of light chain of sequence of sequence SEQ ID NO:40, or a sequence at least 85% identical thereto.

14. The antibody according to any one of claims 1 to 13, which is a chimeric or a humanised antibody.

15. The antibody according to any one of claims 1 to 14, which is an antibody comprising:

a) a heavy chain of sequence SEQ ID NO:41 and/or a light chain of sequence of sequence SEQ ID NO:42; or

b) a heavy chain of sequence SEQ ID NO:43 and/or a light chain of sequence of sequence SEQ ID NO:44; or

c) a heavy chain of sequence SEQ ID NO:45 and/or a light chain of sequence of sequence SEQ ID NO:46; or

d) a heavy chain of sequence SEQ ID NO:47 and/or a light chain of sequence of sequence SEQ ID NO:48; or

e) a heavy chain of sequence SEQ ID NO:49 and/or a light chain of sequence of sequence SEQ ID NO:50.

16. The antibody according to any one of claims 1 to 14, which comprises:

a) a heavy chain of sequence SEQ ID NO:51, SEQ ID NO:5, or SEQ ID NO: 74; and/or

b) a light chain of sequence SEQ ID NO:17, SEQ ID NO:23, SEQ ID NO:29, SEQ ID NO:55, or SEQ ID NO: 75.

17. The antibody according to any one of claims 1 to 16, which comprises:

a) a heavy chain of sequence SEQ ID NO:51 and a light chain of sequence SEQ ID NO:17, or

b) a heavy chain of sequence SEQ ID NO:5 and a light chain of sequence SEQ ID NO:23, or

c) a heavy chain of sequence SEQ ID NO:5 and a light chain of sequence SEQ ID NO:29, or

d) a heavy chain of sequence SEQ ID NO:51 and a light chain of sequence SEQ ID NO:55, or

e) a heavy chain of sequence SEQ ID NO:74 and a light chain of sequence SEQ ID NO:75.

18. An isolated antibody which binds to A3-B3 domain of human and *Macaca fascicularis* CEACAM5 proteins and which comprises

a) a heavy chain consisting of sequence SEQ ID NO:87 or a sequence at least 85% identical thereto; and/or
b) a light chain consisting of sequence SEQ ID NO:88 or a sequence at least 85% identical thereto.

19. The antibody according to any one of claims 1 to 18, which is an antibody fragment.

20. The antibody according to any one of claims 1 to 19, which is a variable heavy chain of a single domain antibody (VHH).

21. The antibody according to any one of claims 1 to 20, which is a bispecific or a multispecific antibody.

22. The antibody according to any one of claims 1 to 21, which is a fragment selected from the group consisting of Fv, Fab, F(ab')2, Fab', dsFv, (dsFv)2, scFv, sc(Fv)2, and diabodies.

23. An isolated nucleic acid comprising a sequence encoding an antibody according to any one of claims 1 to 22.

24. A host cell which has been transformed by a nucleic acid according to claim 23.

25. An immunoconjugate comprising an antibody according to any one of claims to 1 to 22 conjugated or linked to at least one growth inhibitory agent.

26. The immunoconjugate according to claim 25, wherein said growth inhibitory agent is a cytotoxic agent or a radioactive isotope.

27. The immunoconjugate according to claim 25 or 26, wherein said growth inhibitory agent is selected from the group consisting of chemotherapeutic agents, enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins, taxoids, vincas, taxanes, maytansinoid or maytansinoid analogs, tomaymycin or pyrrolobenzodiazepine derivatives, cryptophycin derivatives, leptomycin derivatives,

auristatin or dolastatin analogs, prodrugs, topoisomerase II inhibitors, DNA alkylating agenst, anti-tubulin agents, and CC-1065 or CC-1065 analogs.

28. The immunoconjugate according to claim 26 or 27, wherein said growth inhibitory agent is ($N^{2'}$-deacetyl-$N^{2'}$-(3-mercapto-1-oxopropyl)-maytansine) DM1 or $N^{2'}$-deacetyl-N-$^{2'}$(4-methyl-4-mercapto-1-oxopentyl)-maytansine (DM4).

29. The immunoconjugate according to any one of claims 25 to 28, wherein the antibody is covalently attached via a cleavable or non-cleavable linker to the at least one growth inhibitory agent.

30. The immunoconjugate according to claim 29, wherein said linker is selected from the group consisting of N-succinimidyl pyridyldithiobutyrate (SPDB), 4-(Pyridin-2-yldisulfanyl)-2-sulfo-butyric acid (sulfo-SPDB), and succinimidyl (N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC).

31. The immunoconjugate according to any one of claims 25 to 30, wherein the antibody comprises a heavy chain of sequence SEQ ID NO:5 and a light chain of sequence SEQ ID NO:29.

32. The immunoconjugate according to any one of claims 24 to 31, wherein the immunoconjugate is characterised by a drug-to-antibody ratio (DAR) ranging from 1 to 10.

33. A pharmaceutical composition comprising an antibody according to any one of claims 1 to 22, or an immunoconjugate according to any one of claims 25 to 32, and a pharmaceutically acceptable carrier.

34. An antibody according to any one of claims 1 to 22, or an immunoconjugate according to any one of claims 25 to 32, or a pharmaceutical composition according to claim 33, for use for the treatment of cancer.

35. The antibody, immunoconjugate or pharmaceutical composition for the use according to claim 34, wherein the cancer is CEACAM5 expressing cancer.

36. The antibody, immunoconjugate or pharmaceutical composition for the use according to claim 34 or 35, wherein the cancer is colorectal, stomach, lung, uterus cervix, pancreas, oesophagus, ovary, thyroid, bladder, endometrium, breast, liver, prostate, or skin cancer.

37. An antibody according to any one of claims 1 to 22 for use for *ex vivo* detecting CEACAM5 expression in biological sample of a subject.

38. An antibody for the use according to claim 37, wherein said antibody is labelled with a detectable molecule or substance.

39. An antibody for the use according to claim 37 or 38, wherein said use is for diagnosing the presence of a cancer in a subject, determining susceptibility of a patient having cancer to a therapeutic agent targeting CEACAM5, or monitoring effectiveness of anti-CEACAM5 cancer therapy or detecting cancer relapse after anti-CEACAM5 cancer therapy.

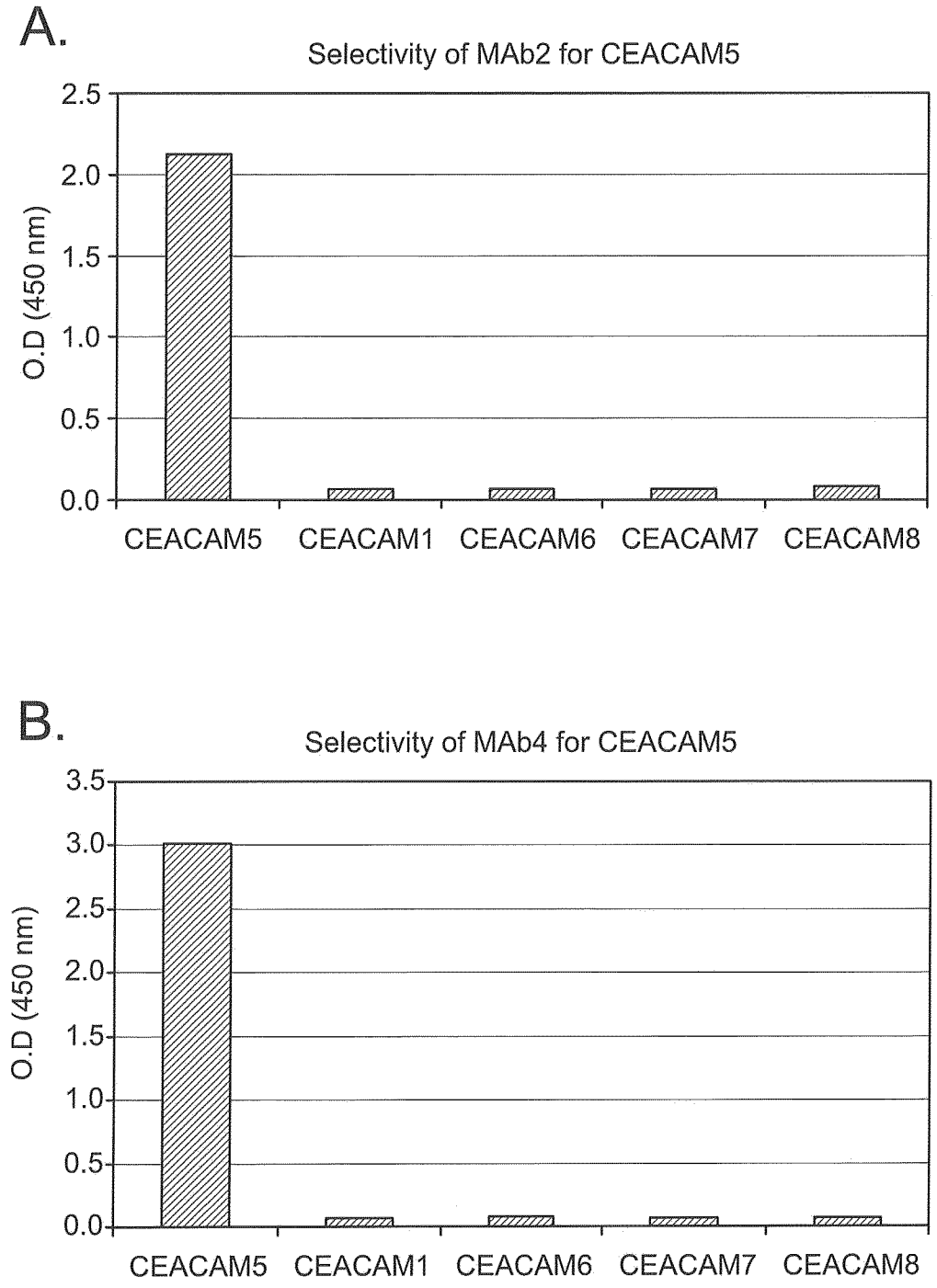
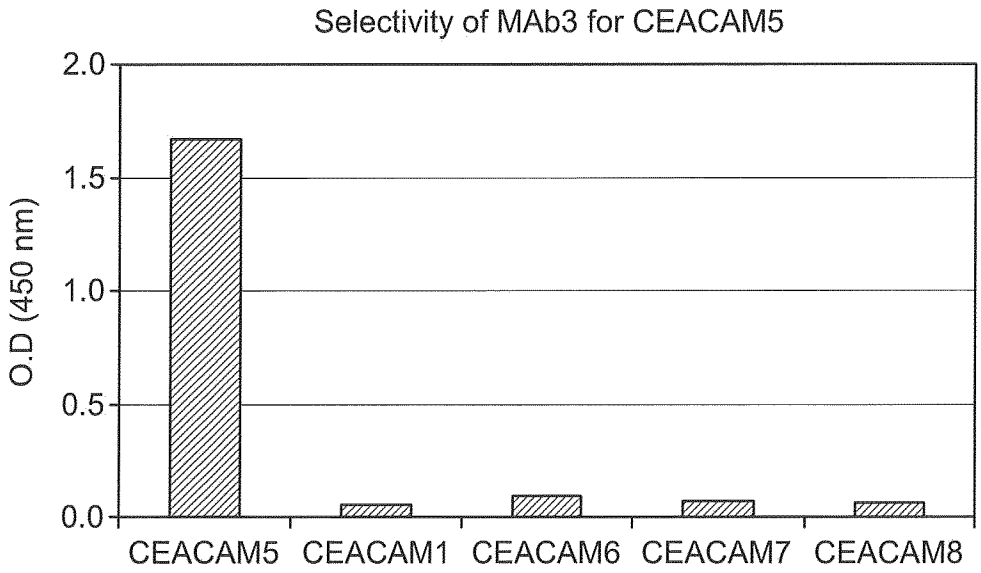


FIG.1 Beginning

C.



D.

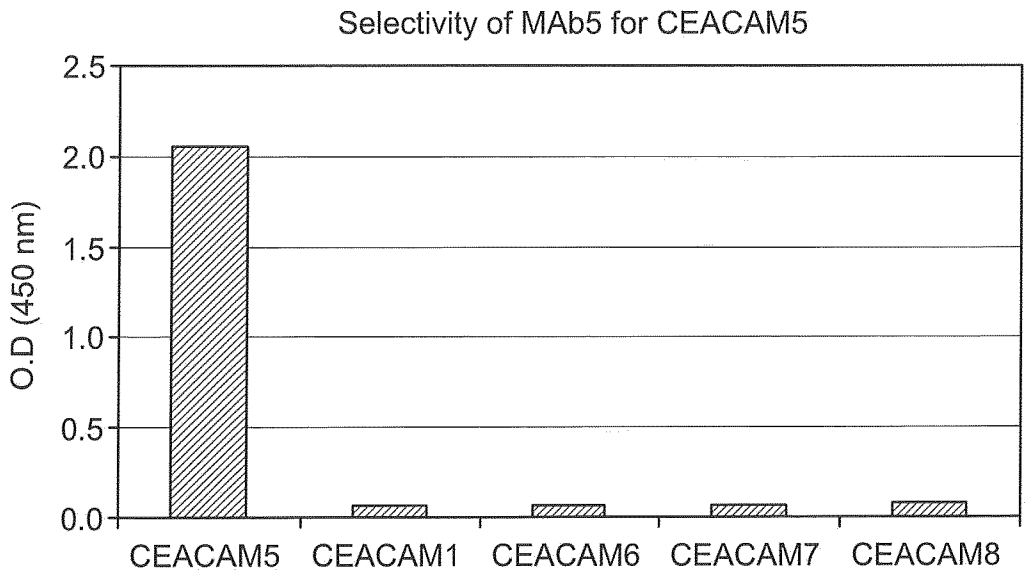


FIG.1 Continuation

E.

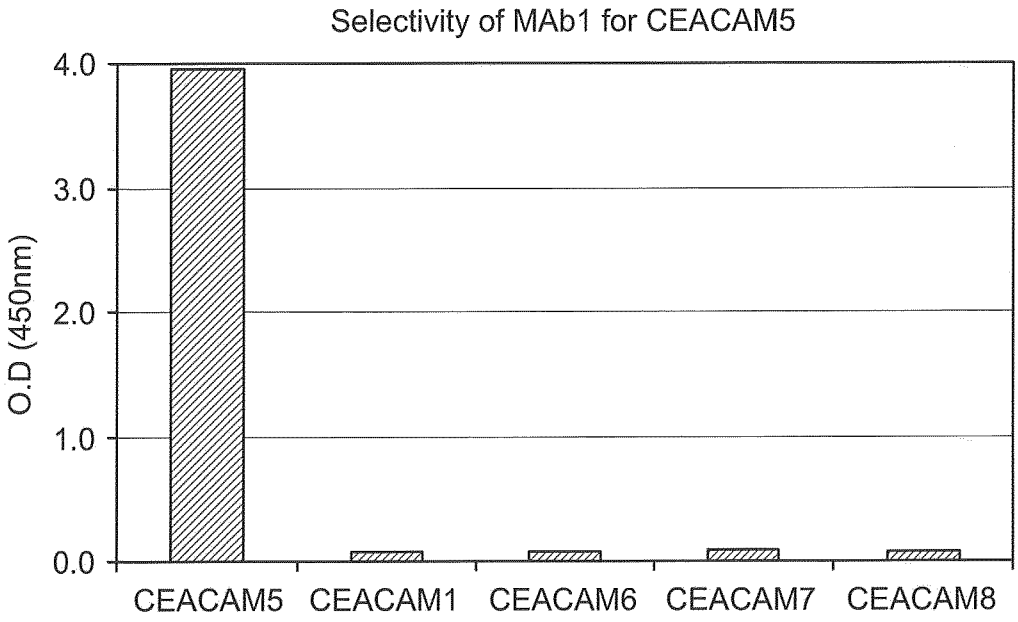

Selectivity of MAb1 for CEACAM5
O.D (450nm)
4.0
3.0
2.0
1.0
0.0
CEACAM5
CEACAM1
CEACAM6
CEACAM7
CEACAM8

FIG.1 End

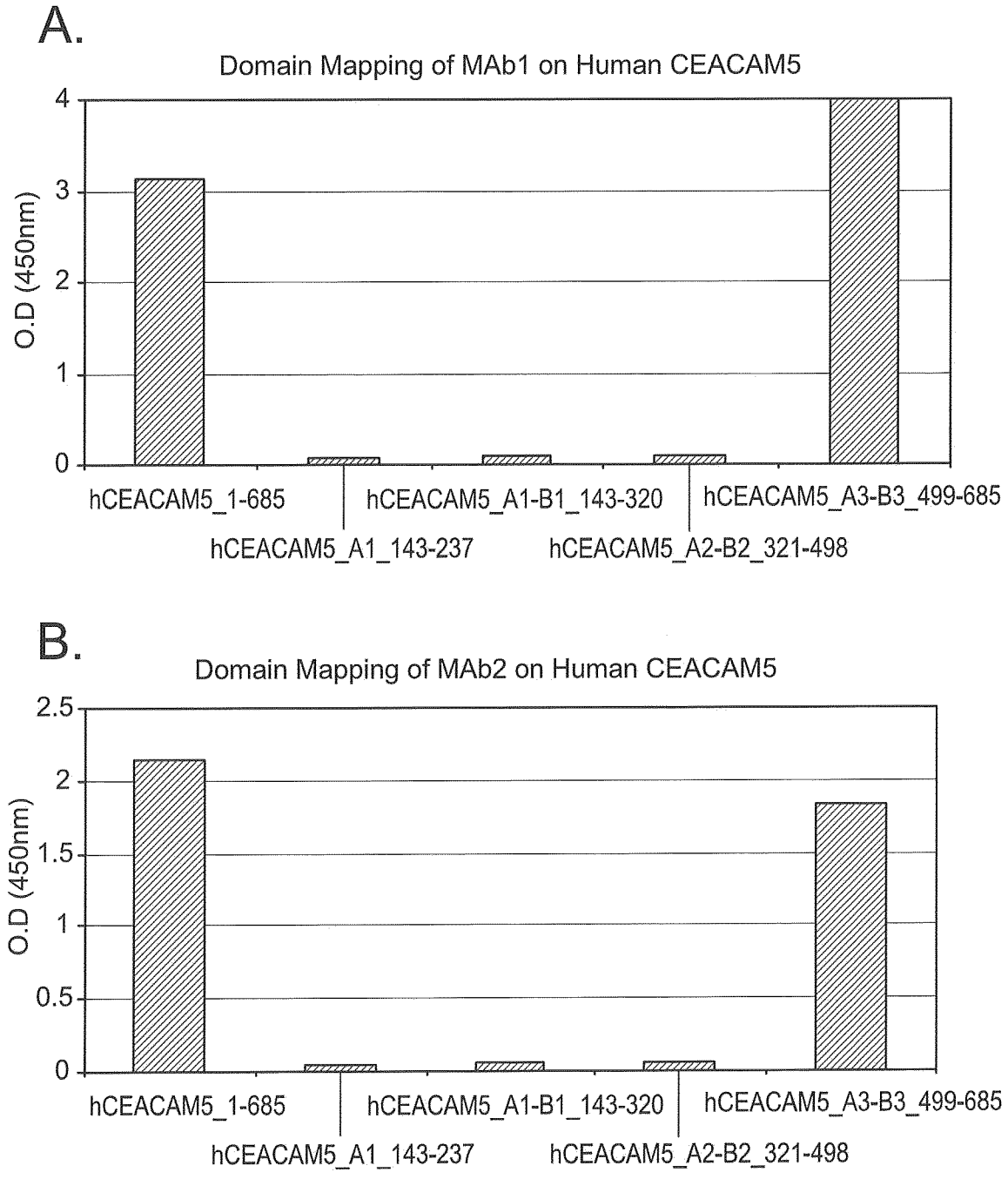


FIG.2 Beginning

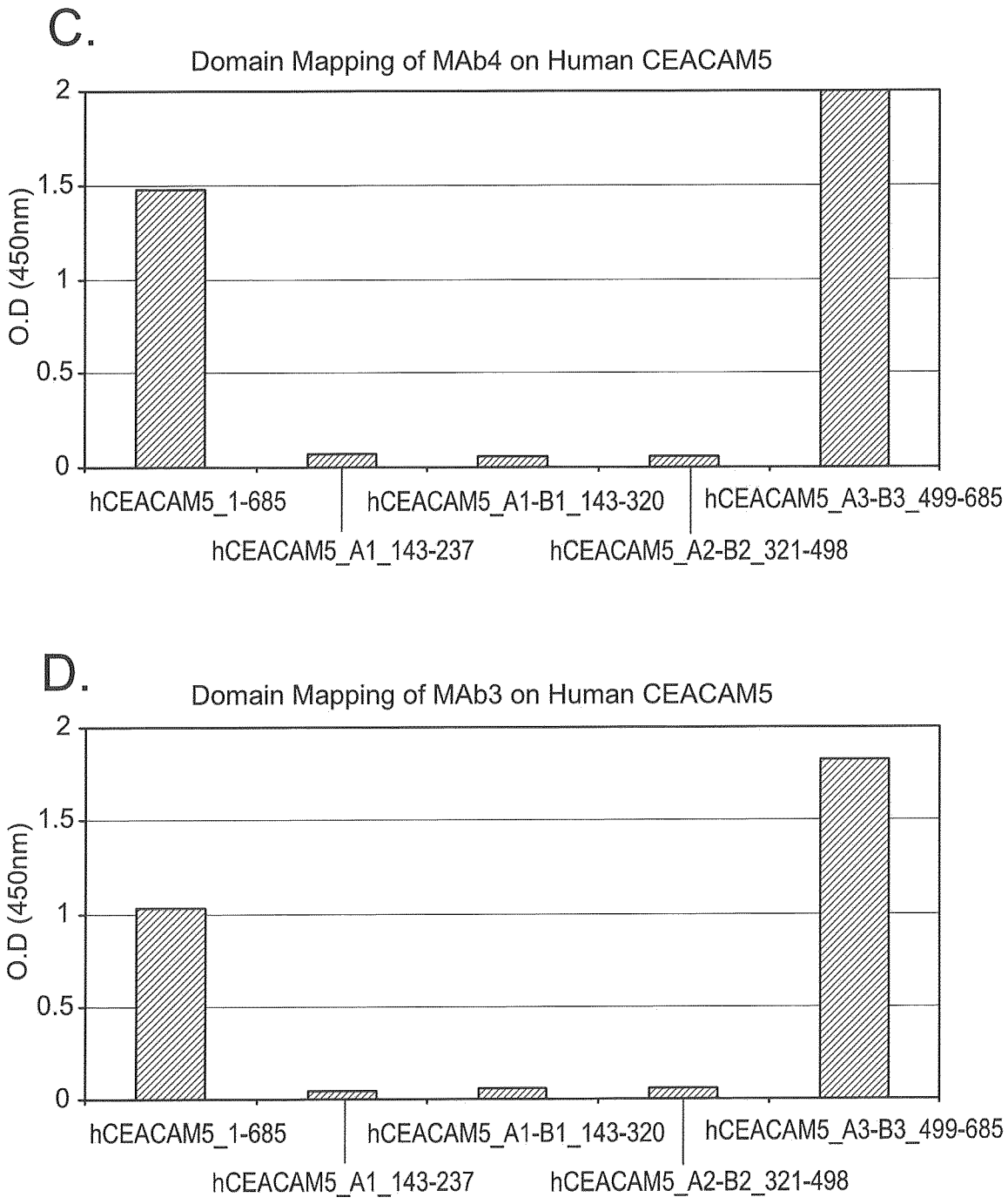


FIG.2 Continuation

E.

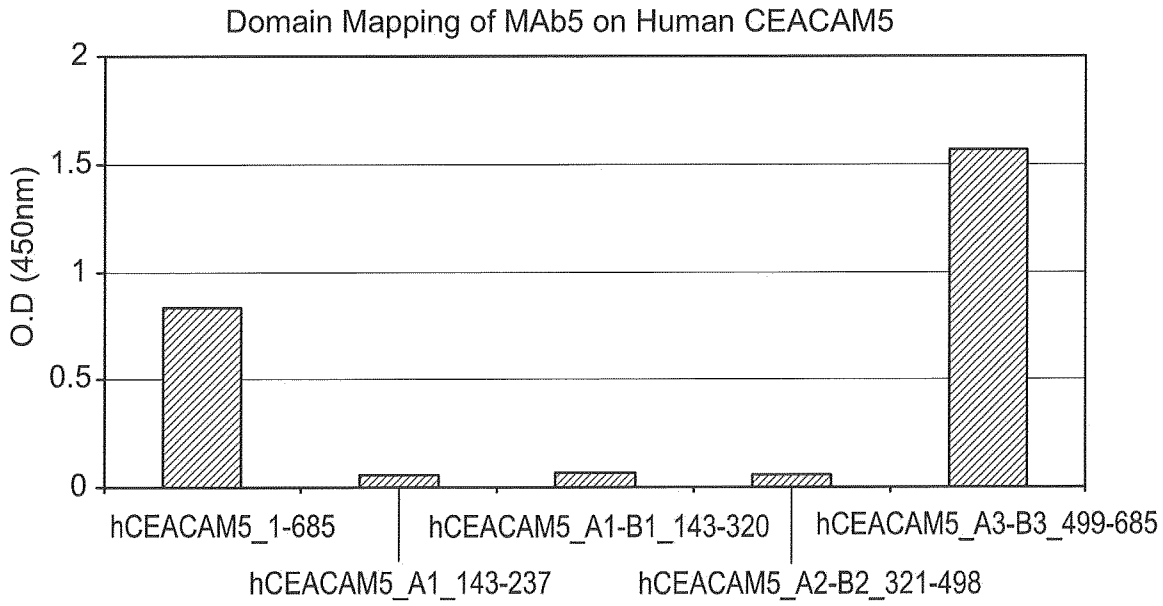

Domain Mapping of MAb5 on Human CEACAM5
O.D (450nm)
2
1.5
1
0.5
0
hCEACAM5_1-685
hCEACAM5_A1_143-237
hCEACAM5_A1-B1_143-320
hCEACAM5_A2-B2_321-498
hCEACAM5_A3-B3_499-685

FIG.2 End

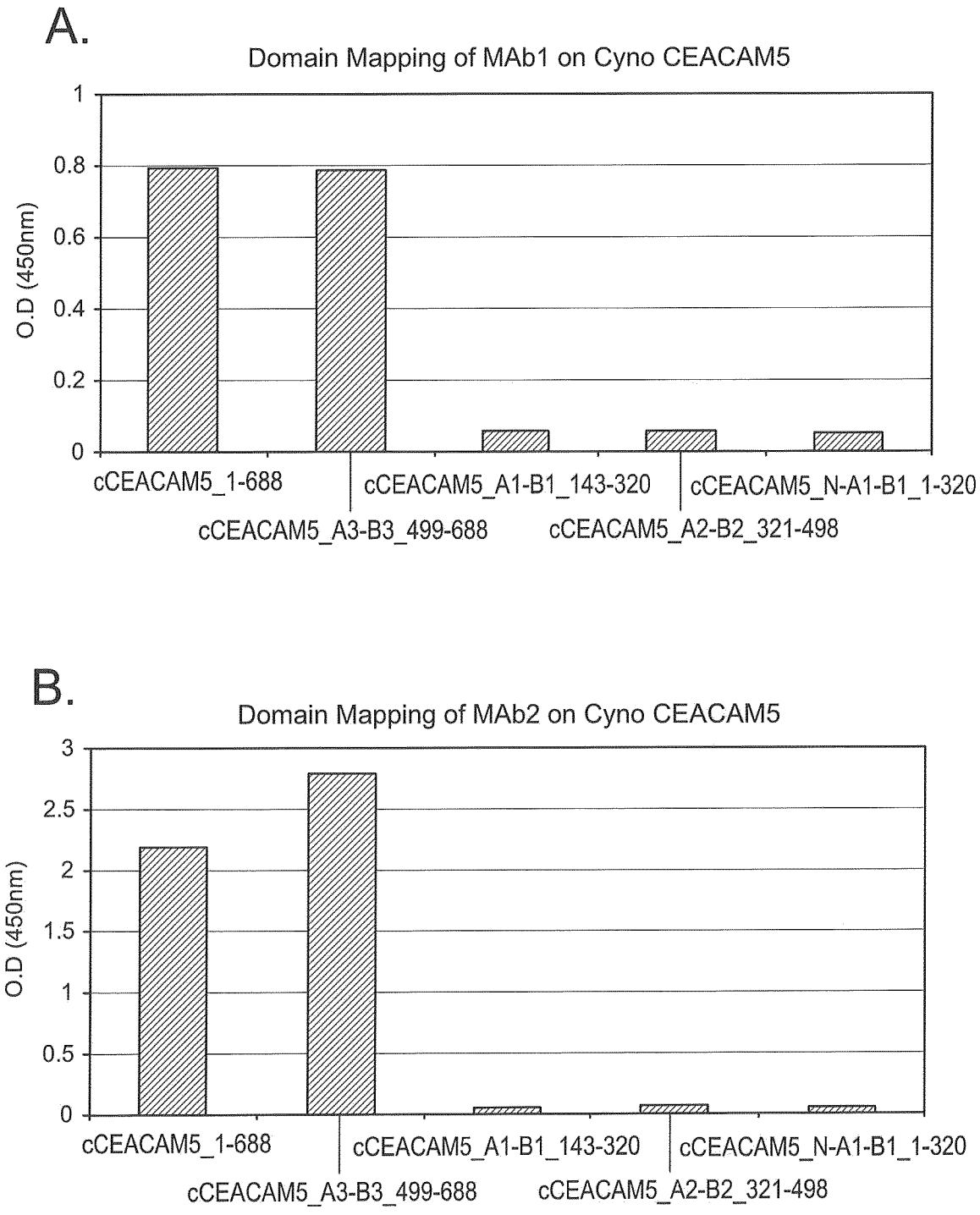
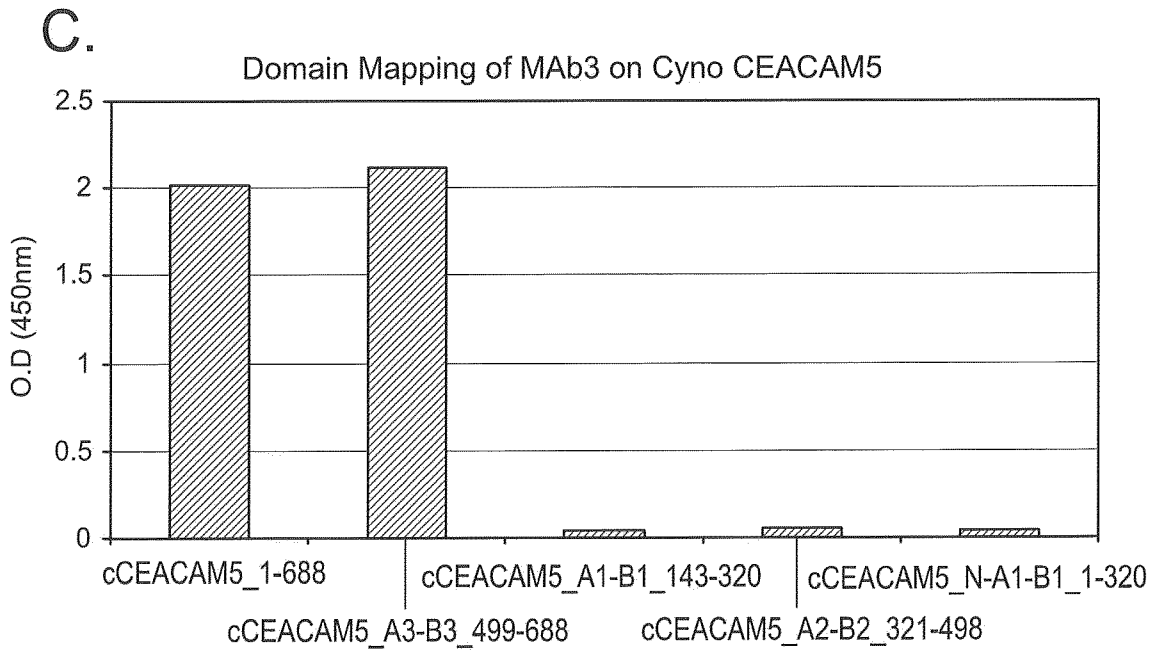


FIG.3 Beginning



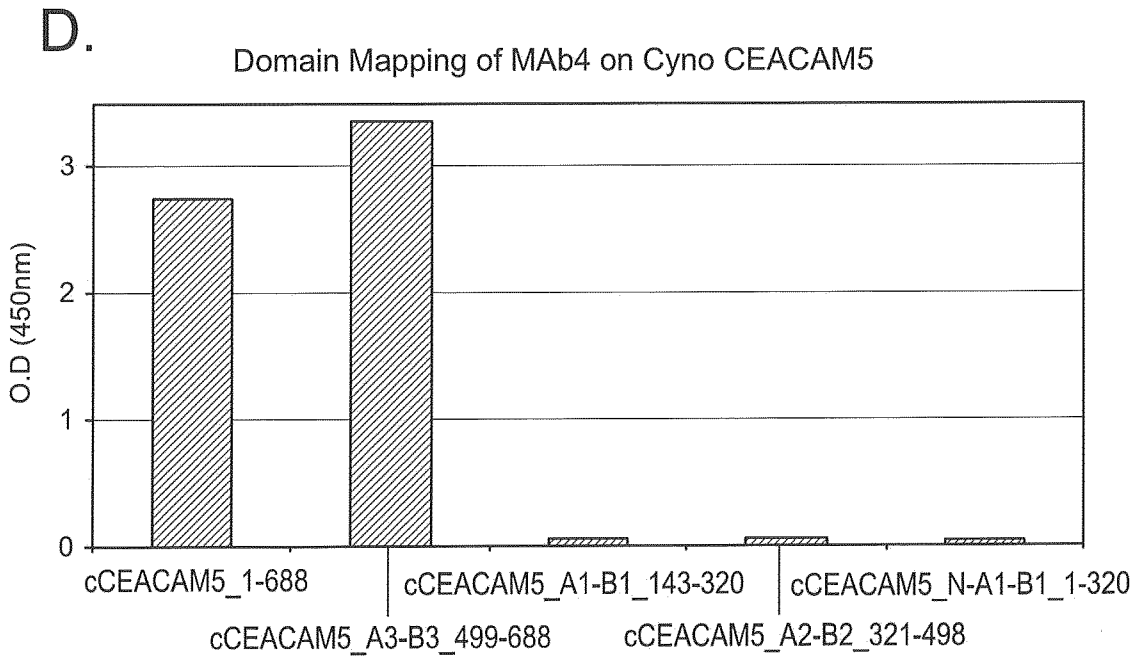


FIG.3 Continuation

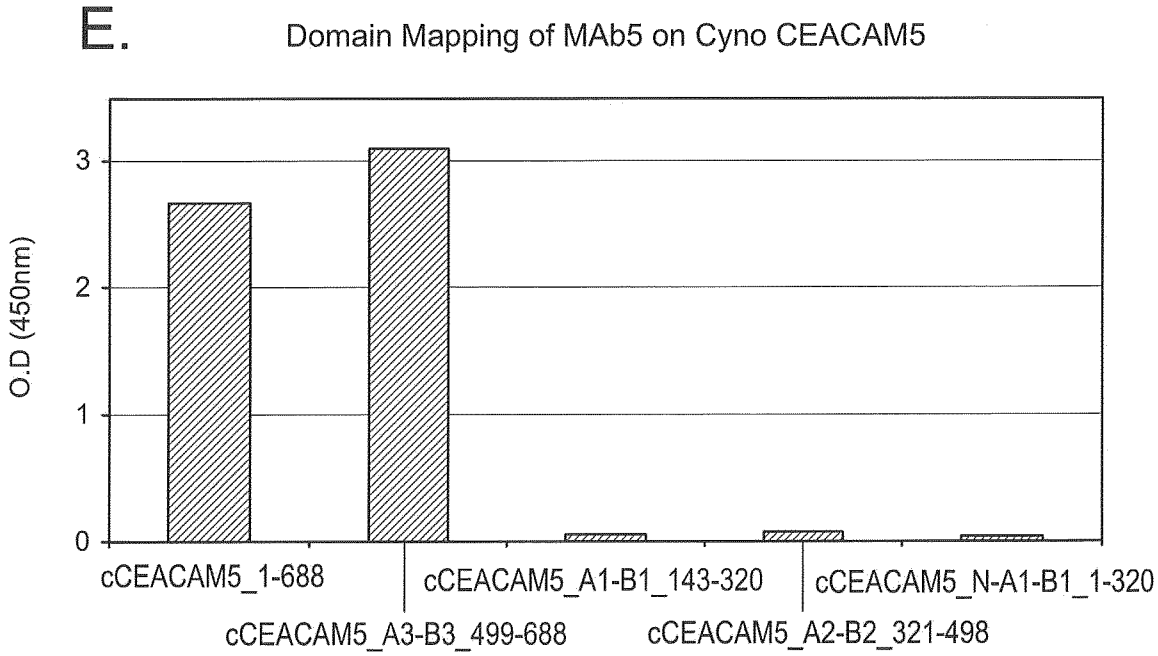

E.
Domain Mapping of MAb5 on Cyno CEACAM5
O.D (450nm)
3
2
1
0
cCEACAM5_1-688
cCEACAM5_A1-B1_143-320
cCEACAM5_N-A1-B1_1-320
cCEACAM5_A3-B3_499-688
cCEACAM5_A2-B2_321-498

FIG.3 End

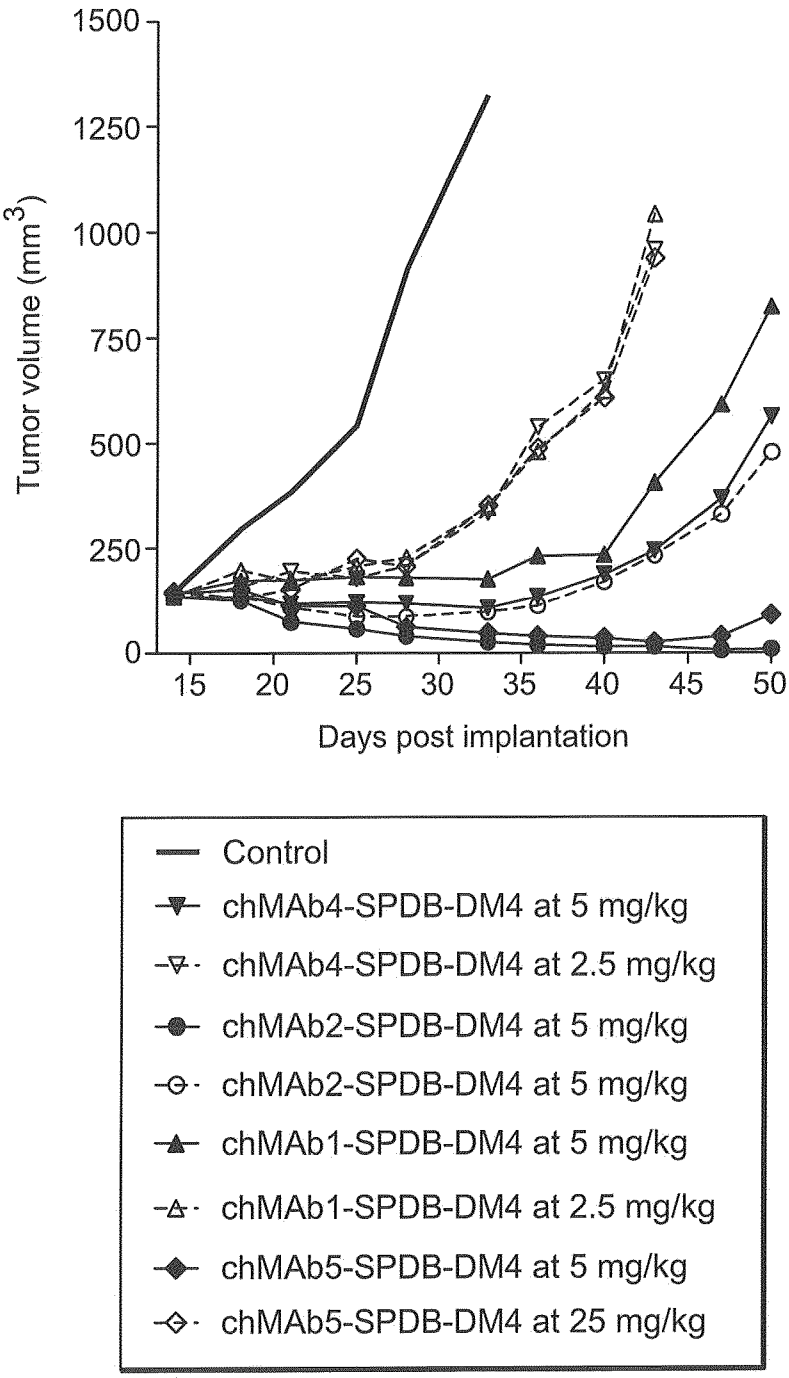

1500
1250
1000
750
500
250
0
Tumor volume (mm3)
15
20
25
30
35
40
45
50
Days post implantation
Control
chMAb4-SPDB-DM4 at 5 mg/kg
chMAb4-SPDB-DM4 at 2.5 mg/kg
chMAb2-SPDB-DM4 at 5 mg/kg
chMAb2-SPDB-DM4 at 5 mg/kg
chMAb1-SPDB-DM4 at 5 mg/kg
chMAb1-SPDB-DM4 at 2.5 mg/kg
chMAb5-SPDB-DM4 at 5 mg/kg
chMAb5-SPDB-DM4 at 25 mg/kg

FIG.4

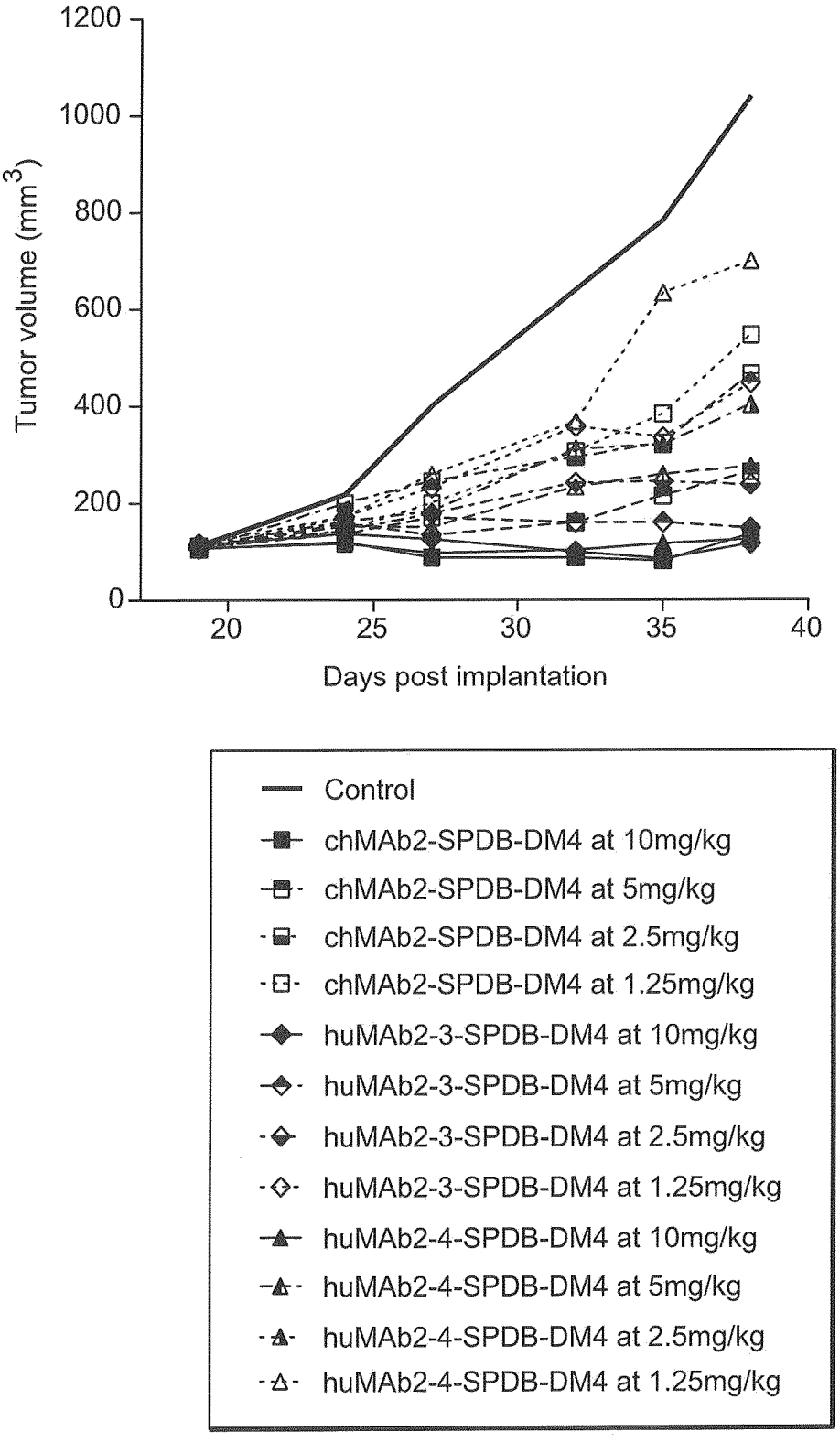

1200
1000
800
600
400
200
0
Tumor volume (mm3)
20
25
30
35
40
Days post implantation
Control
chMAb2-SPDB-DM4 at 10mg/kg
chMAb2-SPDB-DM4 at 5mg/kg
chMAb2-SPDB-DM4 at 2.5mg/kg
chMAb2-SPDB-DM4 at 1.25mg/kg
huMAb2-3-SPDB-DM4 at 10mg/kg
huMAb2-3-SPDB-DM4 at 5mg/kg
huMAb2-3-SPDB-DM4 at 2.5mg/kg
huMAb2-3-SPDB-DM4 at 1.25mg/kg
huMAb2-4-SPDB-DM4 at 10mg/kg
huMAb2-4-SPDB-DM4 at 5mg/kg
huMAb2-4-SPDB-DM4 at 2.5mg/kg
huMAb2-4-SPDB-DM4 at 1.25mg/kg

FIG.5

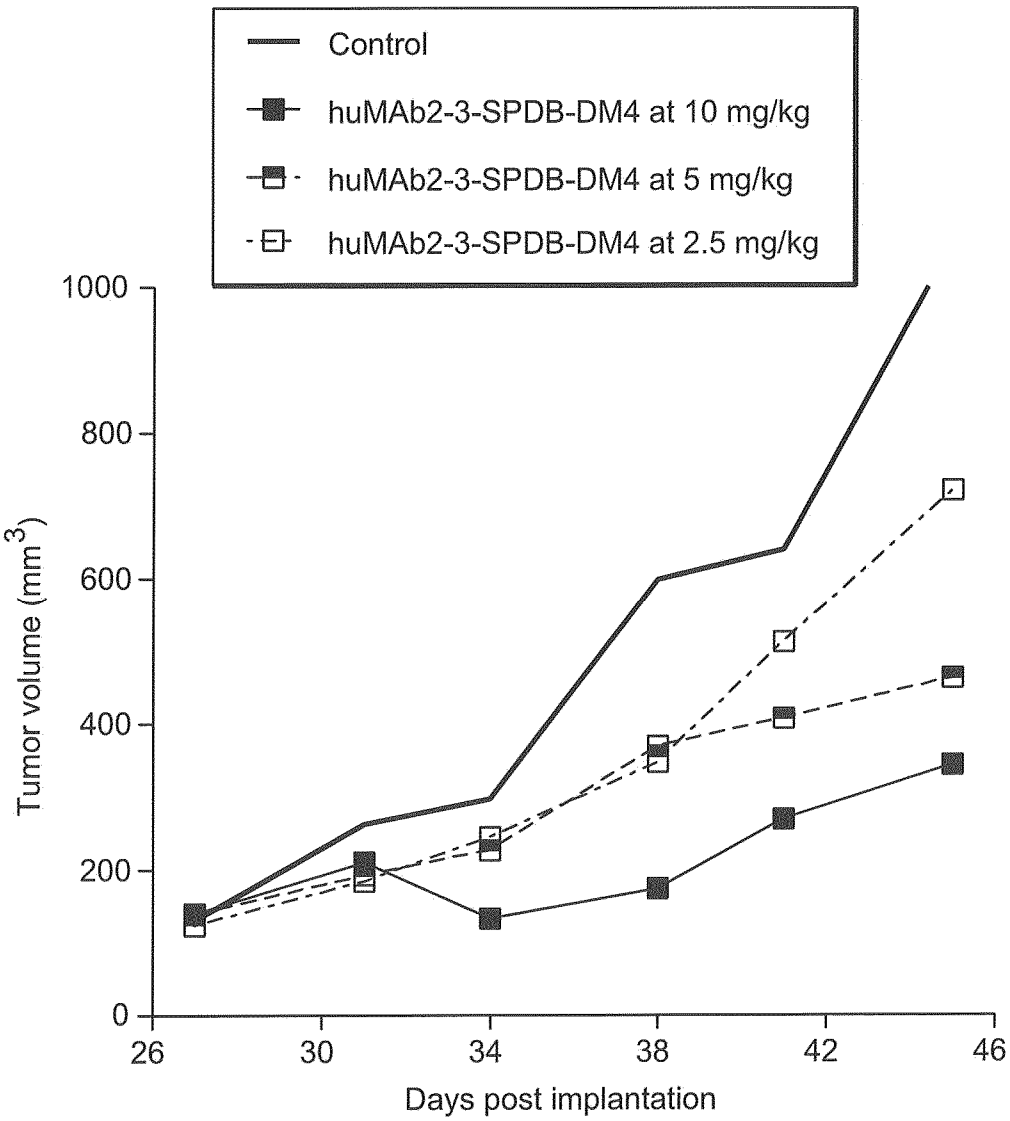

Control
huMAb2-3-SPDB-DM4 at 10 mg/kg
huMAb2-3-SPDB-DM4 at 5 mg/kg
huMAb2-3-SPDB-DM4 at 2.5 mg/kg
Tumor volume (mm3)
1000
800
600
400
200
0
26
30
34
38
42
46
Days post implantation

FIG.6

```
MAb3 VH   (1) EVKLVESGGGLVKPGGSLTLPCAASGFTFSRYAMSWVRQTPEKRLEWVASISSGG-DTYY
MAb1 VH   (1) EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISSGGSYIYY
MAb4 VH   (1) EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYDMSWVRQTPEKRLEWVAFISSYGGRTYY
MAb5 VH   (1) ELQLVESGGVLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPEKRLEWVTYINSGGGITYY
MAb2 VH   (1) EVQLQESGGVLVKPGGSLKLSCAASGFVFSSYDMSWVRQTPEKRLEWVAYISSGGGITYF

MAb3 VH  (60) PDSVKGRFTVSRDNARNILFLQMSSLRSEDTGMYYCARVNYYDSSFLDWWGQGTTLTVSS
MAb1 VH  (61) LDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARPAYYGNPAMDYWGQGTSVTVSS
MAb4 VH  (61) ADTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCAAHYFGTSGPFAYWGQGTLVTVSE
MAb5 VH  (61) PDTVKGRFTISRDNARNTLYLQMSSLKSEDTAIYYCTAHYFGSSGPFAYWGQGTLVTVSA
MAb2 VH  (61) PDTVQGRFTVSRDNAKNTLYLQMNSLKSEDTAIYYCAAHYFGSSGPFAYWGQGTLVTVSA

MAb3 VH   (1) DIVMTQSQRFMSTLEGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASYRYSGVPD
MAb1 VH   (1) DILMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKPLIYSASYRYSGVPD
MAb4 VH   (1) DIQMTQSPASLSASVGETVTITCRASENIYSYFAWYQQKQGKSPQLLVYNAKILAEGVPS
MAb5 VH   (1) DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQLLVYNAKTLTEGVPS
MAb2 VH   (1) DIQMTQSPASLSASVGETVTITCRASENIFSYLAWYQQKQGKSPQLLVYNTKTLAEGVPS

MAb3 VH  (61) RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNNYPLYTFGGGTKLEIK
MAb1 VH  (61) RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLYTFGGGTKLEIK
MAb4 VH  (61) RFSGSGSGTQFSLKINSLQPEDFGTYYCQHHYGIP-FTFGSGTKLELK
MAb5 VH  (61) RFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGTP-FTFGSGTKLEIK
MAb2 VH  (61) RFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGTP-FTFGSGTKLEIK
```

FIG.7

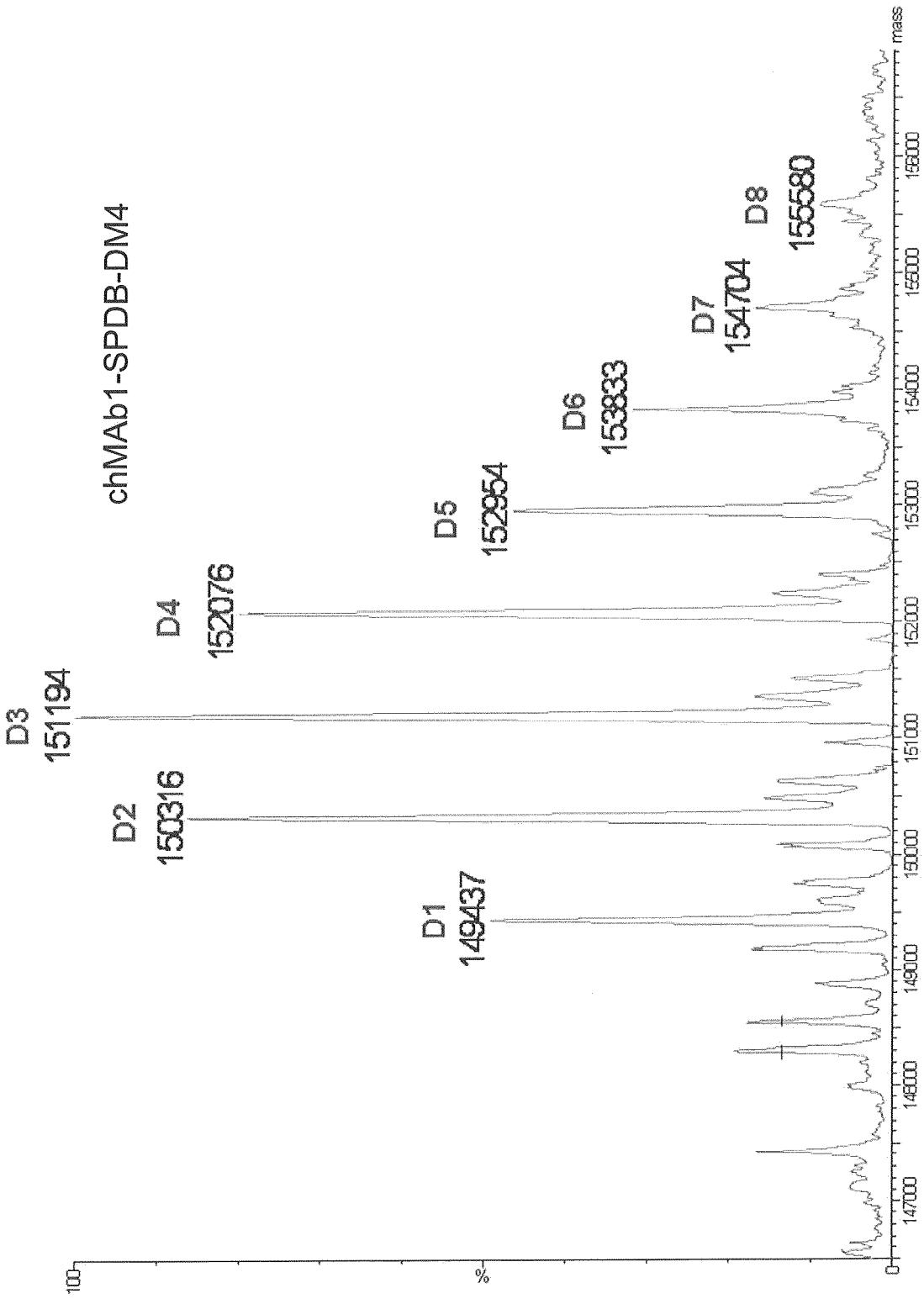

chMAb1-SPDB-DM4
D1
149437
D2
150316
D3
151194
D4
152076
D5
152954
D6
153833
D7
154704
D8
155580
100
%
0
147000
148000
149000
150000
151000
152000
153000
154000
155000
156000
mass

FIG.8

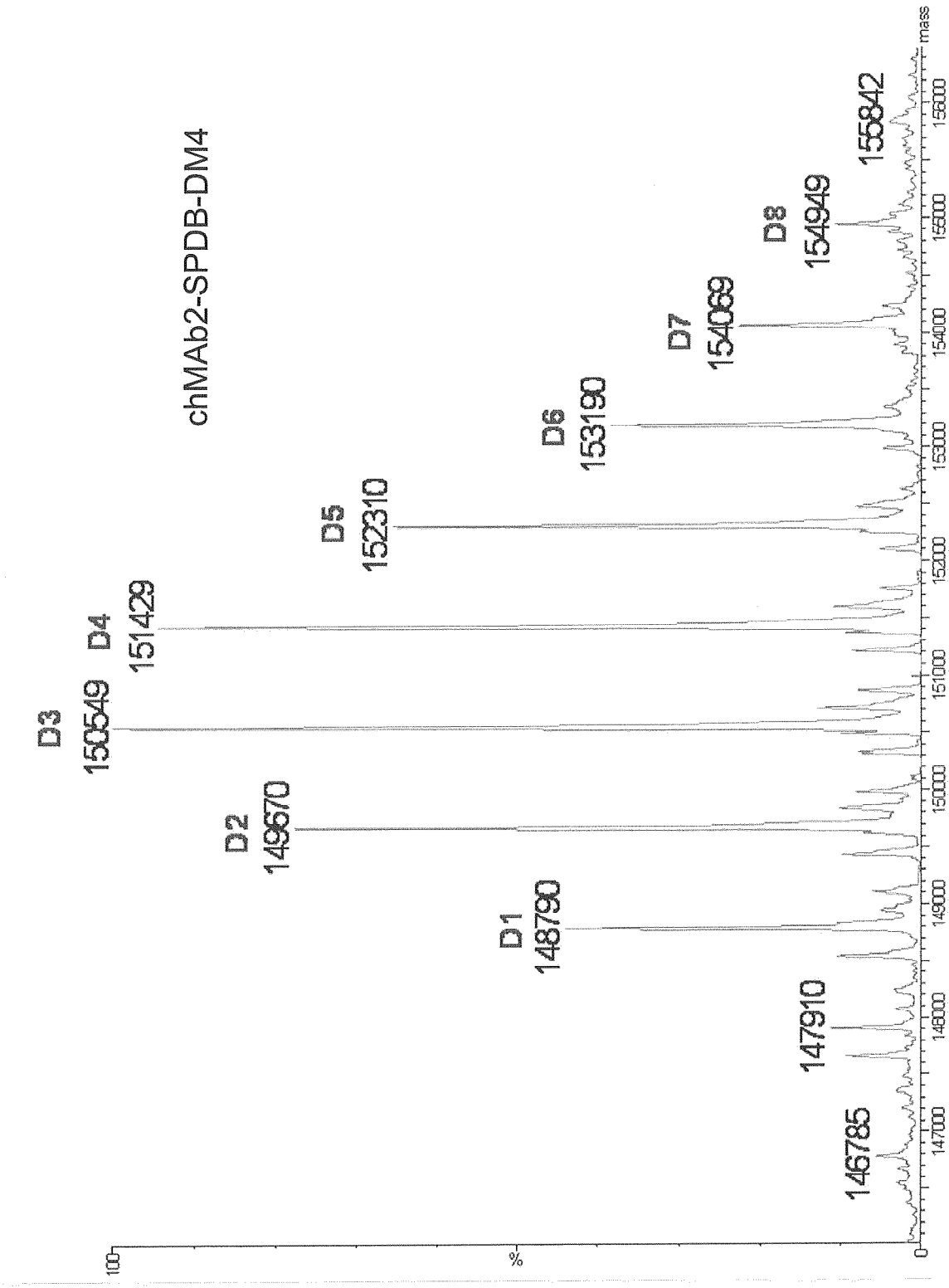

chMAb2-SPDB-DM4
D3
150549
D4
151429
D5
152310
D6
153190
D7
154069
D8
154949
155842
D2
149670
D1
148790
147910
146785
100
%
0
147000
148000
149000
150000
151000
152000
153000
154000
155000
156000
mass

FIG.9

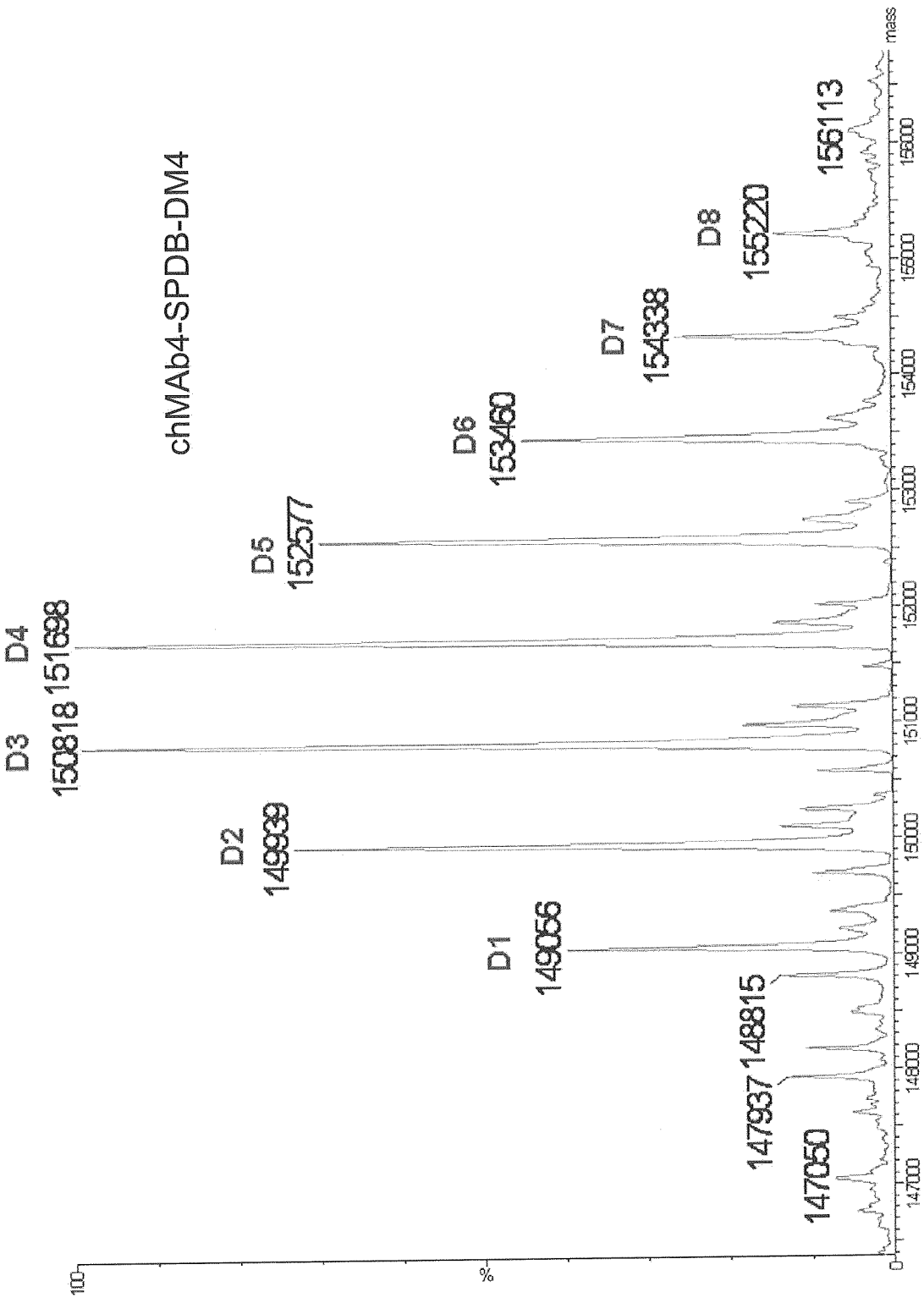

chMAb4-SPDB-DM4
D1
149056
D2
149939
D3
150818
D4
151698
D5
152577
D6
153460
D7
154338
D8
155220
147050
147937
148815
156113
100
%
0
147000
148000
149000
150000
151000
152000
153000
154000
155000
156000
mass

FIG.10

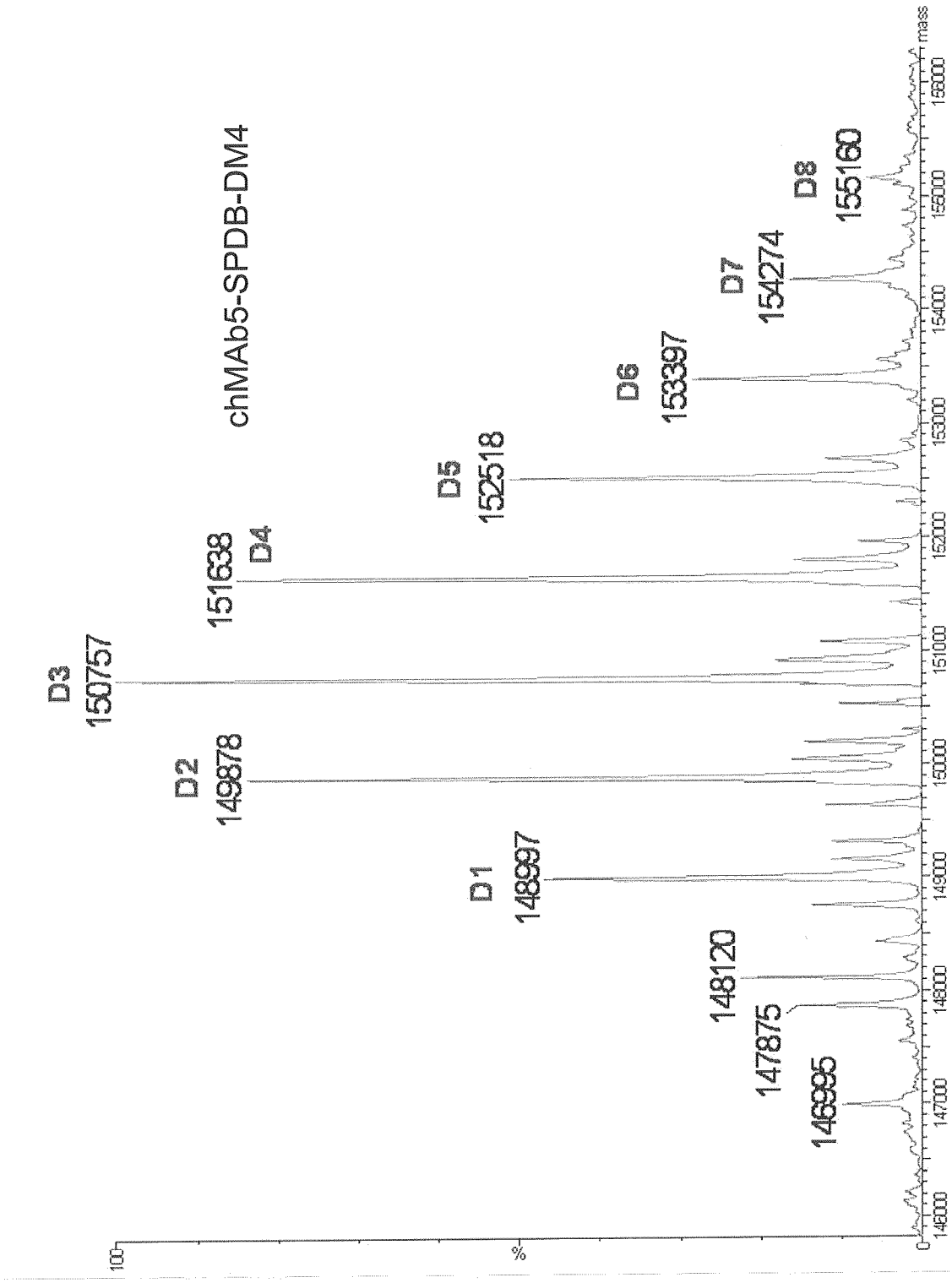

chMAb5-SPDB-DM4
D1
148997
D2
149878
D3
150757
151638
D4
D5
152518
D6
153397
D7
154274
D8
155160
148120
147875
146995
100
%
0
146000
147000
148000
149000
150000
151000
152000
153000
154000
155000
156000
mass

FIG.11

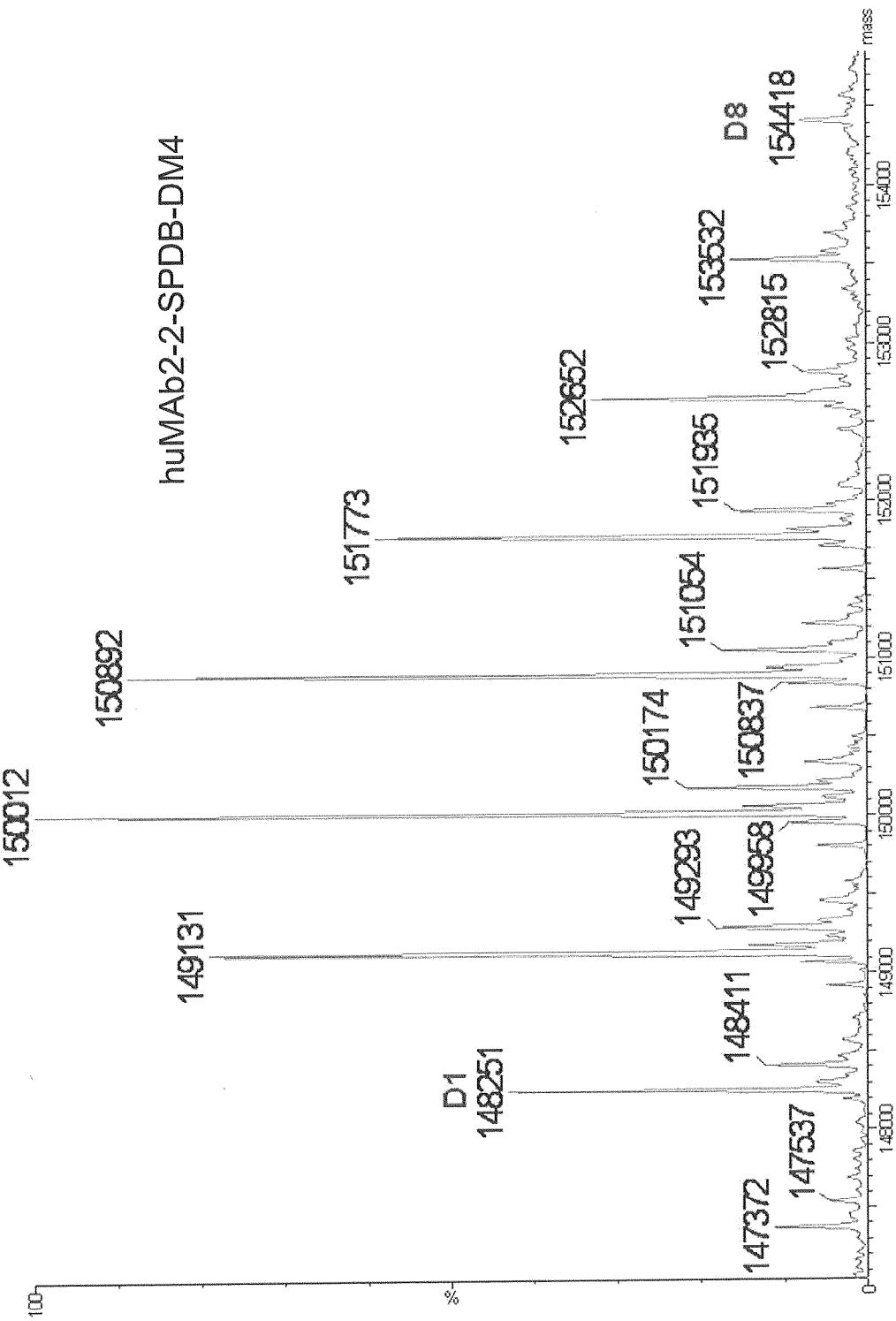

huMAb2-2-SPDB-DM4
100
%
0
147372
147537
D1
148251
148411
149131
149293
149958
150012
150174
150837
150892
151054
151773
151935
152652
152815
153532
D8
154418
mass
148000
149000
150000
151000
152000
153000
154000

FIG.12

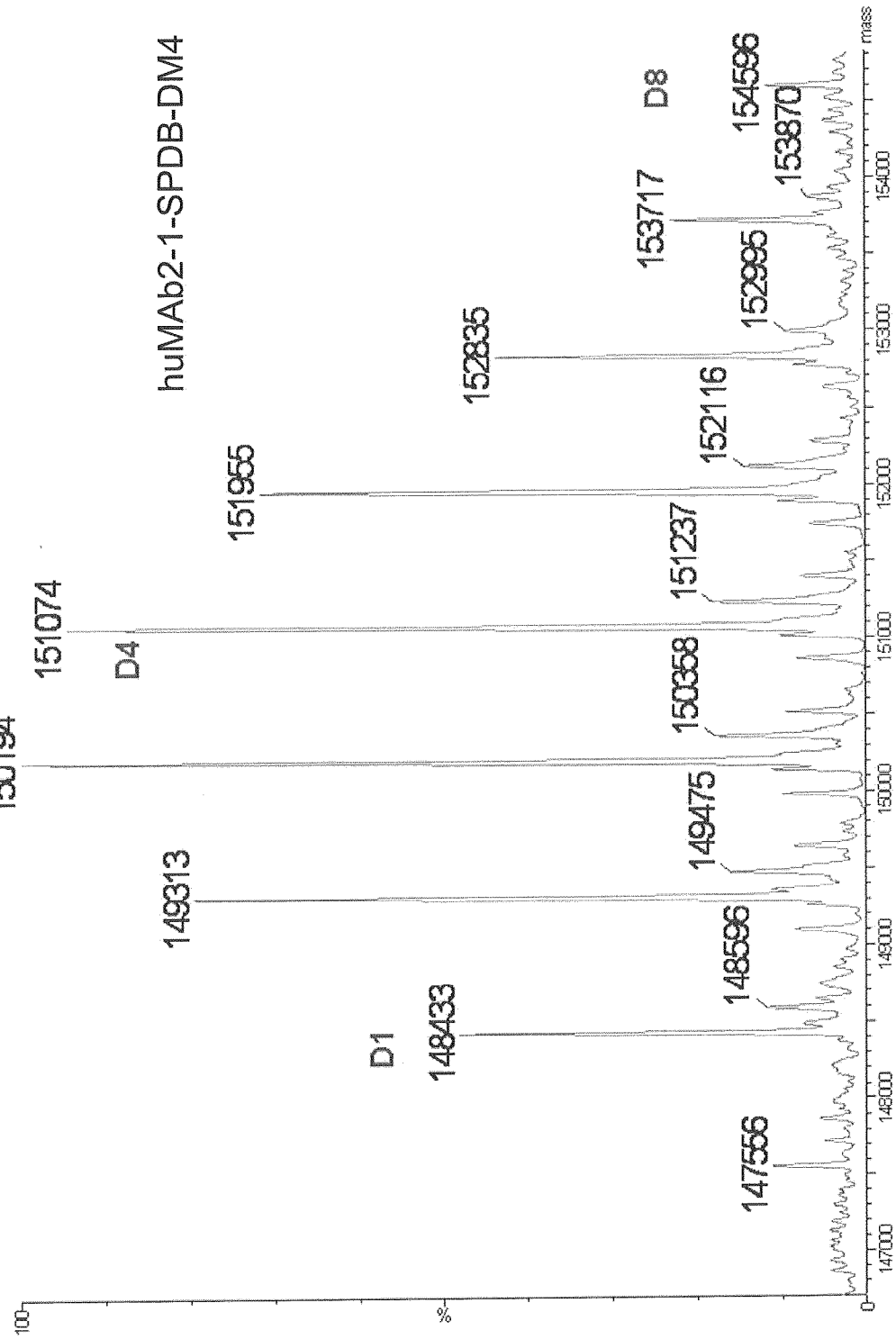

huMAb2-1-SPDB-DM4
D1
D4
D8
147556
148433
148596
149313
149475
150194
150358
151074
151237
151955
152116
152835
152995
153717
153870
154596
100
%
0
147000
148000
149000
150000
151000
152000
153000
154000
mass

FIG.13

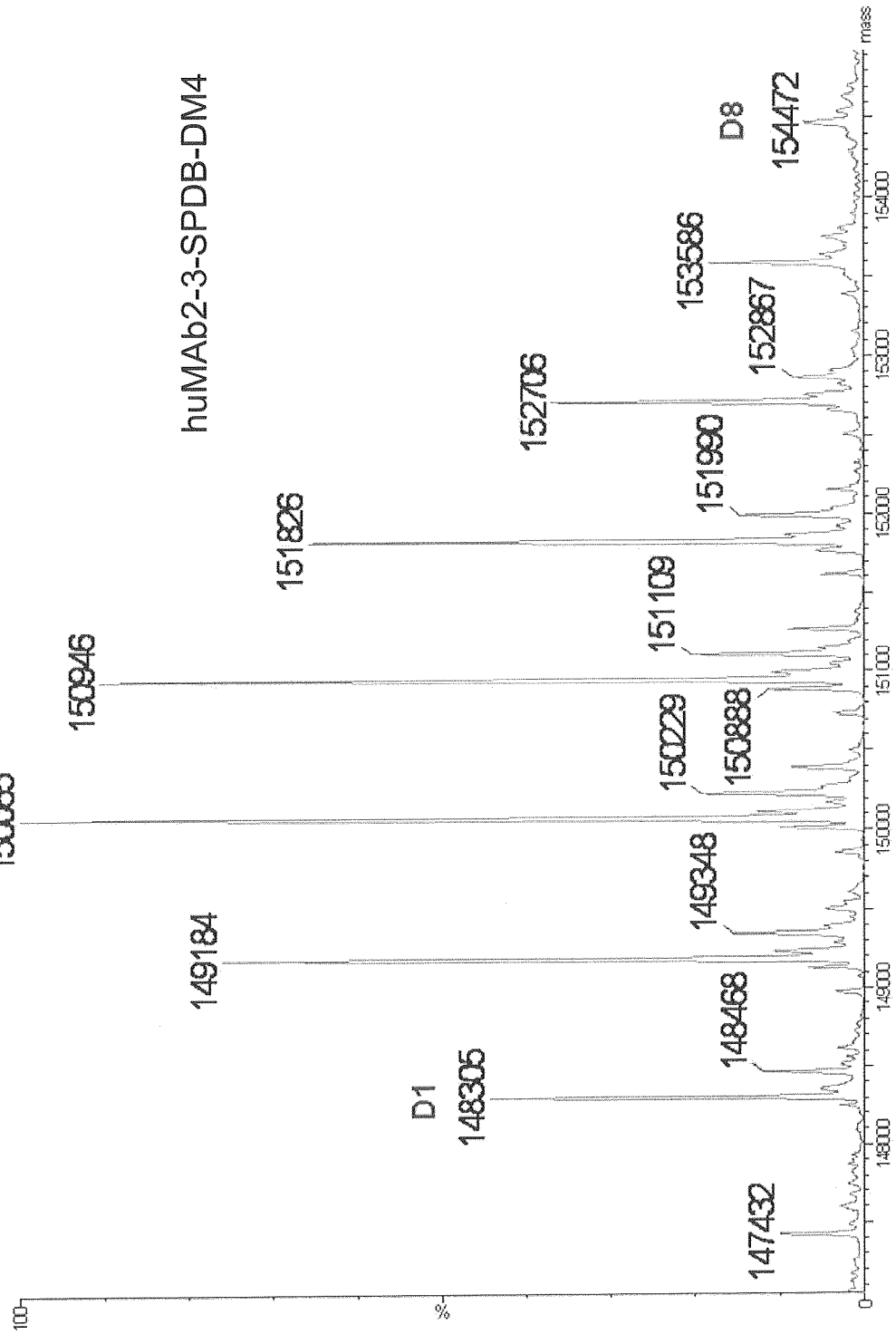

huMAb2-3-SPDB-DM4
100
%
0
147432
D1
148305
148468
149184
149348
150065
150229
150838
150946
151109
151826
151990
152706
152867
153586
D8
154472
mass
148000
149000
150000
151000
152000
153000
154000

FIG.14

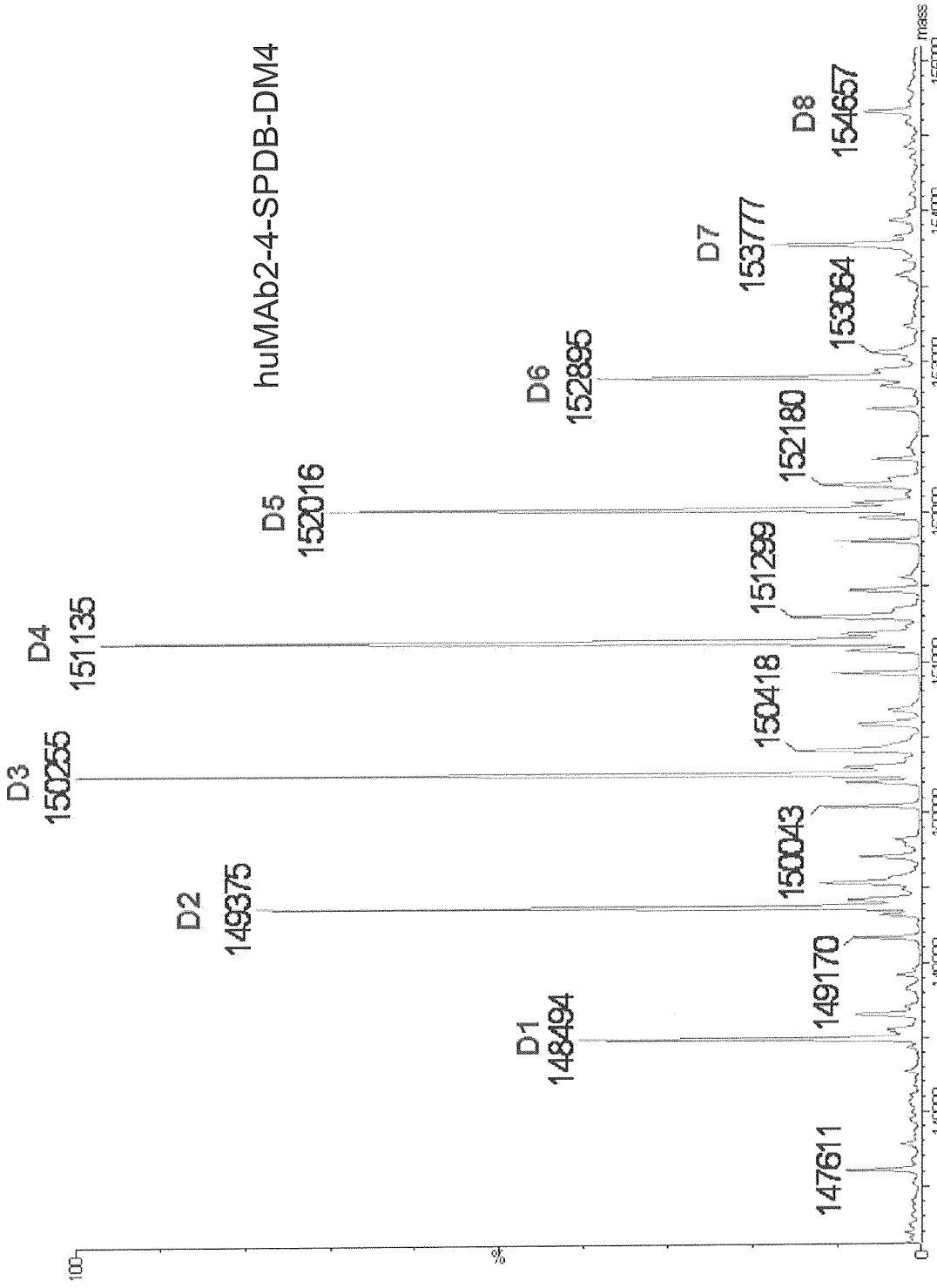

huMAb2-4-SPDB-DM4
D1
148494
D2
149375
D3
150255
D4
151135
D5
152016
D6
152895
D7
153777
D8
154657
147611
149170
150043
150418
151299
152180
153064
100
%
0
mass
148000
149000
150000
151000
152000
153000
154000
155000

FIG.15

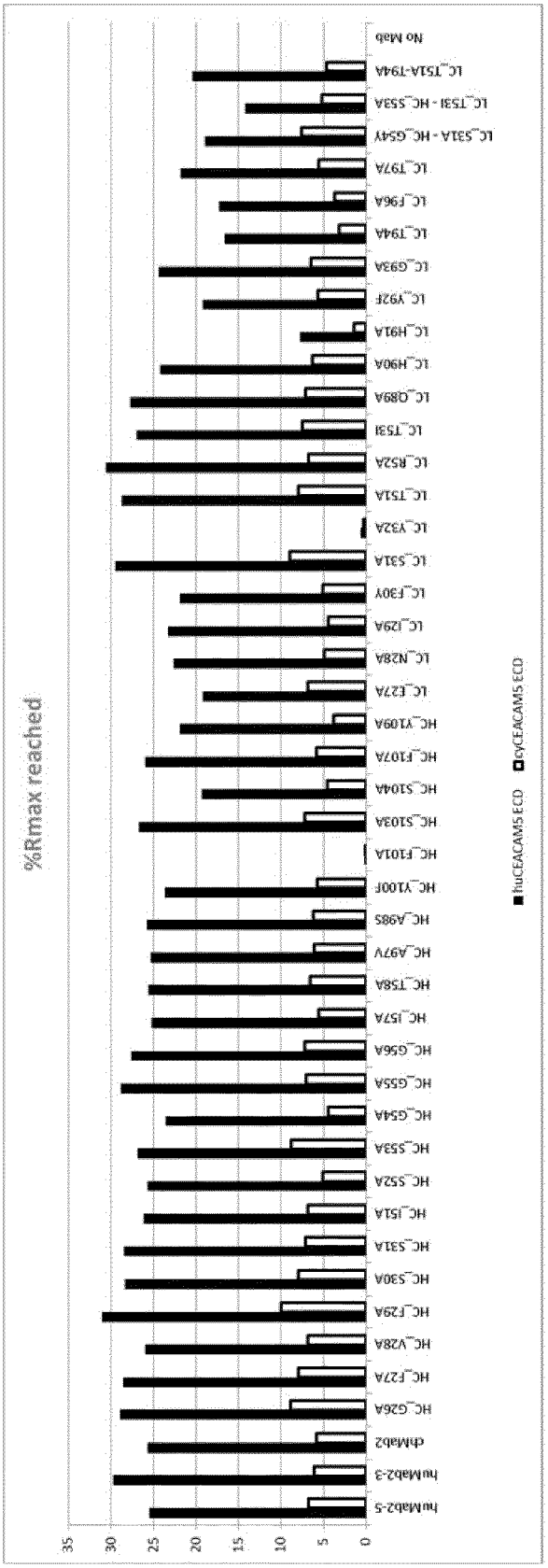

%Rmax reached
huCEACAM5 ECD
cyCEACAM5 ECD
No Mab
LC_T51A-T94A
LC_T51I - HC_S53A
LC_S31A - HC_G54V
LC_T97A
LC_F96A
LC_T94A
LC_G93A
LC_Y92F
LC_H91A
LC_H90A
LC_Q89A
LC_T53I
LC_R52A
LC_T51A
LC_Y32A
LC_S31A
LC_F30Y
LC_I29A
LC_N28A
LC_E27A
HC_Y109A
HC_F107A
HC_S104A
HC_S103A
HC_F101A
HC_Y100F
HC_A98S
HC_A97V
HC_T58A
HC_I57A
HC_G56A
HC_G55A
HC_G54A
HC_S53A
HC_S52A
HC_I51A
HC_S31A
HC_S30A
HC_F29A
HC_V28A
HC_F27A
HC_G26A
chMab2
huMab2-3
huMab2-5
0
5
10
15
20
25
30
35

FIG.16

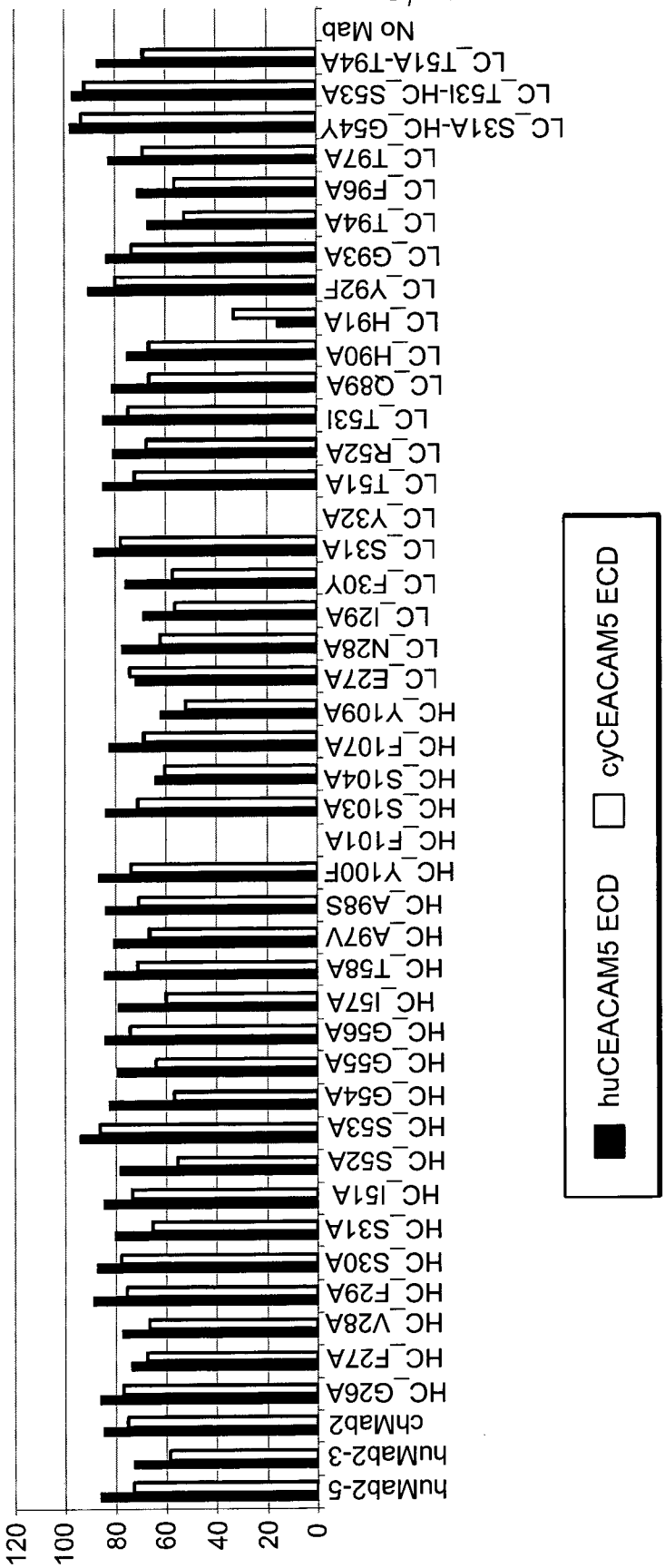

% Remaining signal after 50 seconds
120
100
80
60
40
20
0
huMab2-5
huMab2-3
chMab2
HC_G26A
HC_F27A
HC_V28A
HC_F29A
HC_S30A
HC_S31A
HC_I51A
HC_S52A
HC_S53A
HC_G54A
HC_G55A
HC_G56A
HC_I57A
HC_T58A
HC_A97V
HC_A98S
HC_Y100F
HC_F101A
HC_S103A
HC_S104A
HC_F107A
HC_Y109A
LC_E27A
LC_N28A
LC_I29A
LC_F30Y
LC_S31A
LC_Y32A
LC_T51A
LC_R52A
LC_T531
LC_Q89A
LC_H90A
LC_H91A
LC_Y92F
LC_G93A
LC_T94A
LC_F96A
LC_T97A
LC_S31A-HC_G54Y
LC_T531-HC_S53A
LC_T51A-T94A
No Mab
huCEACAM5 ECD
cyCEACAM5 ECD

FIG.17

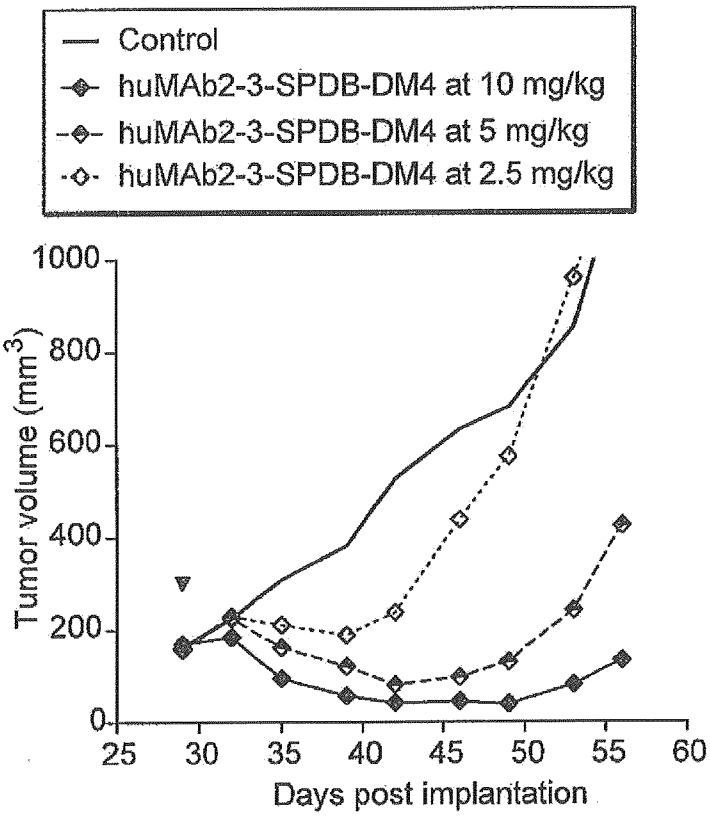

Control
huMAb2-3-SPDB-DM4 at 10 mg/kg
huMAb2-3-SPDB-DM4 at 5 mg/kg
huMAb2-3-SPDB-DM4 at 2.5 mg/kg
Tumor volume (mm3)
1000
800
600
400
200
0
25
30
35
40
45
50
55
60
Days post implantation

FIG.18

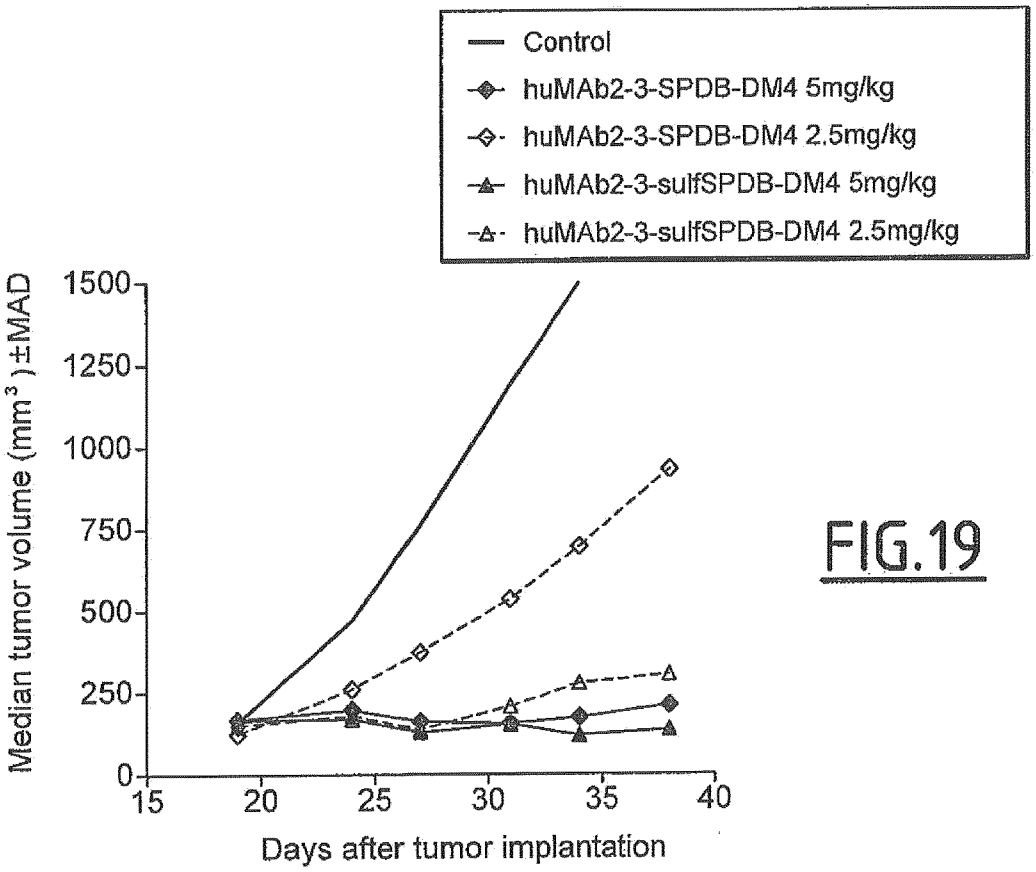
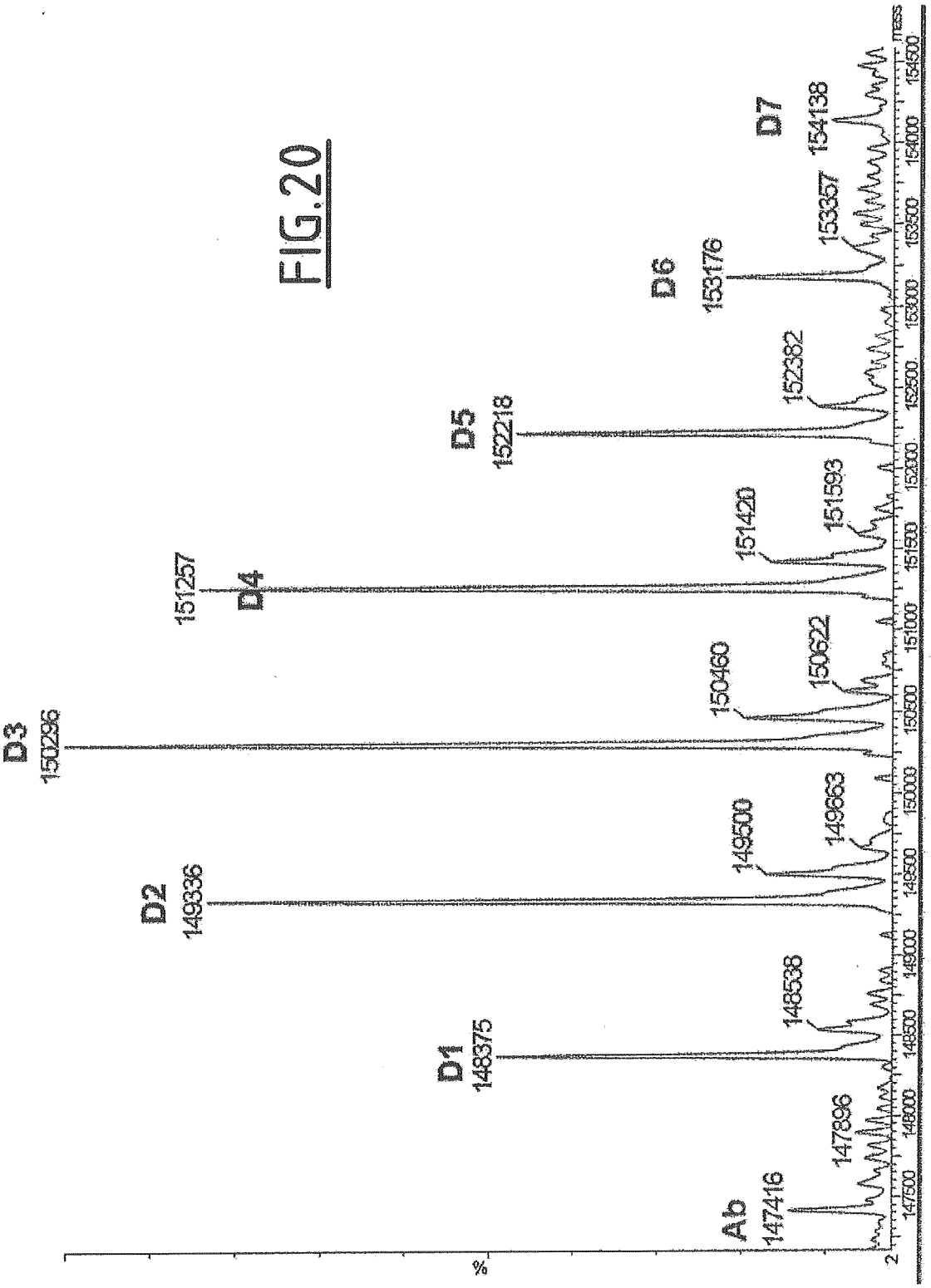

Control
huMAb2-3-SPDB-DM4 5mg/kg
huMAb2-3-SPDB-DM4 2.5mg/kg
huMAb2-3-sulfSPDB-DM4 5mg/kg
huMAb2-3-sulfSPDB-DM4 2.5mg/kg
Median tumor volume (mm3)±MAD
1500
1250
1000
750
500
250
0
15
20
25
30
35
40
Days after tumor implantation

FIG.19

FIG.20


Ab
147416
147896
D1
148375
148538
D2
149336
149500
149663
D3
150296
150460
150622
D4
151257
151420
151593
D5
152218
152382
D6
153176
D7
153357
154138
%
mass

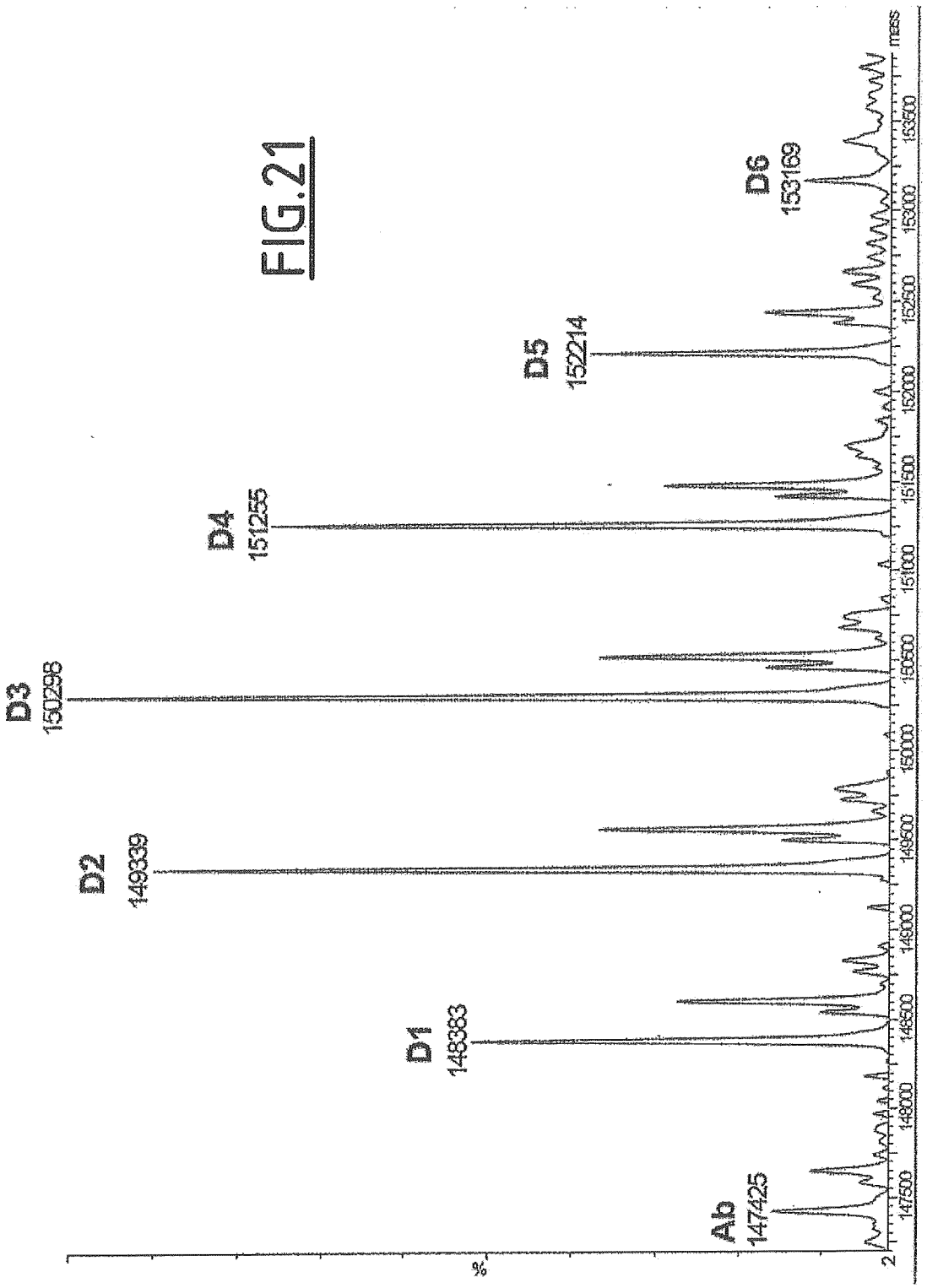

Ab
147425
D1
148383
D2
149339
D3
150298
D4
151255
D5
152214
D6
153169
%
mass

FIG.21

Heavy Chain variable domain alignment

```
Mab2            SEQ ID NO:33  (1) EVQLQESGGVLVKPGGSLKLSCAAS GFVFSSYDMSWVRQTPEKRLEWVAYISSGGGITYF (60)
Mab4            SEQ ID NO:37  (1) EVQLVESGGGLVKPGGSLKLSCAAS GFTFSSYDMSWVRQTPEKRLEWVAFISSYGGRTYY (60)
Mab5            SEQ ID NO:39  (1) ELQLVESGGVLVKPGGSLKLSCAAS GFAFSSYDMSWVRQTPEKRLEWVTYINSGGGITYY (60)
humanized VH1a  SEQ ID NO:5   (1) EVQLQESGPGLVKPGGSLSLSCAAS GFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYA (60)
humanized VH1   SEQ ID NO:51  (1) EVQLQESGPGLVKPGGSLSLSCAAS GFVFSSYDMSWVRQTPERRLEWVAYISSGGGITYF (60)
humanized VHg2  SEQ ID NO:74  (1) EVQLVESGGGLVQPGGSLRLSCAAS GFVFSSYDMSWVRQAPGKGLEWVSYISSGGGITYY (60)

Mab2            SEQ ID NO:33 (61) PDTVQGRFTVSRDNAKNTLYLQMNSLKSEDTAIYYC AAHYFGSSGPFAYWGQGTLVTVSA (120)
Mab4            SEQ ID NO:37 (61) ADTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYC AAHYFGTSGPFAYWGQGTLVTVSA (120)
Mab5            SEQ ID NO:39 (61) PDTVKGRFTISRDNARNTLYLQMSSLKSEDTAIYYC TAHYFGSSGPFAYWGQGTLVTVSA (120)
humanized VH1a  SEQ ID NO:5  (61) PSTVKGRFTVSRDNAKNTLYLQMNSLTSEDTAVYYC AAHYFGSSGPFAYWGQGTLVTVSS (120)
humanized VH1   SEQ ID NO:51 (61) PSTVKGRFTVSRDNAKNTLYLQMNSLTSEDTAIYYC AAHYFGSSGPFAYWGQGTLVTVSA (120)
humanized VHg2  SEQ ID NO:74 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC AAHYFGSSGPFAYWGQGTLVTVSS (120)
```

In ▨ : CDR positions allowing any substitution
In ▨ : CDR positions allowing only conservative substitution
In □ : CDR positions not allowing any substitution

FIG.22

Light Chain variable domain alignment

Mab2	SEQ ID NO:34	(1)	DIQMTQSPASLSASVGETVTITCRAS**ENIFSY**LAWYQQKQGKSPQLLVY**NTK**TLAEGVPS (60)
Mab4	SEQ ID NO:38	(1)	DIQMTQSPASLSASVGETVTITCRAS**ENIYSY**FAWYQQKQGKSPQLLVY**NAK**ILAEGVPS (60)
Mab5	SEQ ID NO:40	(1)	DIQMTQSPASLSASVGETVTITCRAS**ENIYSY**LAWYQQKQGKSPQLLVY**NAK**TLTEGVPS (60)
humanized VL1	SEQ ID NO:17	(1)	DIQMTQSPASLSASVGDTVTITCRAS**ENIFSY**LAWYQQKPGKSPKLLVY**NTK**TLAEGVPS (60)
humanized VL1a	SEQ ID NO:23	(1)	DIQMTQSPASLSASVGDRVTITCRAS**ENIFSY**LAWYQQKPGKSPKLLVY**NTK**TLAEGVPS (60)
humanized VL1c	SEQ ID NO:29	(1)	DIQMTQSPASLSASVGDRVTITCRAS**ENIFSY**LAWYQQKPGKSPKLLVY**NTR**TLAEGVPS (60)
humanized VL1d	SEQ ID NO:55	(1)	DIQMTQSPASLSASVGDTVTITCRAS**ENIFSY**LAWYQQKPGKSPKLLVY**NTR**TLAEGVPS (60)
humanized VLg5	SEQ ID NO:75	(1)	DIQMTQSPSSLSASVGDRVTITCRAS[ENIFSY]LAWYQQKPGKAPKLLIY[NTR]TLQSGVPS (60)

Mab2	SEQ ID NO:34	(61)	RFSGSGSGTQFSLKINSLQPEDFGSYYC**QHHYGTPFT**FGSGTKLEIK (107)
Mab4	SEQ ID NO:38	(61)	RFSGSGSGTQFSLKINSLQPEDFGTYYC**QHHYGIPFT**FGSGTKLELK (107)
Mab5	SEQ ID NO:40	(61)	RFSGSGSGTQFSLKINSLQPEDFGSYYC**QHHYGTPFT**FGSGTKLEIK (107)
humanized VL1	SEQ ID NO:17	(61)	RFSGSGSGTQFSLTISSLQPEDFGSYYC**QHHYGTPFT**FGSGTKLEIK (107)
humanized VL1a	SEQ ID NO:23	(61)	RFSGSGSGTDFSLTISSLQPEDFATYYC**QHHYGTPFT**FGSGTKLEIK (107)
humanized VL1c	SEQ ID NO:29	(61)	RFSGSGSGTDFSLTISSLQPEDFATYYC**QHHYGTPFT**FGSGTKLEIK (107)
humanized VL1d	SEQ ID NO:55	(61)	RFSGSGSGTQFSLTISSLQPEDFGSYYC**QHHYGTPFT**FGSGTKLEIK (107)
humanized VLg5	SEQ ID NO:75	(61)	RFSGSGSGTDFTLTISSLQPEDFATYYC[QHHYGTPFT]FGQGTKLEIK (107)

In ▨ : CDR positions allowing any substitution
In ▧ : CDR positions allowing only conservative substitution
In □ : CDR positions not allowing any substitution

FIG.23

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2013/074291

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

   a. (means)

   ☐ on paper

   ☒ in electronic form

   b. (time)

   ☒ in the international application as filed

   ☐ together with the international application in electronic form

   ☐ subsequently to this Authority for the purpose of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2013/074291

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/30 A61K39/395 A61P35/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	R. BLUMENTHAL ET AL.: "Inhibition of adhesion, invasion, and metastasis by antibodies targeting CEACAM6 (NCA-90) and CEACAM5 (carcinoembryonic antigen).", CANCER RESEARCH, vol. 65, no. 19, 1 October 2005 (2005-10-01), pages 8809-8817, XP055022386, USA abstract figure 1 page 8810, left-hand column, paragraph 2 ----- -/--	1-39

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
10 February 2014	24/02/2014

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Nooij, Frans

3

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	L. PENG ET AL.: "The CEA/CD3-bispecific antibody MEDI-565 (MT111) binds a nonlinear epitope in the full-length but not a short splice variant of CEA.", PLOS ONE, vol. 7, no. 5, E36412, May 2012 (2012-05), pages 1-14, XP002719867, cited in the application abstract page 2, left-hand column, paragraph 3 - right-hand column, paragraph 1 page 6, right-hand column, last paragraph - page 8, right-hand column, paragraph 2	1-39
A	M. OBERST ET AL.: "In vitro pharmacological comparison of a carcinoembryonic antigen (CEA)/CD3 bispecific cynomolgus-reactive biosimilar BiTE antibody (CyS111) biosimilar with the clinical candidate MEDI-565 (MT111).", PROCEEDINGS OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, ANNUAL MEETING, vol. 50, April 2009 (2009-04), page 786, XP008167243, USA cited in the application abstract #3247	1-39
A	WO 2012/117002 A1 (ROCHE GLYCART AG) 7 September 2012 (2012-09-07) paragraph [0009] - paragraph [0011]	1-39
A	M. SCHMIDT ET AL.: "Kinetics of anti-carcinoembryonic antigen antibody internalization: effects of affinity, bivalency, and stability.", CANCER IMMUNOLOGY IMMUNOTHERAPY, vol. 57, 2008, pages 1879-1890, XP019654564, cited in the application abstract page 1888, right-hand column, last paragraph - page 1889, left-hand column, last paragraph	1-39

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2013/074291

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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