Anti-CEACAM6 Antibodies and Uses Thereof

The present invention provides recombinant antigen-binding regions and antibodies and functional fragments containing such antigen-binding regions that are specific for human and Macaca fascicularis CEACAM6 (Carcinoembryonic antigen-related cell adhesion molecule 6, CD66c, Non-specific crossreacting antigen, NCA, NCA-50/90), and which therefore do not significantly cross-react with the closely related human CEACAM1, human CEACAM3, and human CEACAM5. The invention further provides methods to generate this kind of antibodies.

The antibodies, accordingly, can be used to treat cancer and other disorders and conditions associated with the expression of the CEACAM6. The invention also provides nucleic acid sequences encoding the foregoing antibodies, vectors containing the same, pharmaceutical compositions and kits with instructions for use.

BACKGROUND OF THE INVENTION

Antibody-based therapy is an effective and clinically established treatment of various cancers, including solid tumors. For example, HERCEPTIN® has been used successfully to treat breast cancer and RITUXAN® is effective in B-cell related cancer types. Central to the development of a novel successful antibody-based therapy is the isolation of antibodies against cell-surface proteins found to be preferentially expressed on target cells (e.g. cancer cells, immune cells etc) that are able to functionally modify the activity of the corresponding receptor.

Antibody blockade of immune checkpoint molecules for immune cell activation and thus for immunotherapy of cancer is a clinically validated approach. In 2011 the CTLA-4 blocking antibody Ipilimumab has been approved by the FDA for the 2nd line therapy of metastatic melanoma (Yervoy). Another example is the blockade of the PD-1/PD-L1 axis for which several drugs are either approved or currently under clinical development and for which impressive clinical responses have been reported in melanoma, RCC and lung cancer (Henick et al., Expert Opin Ther Targets. 2014 Dec;18(12):1407-20)).

Proteins of the Carcinoembryonic antigen-related cell adhesion molecule (CEACAM) family belong to the immunoglobulin (Ig) supergene family and generally

exhibit a variable (V)-like domain identified as the N domain. The N domain is followed by either none or up to six constant C2-like Ig domains (termed A or B). These extracellular domains are required for CEACAM functionality as homo- and heterophilic intercellular adhesion molecules (Obrinck, Curr Opin Cell Biol. 1997 Oct; 9(5):616-26) or as human and rodent pathogen receptors (Kuespert et al., Curr Opin Cell Biol. 2006 Oct; 18(5):565-71; Voges et al., PLoS One. 2012;7(6):e39908). CEACAM receptors associate as dimers or oligomers and multiple associations with other partners at the membrane and consequently modulate important functions. In addition to their expression in human tissues, the CEACAM gene family is highly conserved in 27 other mammalian species and is best described in mouse, rat, cattle, dog, platypus and opossum (Kammerer and Zimmermann, BMC Biol. 2010 Feb 4; 8:12). The best characterized biological function of CEACAMs is the support of cell-cell adhesion through their homo- and heterophilic interactions, including a role in the differentiation and formation of a three-dimensional tissue structure, angiogenesis, apoptosis, tumor suppression, and metastasis. (Kuespert et al., Curr Opin Cell Biol. 2006 Oct; 18(5):565-71). More details on the family members are described in other reviews (Horst and Wagener, Handb Exp Pharmacol. 2004;(165): 283-341; Gray-Owen and Blumberg, Nat Rev Immunol. 2006 Jun;6(6):433-46).

CEACAM6 (Carcinoembryonic antigen-related cell adhesion molecule 6, CD66c, Non-specific crossreacting antigen, NCA, NCA-50/90) is a glycosylphosphatidylinositol (GPI)-linked cell surface protein with one N-domain and 2 C2-like domains which mediate a number of possible cis or trans directed interactions of CEACAM proteins through their extracellular domains with a variety of membrane receptors, a few of which have been identified. (Beauchemin and Arabzadeh, Cancer Metastasis Rev. 2013 Dec;32(3-4):643-71).

CEACAM6 is expressed in a variety of epithelia of normal human tissue such as colon (Blumenthal et al., BMC Cancer, 2007, Jan 3;7:2.), lung (Kolla et al., Am J Physiol Lung Cell Mol Physiol 296: L1019-L1030) and granulocytes (Kuroki et al., Biochem Biophys Res Commun. 1992 Jan 31;182(2):501-6). In the granulocytic lineage CEACAM6 was expressed at all stages of granulocytic maturation except for the early lineage-committed precursor cell (Strickland et al., J Pathol. 2009 Jul;218(3):380-90); Schölzel et al., American Journal of Pathology, 156 (2), 595-605). CEACAM6 is not expressed in rodents. (Beauchemin et al., Exp Cell Res. 1999 Nov 1;252(2):243-9).

CEACAM6 expression has been described for several cancers. In colon cancer CEACAM6 is upregulated in 55% of the cases and an independent prognostic factor allowing subdivision of patients into low and high-risk groups (Jantscheff et al., J Clin Oncol. 2003 Oct 1;21(19):3638-46). In pancreatic adenocarcinoma 92% (n=82) of analyzed specimens were found to be positive while CEACAM6 expression was more prevalent in high-grade than in low grade PanIN lesions (Duxbury et al., Ann Surg. 2005 Mar;241(3):491-6). This was confirmed in another study where >90% of invasive pancreatic adenocarcinomas (110 of 115 tested) showed a robust (over-) expression of CEACAM6 (Strickland et al., J Pathol. 2009 Jul;218(3):380-90). In addition, Blumenthal et al. reported CEACAM6 expression in breast tumors, in pancreatic tumors, ovarian adenocarcinomas, lung adenocarcinoma, lymph node metastases and metastases from breast, colon and lung tumors. (Blumenthal et al., BMC Cancer. 2007 Jan 3;7:2).

CEACAM6 expression in breast cancer was also reported by others (Maraqa et al., Clin Cancer Res. 2008 Jan 15;14(2):405-11; Poola et al., Clin Cancer Res. 2006 Aug 1;12(15):4773-83; Balk-Moller et al., Am J Pathol. 2014 Apr;184(4):1198-208); Tsang et al., Breast Cancer Res Treat. 2013 Nov;142(2):311-22). In addition CEACAM6 expression has been reported in multiple myeloma (Witzens-Harig et al., Blood 2013 May 30;121(22):4493-503), gastric cancer (Deng et al., Genet Mol Res. 2014 Sep 26;13(3):7686-97) and head and neck cancer (Cameron et al., Mol Cancer. 2012 Sep 28;11:74).

Experimental evidence supports a role for CEACAM6 as important regulator of metastasis. Kim et al. have shown that attenuating CEACAM6 expression in LoVo cells using a CEACAM6-specific siRNA or increasing its expression in HCT116 cells, respectively, impeded or augmented invasion through the extracellular matrix (Kim et al., Clin Chim Acta. 2013 Jan 16;415:12-9). Suppression of CEACAM6 expression leads to elevated E-cadherin promoter activity. Blumenthal et al. showed that CEACAM5 and CEACAM6 contributed to CRC metastatic dissemination which could be blocked by monoclonal antibodies in vivo. (Blumenthal et al., BMC Cancer. 2007 Jan 3;7:2). Also it has been shown that CEACAM6 is expressed in CD133-positive cells in colon cancer samples able to form stem cell-enriched colon spheres for which proliferation, clonogenic potential, as well as in vivo tumorigenic potential were significantly hampered upon its silencing (Gemei et al., Cancer. 2013 Feb 15;119(4):729-38). In breast cancer it was shown that tamoxifen resistant samples are CEACAM6 overexpressing and CEACAM6 was a significant predictor of recurrence of the disease (Maraqa et al., Clin Cancer Res. 2008 Jan 15;14(2):405-11). siRNA

mediated CEACAM6 silencing in a MMU1-tamoxifen-resistant MCF7 cell derivative reversed endocrine resistance, anchorage independence of these cells and invasive properties (Lewis-Wambi et al., Eur J Cancer. 2008 Aug;44(12):1770-9). In lung adenocarcinoma CEACAM6 expression was significantly associated with adverse clinical outcome (Kobayashi et al., Br J Cancer. 2012 Nov 6;107(10):1745-53). In pancreatic cancer CEACAM6 silencing with siRNA reversed the acquired anoikis resistance of Mia(AR) pancreatic tumor cells. Overexpression of CEACAM6 in Capan2 pancreatic cancer cells augmented gemcitabine resistance whereas siRNA-mediated suppression of CEACAM6 expression in BxPC3 cells chemosensitized them to the drug by modulating AKT activity in an Src dependent manner (Duxbury et al., Cancer Res. 2004 Jun 1;64(11):3987-93). These effects corresponded to increased invasiveness of high CEACAM6 expressing cells exhibiting c-src activity and matrix metalloproteinase (MMP9) expression (Duxbury et al., Br J Cancer. 2004 Oct 4;91(7):1384-90).

T-cell responses against tumor-associated antigens have been described in many tumors (Beckhove et al., J Clin Invest. 2004 Jul;114(1):67-76; Choi et al., Blood. 2005 Mar 1;105(5):2132-4; Sommerfeldt et al., Cancer Res. 2006 Aug 15;66(16):8258-65; Schmitz-Winnenthal et al., Cancer Res. 2005 Nov 1;65(21):10079-87.; Jäger et al., Proc Natl Acad Sci U S A. 2000 Apr 25;97(9):4760-5; Romero et al., Adv Immunol. 2006;92:187-224) and often cause an accumulation of tumor specific memory T cells in lymphoid organs or in the blood (Choi et al., Blood. 2005 Mar 1;105(5):2132-4; Feuerer et al., Nat Med. 2001 Apr;7(4):452-8; Letsch et al., Cancer Res. 2003 Sep 1;63(17):5582-6). However, the capacity of T cells to react against autologous tumor cells is generally low (Horna and Sotomayor, Curr Cancer Drug Targets. 2007 Feb;7(1):41-53); Yang and Carbone, Adv Cancer Res. 2004;92:13-27). Many tumors have the capacity to block effector functions of T cells which contributes to the limited activity of tumor immunotherapy. T-cell unresponsiveness against tumor cells has been demonstrated for a broad variety of cancers (Pardoll, Nat Immunol. 2012 Dec;13(12):1129-32).

CEACAM6 also contributes to the regulation of CD8+ T cell response. Recently, Witzens-Harig et al. demonstrated in multiple myeloma expressing several CEACAM family members that treatment with anti-CEACAM6 mAbs or siRNA silencing CEACAM6 reinstated T cell reactivity against malignant plasma cells indicating a role for CEACAM6 in CD8+ T cell response regulation (Witzens-Harig et al., Blood 2013 May 30;121(22):4493-503). So far, a receptor for CEACAM6 on T cells has not been

identified. However, co-culture of CEACAM6 positive myeloma cells with T cells resulted in the modulation of T cell signaling events including an activation of SHP phosphatases by CEACAM6 ligation (Lin and Weiss, J Cell Sci. 2001 Jan;114(Pt 2):243-4; Latour et al., Mol Cell Biol. 1997 Aug;17(8):4434-41; Wen et al., J Immunol. 2010 Dec 1;185(11):6413-9). CEACAM6 has no intrinsic signaling capacity, and its inhibitory capacity is presumably mediated by binding to receptors on the T cell surface. Such a receptor can be for example CEACAM1 for which mechanism for the modulation of innate and adaptive immune responses have been described. CEACAM1 (CD66a) possesses a cytoplasmic tail containing an immunoreceptor tyrosine-based inhibitory (ITIM) motif. CEACAM1 is stored in intracellular vesicles and upon T cell activation is rapidly (24 h to 72 h) externalized and expressed on the T cell surfacewhere it mediates the blockade of T-cell effector functions after homo- or heterophilic binding to ligands expressed on target cells (Gray-Owen and Blumberg, Nat Rev Immunol. 2006 Jun;6(6):433-46). The nature of this binding is unknown and could be either homo- or heterophilic binding to other CEACAMs or binding to other components of the extracellular matrix, growth factor receptors, integrins, or cadherins. Homophilic interactions have been reported between CEACAM1 and CEACAM1 (Ortenberg et al., Mol Cancer Ther. 2012 Jun;11(6):1300-10). Heterophilic CEACAM interactions have been described for example between CEACAM1 and CEACAM5, and CEACAM6 and CEACAM8 (Cavallaro and Christofori, Nat Rev Cancer. 2004 Feb;4(2):118-32).

As described above CEACAM6 is a very attractive target for therapeutic intervention in cancer immunotherapy. As noted, CEACAM6 is a member of a family of highly homologous proteins. An antibody suitable for human therapy, which is relieving immunosuppression of CEACAM6, must therefore be able to distinguish between CEACAM6 and other paralogous proteins like CEACAM1, CEACAM3, CEACAM5, which each display different functions and tissue distributions, to restrict its mode of action and localization to CEACAM6 and to avoid unwanted adverse side effects.

As CEACAM6 is not only expressed on tumor cells but also on normal tissues (especially granulocytes but also epithelial cells of e.g. lung and gastrointestinal cells – Chan and Stanners, Mol Ther. 2004 Jun;9(6):775-85; Strickland et al., J Pathol. 2009 Jul;218(3):380-90), it is absolutely crucial to be able to predict the adverse side effect profile of the therapeutic antibody. This is all the more important, since the anticipated mode of action will be inhibition of immunosuppression, i.e. an immunoactivation, which can result in serious hazards (incident of CD28 superagonist TGN1412 trial;

Suntharalingam et al., N Engl J Med. 2006 Sep 7;355(10):1018-28). So indirect effects on the immune system on top of direct effects on granulocytes need to be carefully assessed. To enable the development of a human therapeutic antibody and a predictive pre-clinical tolerability testing, it is mandatory for the antibody to exhibit relevant cross-reactivity to a toxicology relevant species, in case of CEACAM6 to non-human primates, preferentially Macaca fascicularis (cynomolgus).

As a prerequisite, a therapeutic antibody needs to bind with high affinity to human CEACAM6 on cells, to bind selectively to CEACAM6 (without binding to any paralogs), to be cross-reactive to monkey CEACAM6 within one order of magnitude of monovalent K_D (to safely reflect binding on normal tissues in the toxicology monkey model even at low surface densities under non-avidity based binding conditions), to bind to a similar epitope as on human CEACAM6, to be able to relieve CEACAM6-mediated immunosuppression, to be non-immunogenic in human therapy (i.e. a human or humanized antibody), and to be stable enough to allow for clinical development, formulation and storage over extended periods of time as a pharmaceutical. The latter is important as it has been noted earlier that physical degradation (especially aggregation) may enhance immune response to a therapeutic protein (Hermeling et al., Pharm Res. 2004 Jun;21(6):897-903) and aggregation is closely connected to unfolding of IgG and its thermal stability (Vermeer and Norde, Biophys J. 2000 Jan;78(1):394-404).

Several anti-CEACAM6 antibodies exist. Most of them are non-human reagent antibodies, many of them are polyclonal. The specificity and selectivity to human CEACAM6 as well as cross-reactivity to monkey CEACAM6 is in most of the cases not disclosed or known.

Therapeutic antibodies directed against CEACAM6 are also known in the art. Some are not selective to human CEACAM6 (e.g. MN-3 from Immunomedics, Neo201/h16C3 from Neogenix; both binding in addition to human CEACAM5). A single domain antibody 2A3 and its fusion variants (WO2012040824 and Niu et al., J Control Release. 2012 Jul 10;161(1):18-24) are not characterized with respect to selectivity and cross-reactivity to monkey CEACAM6.

Selective anti-CEACAM6 antibodies apparently cross-reactive to monkey CEACAM6 are not disclosed (Strickland et al., J Pathol. 2009 Jul;218(3):380-90).

The murine antibody 9A6 (Genovac/Aldevron) is the only antibody described to be able to modulate the immunosuppressive activity of CEACAM6 (Witzens-Harig et

al., Blood 2013 May 30;121(22):4493-503). 9A6 inhibits the immunosuppressive activity of CEACAM6, leading to enhanced cytokine secretion by T cells in vitro and anti-tumor efficacy in vivo (Khandelwal et al., Poster Abstract 61, Meeting Abstract from 22nd Annual International Cancer Immunotherapy Symposium October 6-8, 2014, New York City, USA). Although its selectivity appears appropriate, it was previously not characterized with regards to its cross-reactivity to monkey CEACAM6. In addition, its murine nature precludes a direct therapeutic application in humans.

As shown in the examples, the antibody 9A6 binds to recombinant human CEACAM6 but no binding to recombinant Macaca mulatta or Macaca fascicularis CEACAM6 was detected. For comparison, Neo201—hIgG1 was also tested. This antibody displayed high affinity binding to both human and monkey CEACAM6. But Neo201 binds to human CEACAM5 and CEACAM6 and is therefore not specific for CEACAM6.

In conclusion there is high need for a therapeutic monoclonal antibody that comprises the following features:

i. The antibody is a high affinity binder of human CEACAM6.

ii. The antibody is selective to CEACAM6, not binding to any paralogs, especially CEACAM1, CEACAM3, and CEACAM5.

iii. The antibody is cross-reactive to monkey CEACAM6 within one order of magnitude of monovalent K_D.

iv. The antibody is non-immunogenic in human therapy, i.e. it is a human or humanized antibody.

v. The antibody is able to relieve CEACAM6-mediated immunosuppression.

Such an antibody does not exist in the prior art. 9A6 binding to N-terminal domain 1 of human CEACAM6 is the only known anti-CEACAM6 antibody that is able to relieve CEACAM6-mediated immunosuppression, yet lacks cross-reactivity to monkey CEACAM6 apart from being a mouse antibody. Neo201 binds to a different domain outside of N-terminal domain 1 of CEACAM6. Therapeutic efficacy of Neo201-hIgG1 has been published to be based on ADCC (Proceedings of the 102nd Annual Meeting of the American Association for Cancer Research; 2011 Apr 2-6; Orlando, FL.

Philadelphia (PA): AACR: Du et al., Cancer Res April 15, 2011; 71(8 Supplement): 4582).

The inventors assumed that relief of CEACAM6-mediated immunosuppression is connected to binding to N-terminal domain 1. But generation of antibodies binding to N-terminal domain 1 of CEACAM6 results in a challenging selectivity problem.

The sequence alignment in Figure 1 shows a very high degree of similarity of protein sequences of human CEACAM6 and human CEACAM3, human CEACAM5 and human CEACAM1 throughout the entire extracellular region. The target region (domain 1 of human CEACAM6) is especially similar to other CEACAMs, which is also reflected in Table 7. The paralogs of human CEACAM6 (e.g. CEACAM1, CEACAM3, and CEACAM5) are much more similar to human CEACAM6 than the cynomolgus ortholog. In fact, there are only 2 positions in the N-terminal region in the primary sequence that are identical in human and cynomolgus CEACAM6 but different from amino acids in the other human paralogs (marked in Figure 1 with asterisks).

Unexpectedly the inventors were able to find a method to generate antibodies comprising all of the desired selectivity and functional features.

SUMMARY OF THE INVENTION

This invention is related to antibodies, or antigen-binding antibody fragments thereof, or variants thereof which display high affinity for human and Macaca fascicularis CEACAM6 protein, and which do not significantly cross-react with the closely related human CEACAM1, human CEACAM3, and human CEACAM5. This means the antibodies, or antigen-binding antibody fragments thereof, or variants thereof are selective for CEACAM6. The antibodies provided bind to the N-terminal domain 1 which is highly conserved among these proteins.

The anti-CEACAM6 antibodies of this invention are able to change in vitro the cytokine profile of tumor specific T cells towards a more cytotoxic and / or activated phenotype characterized by increased IFN-gamma, and / or IL-2 and / or TNF-alpha secretion. Therefore the antibodies of this invention are able to relieve CEACAM6-mediated immunosuppression, and induce an immunoactivation, which finally results in an anti-tumor efficacy in vivo.

The antibodies of this invention, or antigen-binding antibody fragments thereof, or variants thereof interfere with CEACAM6 and CEACAM1 interaction which might be a mechanism for the modulation of innate and adaptive immune responses.

The antibodies of the invention are thus suitable for the treatment of cancer as well as metastases thereof, in particular CEACAM6 expressing tumors, such as colorectal cancer, non-small-cell lung cancer (NSCLC), small cell lung cancer (SCLC), pancreatic cancer, gastric cancer, breast cancer and multiple myeloma.

The invention describes antibodies that are distinguished from existing anti-CEACAM6 antibodies, in that they are able to bind to human and Macaca fascicularis CEACAM6 within one order of magnitude of monovalent K_D (to safely reflect binding on normal tissues in toxicology monkey model even at low surface densities under non-avidity based binding conditions) and do not significantly cross-react with the closely related paralogs CEACAM1, CEACAM3, and CEACAM5. So these antibodies are suitable for preclinical toxicological studies in cynomolgus monkeys to evaluate their safety profiles. As CEACAM6 is not only expressed on tumor cells but also on normal tissues (especially granulocytes but also epithelial cells of e.g. lung and gastrointestinal cells – Chan and Stanners, Mol Ther. 2004 Jun;9(6):775-85; Strickland et al., J Pathol. 2009 Jul;218(3):380-90), it is absolutely crucial to be able to predict the adverse side effect profile of the therapeutic antibody. This is all the more important, since the anticipated mode of action will be inhibition of immunosuppression, i.e. an immunoactivation, which can result in serious hazards (incident of CD28 superagonist TGN1412 trial), so indirect effects on immune system on top of direct effects on granulocytes need to be carefully assessed.

Highly preferred anti-CEACAM6 antibodies of the invention are depicted in Table 1 characterized by their structural features.

In some embodiments, the anti-CEACAM6 antibody of the invention binds to an epitope of human CEACAM6, wherein said epitope comprises one or more amino acid residues selected from the group consisting of Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In certain embodiments, the anti-CEACAM6 antibody of the invention binds to an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In some embodiments, the anti-CEACAM6 antibody of the invention interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises one, two, three four, five, eight, ten, fifteen or more amino acid residues selected from the group consisting of Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In certain embodiments, the anti-CEACAM6 antibody of the invention interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

An anti-CEACAM6 antibody of the invention might be co-administered with known medicaments, and in some instances the antibody might itself be modified. For example, an antibody could be conjugated to a cytotoxic agent, immunotoxin, toxophore or radioisotope to potentially further increase efficacy.

The invention further provides antibodies which constitute a tool for diagnosis of malignant or dysplastic conditions in which CEACAM6 expression is elevated compared to normal tissue. Provided are anti-CEACAM6 antibodies conjugated to a detectable marker. Preferred markers are a radiolabel, an enzyme, a chromophore or a fluorophore.

The invention is also related to polynucleotides encoding the antibodies of the invention, or antigen-binding fragments thereof, cells expressing the antibodies of the invention, or antigen-binding fragments thereof, methods for producing the antibodies of the invention, or antigen-binding fragments thereof, methods for inhibiting the growth of dysplastic cells using the antibodies of the invention, or antigen-binding fragments thereof, and methods for treating and detecting cancer using the antibodies of the invention, or antigen-binding fragments thereof.

The invention is also related to isolated nucleic acid sequences, each of which can encode an aforementioned antibody or antigen-binding fragment thereof that is specific for an epitope of CEACAM6. Nucleic acids of the invention are suitable for recombinant production of antibodies or antigen-binding antibody fragments. Thus, the invention also relates to vectors and host cells containing a nucleic acid sequence of the invention.

Compositions of the invention may be used for therapeutic or prophylactic applications. The invention, therefore, includes a pharmaceutical composition

comprising an inventive antibody or antigen-binding fragment thereof and a pharmaceutically acceptable carrier or excipient therefore. In a related aspect, the invention provides a method for treating a disorder or condition associated with the undesired presence of CEACAM6 expressing cells. In a preferred embodiment the aforementioned disorder is cancer. Such method contains the steps of administering to a subject in need thereof an effective amount of the pharmaceutical composition that contains an inventive antibody as described or contemplated herein.

Further this invention is related to methods to generate this kind of antibodies. The invention provides instructions for using an antibody library to isolate one or more members of such library that binds specifically to CEACAM6. In addition, the invention provides instruction for immunizing mice to produce hybridoma cell lines that secrete antibodies that bind specifically to CEACAM6 and which are cross-reactive to Macaca fascicularis (cynomolgus monkey) CEACAM6. Instructions for humanization of murine antibodies that bind specifically to CEACAM6 are also provided by the invention.

DESCRIPTION OF THE FIGURES

Figure 1: Protein sequence alignment of extracellular regions of human CEACAM6 paralogs as well as Macaca fascicularis (cynomolgus monkey) CEACAM6 ortholog. Numbers indicate amino acid position after removal of signal peptide sequence. Positions in N-terminal region in the primary sequence that are identical in human and cynomolgus CEACAM6 but different from amino acids in this position in the other human paralogs are marked with asterisks. N-terminal domain 1 is boxed.

Figure 2: Amino acid sequences of the variable domains VL and VH of TPP-2971. Sequences grafted into human frameworks are highlighted as underlined bold letters. CDRs according to Kabat definition are written as italic letters. Grey shaded letters represent differences of the sequences from TPP-3187 in comparison to TPP-2971.

Figure 3: Amino acid sequences of the variable domains VL and VH of TPP-3310 and TPP-3714. Sequences derived from the murine CDRs of TPP-2971 are

highlighted as underlined bold letters. CDRs according to Kabat definition are written as italic letters. The antibodies TPP-3310 and TPP-3714 differ in two amino acids within the VH framework highlighted as underlined non-bold letters.

Figure 4: Amino acid sequences of the variable domains VL and VH of TPP-3820 and TPP-3821. Sequences derived from the murine CDRs of TPP-3187 are highlighted as underlined bold letters. CDRs according to Kabat definition are written as italic letters. The antibodies TPP-3820 and TPP-3821 differ in two amino acids within the VH framework highlighted as underlined non-bold letters.

Figure 5: In vitro pharmacological effect of anti-CEACAM6 antibodies on IFN-gamma secretion of survivin peptide specific T cells and extent of this secretion. **A+B**. IFN-gamma ELISpot assay of survivin-peptide specific T cells and KS tumor cells. 10,000 KS tumor cells were co-cultivated together with 2,500 Survivin TC for 20 h. The antibody concentration in the co-culture was 30 µg/ml. **C**. IFN-gamma ELISA assay of survivin-peptide specific TC and KS tumor cells. 10,000 KS tumor cells were co-cultivated together with 20,000 Survivin TC for 20 h. The antibody concentration in the coculture was 30 µg/ml. X-axis shows the different conditions tested: in A: 1 = 10,000 KS cells; 2 = 2,500 T cells; 3 = no antibody treatment; 4 = isotype-matched antibody control; 5 = TPP-3470 (9A6-hIgG2) 6 = TPP-3323; in B: 1 = 10,000 KS cells; 2 = 2,500 T cells; 3 = no antibody treatment; 4 = isotype-matched antibody control; 5 = TPP-3470 (9A6-hIgG2) 6 = TPP-3310; 7 = TPP-3707; in C: 1 = 10,000 KS cells; 2 = 20,000 T cells; 3 = no antibody treatment; 4 = isotype-matched antibody control; 5 = TPP-3470 (9A6-hIgG2) 6 = TPP-3310; 7 = TPP-3707; the Y-axis corresponds to the IFN-gamma spot-counts per well (in A and B) or IFN-gamma concentration in pg/ml (in C). Asterisks indicate statistically significant results according to Student´s t test, unpaired, two-tailed. Error bars represent SEM.

Figure 6: In vitro pharmacological effect of anti-CEACAM6 antibodies on cytokine secretion (IFN-gamma, IL-2 and TNF-alpha) of survivin peptide specific T cells. **A.** IFN-gamma Luminex analysis. **B**. IL-2 Luminex analysis. **C**. TNFa Luminex analsysis. Luminex cytokine analysis of survivin-peptide specific TC and KS tumor cells. 10,000 KS tumor cells were co-cultivated together with 20,000 Survivin TC for 20

h. The antibody concentration in the coculture was 30 µg/ml. X-axis depicts the different conditions tested: 1 = 10,000 KS cells; 2 = 20,000 T cells; 3 = no antibody treatment; 4 = isotype-matched antibody control; 5 = TPP-3470 (9A6-hIgG2) 6 = TPP-3310; 7 = TPP-3707; the Y-axis corresponds to the cytokine concentration in pg/ml.

Figure 7: Effect of anti-CEACAM6 antibodies on tumor growth *in vivo*. 2 x 10^6 KS breast cancer cells were inoculated s.c. On day 23 and 27 tumor-antigen specific T cells (survivin-peptide specific) were injected i.v. 200 µg of anti-CEACAM6 antibodies or the matched isotype control were administered i.p. on day 22, 24, 26 and 28. Tumor growth was assessed every 2-3 days. Error bars represent SEM. Y-axis = tumor surface (mm^2); X-axis = days; TC = survivin-peptide specific T cells. 1 = PBS-treated; 2 = treatment with T cells and isotype matched antibody control; 3 = treatment with T cells and TPP-3470 (9A6-hIgG2); 4 = treatment with T cells and TPP-3310; 5 = treatment with T cells and TPP-3707.

Figure 8: Annotated sequences of preferred anti-CEACAM6 antibodies of this invention. Provided are protein and DNA sequences for heavy and light chains of IgGs as well as for VH and VL regions of selected antibodies. Below the sequences important regions are annotated (VH and VL regions in full length IgGs, and the CDR regions (H-CDR1, H-CDR2, H-CDR3, L-CDR1, L-CDR2, L-CDR3)).

Figure 9: Cartoon representation of the single N-terminal domain 1 of human CEACAM6 (TPP-1794, white) bound to the Fab fragment APP-1574 (heavy and light chains are colored dark and light gray, respectively).

Figure 10: Details of the protein interface shown in Figure 9. Selected residues are depicted in stick representation and colored as in Figure 9. The numbering corresponds to TPP-1794 (SEQ-ID NO: 169)

Figure 11: xCELLigence cytotoxicity assay using survivin-peptide specific $CD8^+$ T cells.

A. 20,000 KS breast cancer tumor cells in co-culture with 20,000 survivin specific T cells **B.** 40,000 HCT-116-hC6 tumor cells in co-culture with 20,000 survivin specific T cells. Cytotoxicity was monitored for ~100 h. Antibodies were used at 30 µg/ml final concentration: #1, time point of T cell addition; #2, tumor cells only; #3, no antibody; #4, isotype-matched antibody control; #5, anti-PD-L1 Ab as human IgG2; #6, TPP-3470 9A6 Ab as human IgG2; #7 TPP-3310 hIgG2. Asterisks indicate statistically significant results according to Student´s t test, unpaired, two-tailed. X, x-axis, Time (Hours); Y, Y-Axis, normalized cell index.

Figure 12: xCELLigence cytotoxicity assay using patient-derived T cells of a pancreatic cancer (TIL-12).

A and **B**: 10,000 HCC2935 tumor cells in co-culture with 50,000 pancreatic cancer infiltrating lymphocyte cells (TIL-12). Cytotoxicity was monitored for ~150 h. An anti-CD3 x EpCAM bispecific mAb (0.25 ng/ml) has been added in co-culture to direct T cells against the tumor cells independent of HLA.

A: #1,T cell addition; #2 tumor cells only; #3, no antibody; #4, isotype-matched antibody control; #5, anti-PD-L1 Ab as human IgG2; #6, TPP-3470; #7 TPP-3310; Antibodies were used at 30 µg/ml.

B: Concentration dependency of TPP-3310-mediated effect: #1, T cell addition; #2, tumor cells only; #3, TPP-3310 at 0.07 µg/ml; #4, TPP-3310 at 0.02 µg/ml; #5, isotype-matched antibody control at 50 µg/ml; #6, TPP-3310 at 0.021 µg/ml; #7, TPP-3310 at 0.062 µg/ml; #8, TPP-3310 at 1.85 µg/ml; #9, TPP-3310 at 5.5 µg/ml; #10, TPP-3310 at 16.67 µg/ml; #11, TPP-3310 at 50 µg/ml;

X- x-axis, Time (hours); Y, Y-Axis, normalized cell index

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based on the discovery of novel antibodies that have a specific affinity for CEACAM6 and can deliver a therapeutic benefit to a subject. The antibodies of the invention, which may be human, humanized or chimeric, can be used in many contexts, which are more fully described herein.

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by one of ordinary skill in the art to which this invention belongs. The following references, however, can provide one of skill in the art to which this invention pertains with a general definition of many of the terms used in this invention, and can be referenced and used so long as such definitions are consistent with the meaning commonly understood in the art. Such references include, but are not limited to, Singleton et al., Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); Hale & Marham, The Harper Collins Dictionary of Biology (1991); and Lackie et al., The Dictionary of Cell & Molecular Biology (3d ed. 1999); and Cellular and Molecular Immunology, Eds. Abbas, Lichtman and Pober, 2nd Edition, W.B. Saunders Company. Any additional technical resource available to the person of ordinary skill in the art providing definitions of terms used herein having the meaning commonly understood in the art can be consulted. For the purposes of the present invention, the following terms are further defined. Additional terms are defined elsewhere in the description. As used herein and in the appended claims, the singular forms "a," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "a gene" is a reference to one or more genes and includes equivalents thereof known to those skilled in the art, and so forth.

The terms "polypeptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer. Unless otherwise indicated, a particular polypeptide sequence also implicitly encompasses conservatively modified variants thereof.

Amino acids may be referred to herein by their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

As used herein "CEACAM6" designates the "carcinoembryonic antigen-related cell adhesion molecule 6", also known as "CD66c" (Cluster of Differentiation 66c), or Non-specific crossreacting antigen, or NCA, or NCA-50/90. CEACAM6 is a glycosylphosphatidylinositol (GPI)-linked cell surface protein involved in cell-cell adhesion. CEACAM6 is highly expressed on the surface of different tumor cells like colon, pancreatic, breast and lung cancer.

A reference sequence for human CEACAM6 is available from UniProtKB/Swiss-Prot data base under accession number P40199.3 (SEQ-ID NO:179 = TPP-4639), including signal peptide (positions 1-34) and propetide chain (positions 321 – 344). A single nucleotide polymorphism has been observed at position 239 (G to V exchange). The mature extracellular domain of human CEACAM6 consists of amino acids at position 35-320 of SEQ-ID No: 179.

human CEACAM6 (SEQ-ID NO:179)

MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQNRIG
YSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEA
TGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWVNGQSLPVSPRLQLSNGNMTLTLLS
VKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGPTISPSKANYRPGENLNLSCHAASNPPAQYSWFIN
GTFQQSTQELFIPNITVNNSGSYMCQAHNSATGLNRTTVTMITVSGSAPVLSAVATVGITIGVLARVALI

A Macaca fascicularis (cynomolgus monkey) protein sequence of CEACAM6 was deduced by the inventors and is represented by TPP-4189 (SEQ-ID No: 177). The mature extracellular domain of cynomolgus CEACAM6 consists of amino acids at position 35-320 of SEQ-ID No: 177.

Macaca fascicularis (cynomolgus monkey) CEACAM6 (SEQ-ID NO:177)

MGPPSAPPCRICVPWKEVLLTASLLTFWSPPTTAQLTIESRPFNVAEGKEVLLLAHNLPQNTLG
FNWYKGERVDAKRLIVAYVIGTQQTTPGPAHSGREMIYSNASLLIQNVTQNDTGSYTLQAIKEDLVTEEA
TGRFWVYPELPKPYITSNNSNPVEDKDAVDFTCEPDIHSTTYLWWVNDQSLPVSPRLQLSNGNRTLTLLS
VKRNDAGAYECEIQNPVSANLSDPVILNVLYGPDVPTISPSNSNYRPGENLNLSCHAASNPTAQYSWFVN
GTFQQSTQELFIPNITVNNSGSYMCQAYNSATGLNRTTVMMITVSGSAPGLSAVATVGIMIGVLARVALI

Domain organization of human and Macaca fascicularis (cynomolgus monkey) CEACAM6 is as follows (based on UniProtKB/Swiss-Prot data base sequence under accession number P40199.3 and SEQ-ID NO:179 = TPP-4639 & SEQ-ID No: 177 = TPP-4189, respectively):

Human and cynomolgus CEACAM6 domains	**Positions on SEQ-ID NO:179 = TPP-4639 and SEQ-ID No: 177 = TPP-4189, respectively**
Domain 1 also known as N domain also known as N-terminal domain 1 (Ig-like V-type)	35 – 142
Domain 2 also known as A domain (Ig-like C2-type 1)	145 – 232
Domain 3 also known as B domain (Ig-like C2-type 2)	237 – 314

human CEACAM1 full-length protein is available from UniProtKB/Swiss-Prot data base under accession number P13688.2 (SEQ-ID No: 173 = TPP-4185). The mature extracellular domain of human CEACAM1 consists of amino acids at position 35-428 of SEQ-ID No: 173.

human CEACAM1 (SEQ-ID NO:173)

MGHLSAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG
YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEA
TGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQSLPVSPRLQLSNGNRTLTLLS
VTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISPSDTYYRPGANLSLSCYAASNPPAQYSWLIN
GTFQQSTQELFIPNITVNNSGSYTCHANNSVTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSV
NLTCSTNDTGISIRWFFKNQSLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNV
NYNALPQENGLSPGAIAGIVIGVVALVALIAVALACFLHFGKTGRASDQRDLTEHKPSVSNHTQDHSNDP
PNKMNEVTYSTLNFEAQQPTQPTSASPSLTATEIIYSEVKKQ

human CEACAM3 full-length protein is available from UniProtKB/Swiss-Prot data base under accession number P40198.2 (SEQ-ID No: 175 = TPP-4187). The mature extracellular domain of human CEACAM3 consists of amino acids at position 35-155 of SEQ-ID No: 175.

human CEACAM3 (SEQ-ID NO:175)

MGPPSASPHRECIPWQGLLLTASLLNFWNPPTTAKLTIESMPLSVAEGKEVLLLVHNLPQHLFG
YSWYKGERVDGNSLIVGYVIGTQQATPGAAYSGRETIYTNASLLIQNVTQNDIGFYTLQVIKSDLVNEEA
TGQFHVYQENAPGLPVGAVAGIVTGVLVGVALVAALVCFLLLAKTGRTSIQRDLKEQQPQALAPGRGPSH
SSAFSMSPLSTAQAPLPNPRTAASIYEELLKHDTNIYCRMDHKAEVAS

human CEACAM5 full-length protein is available from UniProtKB/Swiss-Prot data base under accession number P06731.3 (SEQ-ID No: 176 = TPP-4188). The mature extracellular domain of human CEACAM5 consists of amino acids at position 35-685 of SEQ-ID No: 176.

human CEACAM5 (SEQ-ID NO:176)

MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG
YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHVIKSDLVNEEA
TGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQSLPVSPRLQLSNGNRTLTLFN
VTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVN
GTFQQSTQELFIPNITVNNSGSYTCQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALT
CEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNKLSVDHSDPVILNVLYG
PDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSAS
GHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNR
TLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPPDSSYLSGANLNLSCHSASNPSPQ
YSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSITVSASGTSPGLSAGATVGIMIG
VLVGVALI

The terms "anti-CEACAM6 antibody" and "an antibody that binds to CEACAM6" refer to an antibody that is capable of binding CEACAM6 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting CEACAM6. In one embodiment, the extent of binding of an anti-CEACAM6 antibody to an unrelated, non-CEACAM6 protein is less than about 5%, or preferably less than

about 2% of the binding of the antibody to CEACAM6 as measured, e.g., by a surface plasmon resonance (SPR). In certain embodiments, an antibody that binds to CEACAM6 has a dissociation constant (K_D) of ≤ 1 μM, ≤ 100 nM, ≤ 10 nM, ≤ 1 nM, ≤ 0.1 nM, ≤ 0.01 nM, or ≤ 0.001 nM (e.g. 10^{-8} M or less, e.g. from 10^{-8} M to 10^{-13} M, e.g., from 10^{-9} M to 10^{-13} M). In certain embodiments, an anti-CEACAM6 antibody binds to an epitope of CEACAM6 that is conserved among CEACAM6 from different species.

The term "antibody", as used herein, is intended to refer to immunoglobulin molecules, preferably comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains which are typically inter-connected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region can comprise e.g. three domains CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light chain constant region is comprised of one domain (CL). The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL is typically composed of three CDRs and up to four FRs arranged from amino-terminus to carboxy-terminus e.g. in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

As used herein, the term "Complementarity Determining Regions" (CDRs; e.g., CDR1, CDR2, and CDR3) refers to the amino acid residues of an antibody variable domain the presence of which are necessary for antigen binding. Each variable domain typically has three CDR regions identified as CDR1, CDR2 and CDR3. Each complementarity determining region may comprise amino acid residues from a "complementarity determining region" as defined by Kabat (e.g. about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the light chain variable domain and 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy chain variable domain; (Kabat et al., Sequences of Proteins of Immulological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (e.g. about residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the light chain variable domain and 26- 32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy chain variable domain (Chothia and Lesk; J Mol Biol 196: 901-917 (1987)). In some instances, a complementarity determining region can include amino acids from both a CDR region defined according to Kabat and a hypervariable loop.

Depending on the amino acid sequence of the constant domain of their heavy chains, intact antibodies can be assigned to different "classes". There are five major classes of intact antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these maybe further divided into "subclasses" (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2. A preferred class of immunoglobulins for use in the present invention is IgG.

The heavy-chain constant domains that correspond to the different classes of antibodies are called [alpha], [delta], [epsilon], [gamma], and [mu], respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known. As used herein antibodies are conventionally known antibodies and functional fragments thereof.

A “functional fragment” or “antigen-binding antibody fragment” of an antibody/immunoglobulin hereby is defined as a fragment of an antibody/immunoglobulin (e.g., a variable region of an IgG) that retains the antigen-binding region. An “antigen-binding region” of an antibody typically is found in one or more hyper variable region(s) of an antibody, e.g., the CDR1, -2, and/or –3 regions; however, the variable “framework” regions can also play an important role in antigen binding, such as by providing a scaffold for the CDRs. Preferably, the “antigen-binding region” comprises at least amino acid residues 4 to 103 of the variable light (VL) chain and 5 to 109 of the variable heavy (VH) chain, more preferably amino acid residues 3 to 107 of VL and 4 to 111 of VH, and particularly preferred are the complete VL and VH chains (amino acid positions 1 to 109 of VL and 1 to 113 of VH; numbering according to WO 97/08320).

“Functional fragments”, “antigen-binding antibody fragments”, or “antibody fragments” of the invention include but are not limited to Fab, Fab', Fab'-SH, $F(ab')_2$, and Fv fragments; diabodies; single domain antibodies (DAbs), linear antibodies; single-chain antibody molecules (scFv); and multispecific, such as bi- and tri-specific, antibodies formed from antibody fragments (C. A. K Borrebaeck, editor (1995) Antibody Engineering (Breakthroughs in Molecular Biology), Oxford University Press; R. Kontermann & S. Duebel, editors (2001) Antibody Engineering (Springer Laboratory Manual), Springer Verlag). An antibody other than a "multi-specific" or "multi-functional" antibody is understood to have each of its binding sites identical. The $F(ab')_2$ or Fab may be engineered to minimize or completely remove the intermolecular disulfide interactions that occur between the CH1 and CL domains.

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

Variants of the antibodies or antigen-binding antibody fragments contemplated in the invention are molecules in which the binding activity of the antibody or antigen-binding antibody fragment is maintained.

“Binding proteins” contemplated in the invention are for example antibody mimetics, such as Affibodies, Adnectins, Anticalins, DARPins, Avimers, Nanobodies (reviewed by Gebauer M. et al., Curr. Opinion in Chem. Biol. 2009; 13:245-255; Nuttall S.D. et al., Curr. Opinion in Pharmacology 2008; 8:608-617).

A “human” antibody or antigen-binding fragment thereof is hereby defined as one that is not chimeric (e.g., not “humanized”) and not from (either in whole or in part) a non-human species. A human antibody or antigen-binding fragment thereof can be derived from a human or can be a synthetic human antibody. A “synthetic human antibody” is defined herein as an antibody having a sequence derived, in whole or in part, in silico from synthetic sequences that are based on the analysis of known human antibody sequences. In silico design of a human antibody sequence or fragment thereof can be achieved, for example, by analyzing a database of human antibody or antibody fragment sequences and devising a polypeptide sequence utilizing the data obtained there from. Another example of a human antibody or antigen-binding fragment thereof is one that is encoded by a nucleic acid isolated from a library of antibody sequences of human origin (e.g., such library being based on antibodies taken from a human natural source). Examples of human antibodies include antibodies as described in Söderlind et al., Nature Biotech. 2000, 18:853-856.

A “humanized antibody” or humanized antigen-binding fragment thereof is defined herein as one that is (i) derived from a non-human source (e.g., a transgenic mouse which bears a heterologous immune system), which antibody is based on a

human germline sequence; (ii) where amino acids of the framework regions of a non-human antibody are partially exchanged to human amino acid sequences by genetic engineering or (iii) CDR-grafted, wherein the CDRs of the variable domain are from a non-human origin, while one or more frameworks of the variable domain are of human origin and the constant domain (if any) is of human origin.

A “chimeric antibody” or antigen-binding fragment thereof is defined herein as one, wherein the variable domains are derived from a non-human origin and some or all constant domains are derived from a human origin.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible mutations, e.g., naturally occurring mutations, that may be present in minor amounts. Thus, the term "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. In addition to their specificity, monoclonal antibody preparations are advantageous in that they are typically uncontaminated by other immunoglobulins. The term "monoclonal” is not to be construed as to require production of the antibody by any particular method. The term monoclonal antibody specifically includes chimeric, humanized and human antibodies.

An "isolated" antibody is one that has been identified and separated from a component of the cell that expressed it. Contaminant components of the cell are materials that would interfere with diagnostic or therapeutic uses of the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes.

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

As used herein, an antibody “binds specifically to”, is “specific to/for” or “specifically recognizes” an antigen of interest, e.g. a tumor-associated polypeptide antigen target, is one that binds the antigen with sufficient affinity such that the

antibody is useful as a therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins or does not significantly cross-react with proteins other than orthologs and variants (e.g. mutant forms, splice variants, or proteolytically truncated forms) of the aforementioned antigen target. The term "specifically recognizes" or "binds specifically to" or is "specific to/for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by an antibody, or antigen-binding fragment thereof, having a monovalent K_D for the antigen of less than about 10^{-4} M, alternatively less than about 10^{-5} M, alternatively less than about 10^{-6} M, alternatively less than about 10^{-7} M, alternatively less than about 10^{-8} M, alternatively less than about 10^{-9} M, alternatively less than about 10^{-10} M, alternatively less than about 10^{-11} M, alternatively less than about 10^{-12} M, or less. An antibody “binds specifically to,” is “specific to/for” or “specifically recognizes” an antigen if such antibody is able to discriminate between such antigen and one or more reference antigen(s). In its most general form, “specific binding”, “binds specifically to”, is “specific to/for” or “specifically recognizes” is referring to the ability of the antibody to discriminate between the antigen of interest and an unrelated antigen, as determined, for example, in accordance with one of the following methods. Such methods comprise, but are not limited to surface plasmon resonance (SPR), Western blots, ELISA-, RIA-, ECL-, IRMA-tests and peptide scans. For example, a standard ELISA assay can be carried out. The scoring may be carried out by standard color development (e.g. secondary antibody with horseradish peroxidase and tetramethyl benzidine with hydrogen peroxide). The reaction in certain wells is scored by the optical density, for example, at 450 nm. Typical background (=negative reaction) may be 0.1 OD; typical positive reaction may be 1 OD. This means the difference positive/negative is more than 5-fold, 10-fold, 50-fold, and preferably more than 100-fold. Typically, determination of binding specificity is performed by using not a single reference antigen, but a set of about three to five unrelated antigens, such as milk powder, BSA, transferrin or the like.

"Binding affinity" or “affinity” refers to the strength of the total sum of non-covalent interactions between a single binding site of a molecule and its binding partner. Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1 : 1 interaction between members of a binding pair (e.g. an antibody and an antigen). The dissociation constant “K_D” is commonly used to describe the affinity between a molecule (such as an antibody) and its binding partner (such as an antigen) i.e. how tightly a ligand binds to a particular protein. Ligand-

protein affinities are influenced by non-covalent intermolecular interactions between the two molecules. Affinity can be measured by common methods known in the art, including those described herein. In one embodiment, the "K_D" or "K_D value" according to this invention is measured by using surface plasmon resonance assays using suitable devices including but not limited to Biacore instruments like Biacore T100, Biacore T200, Biacore 2000, Biacore 4000, a Biacore 3000 (GE Healthcare Biacore, Inc.), or a ProteOn XPR36 instrument (Bio-Rad Laboratories, Inc.).

As used herein, the term “epitope” includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains, or combinations thereof and usually have specific three dimensional structural characteristics, as well as specific charge characteristics.

An "antibody that binds to the same epitope" as a reference antibody or “an antibody which competes for binding” to a reference antibody refers to an antibody that blocks binding of the reference antibody to its antigen in a competition assay by 10%, 20%, 30%, 40%, 50% or more, and conversely, the reference antibody blocks binding of the antibody to its antigen in a competition assay by 10%, 20%, 30%, 40%, 50% or more. An exemplary competition assay is provided herein.

An “antibody which binds to an epitope of a target protein Z wherein said epitope comprises the amino acid residues X1, X2, X3, ...” is an antibody which comprises atoms within 5 Å, preferentially within 4 Å, to atoms of said amino acid residues X1, X2, X3, ... of the target protein Z after binding of the antibody to its target protein. Such epitopes can be determined by using an X-ray crystal structure as exemplified in example 16.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc gamma receptors (FcγRs) present on certain cytotoxic cells (e.g. 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 e.g. with cytotoxins. To assess ADCC activity of an antibody of interest, an in vitro ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 or U.S. Patent No. 6,737,056 (Presta), may be performed. Useful effector cells for such assays include PBMC and NK cells.

"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 (C1q) to antibodies (of the appropriate subclass), which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., J. Immunol. Methods 202: 163 (1996), may be performed. Polypeptide variants with altered Fc region amino acid sequences (polypeptides with a variant Fc region) and increased or decreased C1q binding are described, e.g., in US Patent No. 6,194,551 Bl and WO 1999/51642.

As used herein, a “naked antibody” refers to an antibody that is not conjugated to a heterologous moiety (e.g. a cytotoxic moiety) or radiolabel. This naked antibody may be present in a pharmaceutical composition.

The term “immunoconjugate” (interchangeably referred to as "antibody-drug conjugate," or "ADC") refers to an antibody conjugated to one or more cytotoxic or cytostatic agents, such as a chemotherapeutic agent, a drug, a growth inhibitory agent, a toxin (e.g., a protein toxin, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate). Immunoconjugates have been used for the local delivery of cytotoxic agents, i.e., drugs that kill or inhibit the growth or proliferation of cells, in the treatment of cancer (e.g. Liu et al., Proc Natl. Acad. Sci. (1996), 93, 8618-8623)). Immunoconjugates allow for the targeted delivery of a drug moiety to a tumor, and intracellular accumulation therein, where systemic administration of unconjugated drugs may result in unacceptable levels of toxicity to normal cells and/or tissues. Toxins used in antibody-toxin conjugates include bacterial toxins such as diphtheria toxin, plant toxins such as ricin, small molecule toxins such as geldanamycin. The toxins may exert their cytotoxic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition.

"Percent (%) sequence identity" with respect to a reference polynucleotide or polypeptide sequence, respectively, is defined as the percentage of nucleic acid or amino acid residues, respectively, in a candidate sequence that are identical with the nucleic acid or amino acid residues, respectively, in the reference polynucleotide or polypeptide sequence, respectively, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Conservative substitutions are not considered as part of the sequence identity. Preferred are un-gapped alignments. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN

or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

"Sequence homology" indicates the percentage of amino acids that either is identical or that represent conservative amino acid substitutions.

The term “maturated antibodies” or “maturated antigen-binding fragments” such as maturated Fab variants includes derivatives of an antibody or antibody fragment exhibiting stronger binding - i. e. binding with increased affinity - to a given antigen such as the extracellular domain of a target protein. Maturation is the process of identifying a small number of mutations e.g. within the six CDRs of an antibody or antibody fragment leading to this affinity increase. The maturation process is the combination of molecular biology methods for introduction of mutations into the antibody and screening for identifying the improved binders.

An “antagonistic” antibody or a “blocking” antibody is one which significantly inhibits (either partially or completely) a biological activity of the antigen it binds.

An "agonistic" antibody or an antibody with “agonistic activity” is one that binds to its target and induces the activation (either partially or completely) of the respective target, that e.g. leads to activation of the signaling pathways or biological effects (either partially or completely) that are mediated by the respective target. An "agonistic" antibody or an antibody with “agonistic activity” as used herein is an antibody which may mimic at least one of the functional activities of a polypeptide of interest.

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

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

The terms "host cell", "host cell line", and "host cell culture" are used interchangeably and refer to cells into which exogenous nucleic acid has been

introduced, including the progeny of such cells. Host cells include "transformants", "transformed cells", “transfectants”, “transfected cells”, and “transduced cells”, which include the primary transformed/transfected/transduced cell and progeny derived therefrom without regard to the number of passages. Progeny may not be completely identical in nucleic acid content to a parent cell, but may contain mutations. Mutant progeny that have the same function or biological activity as screened or selected for in the originally transformed cell are included herein.

Antibodies of this invention

This invention is related to antibodies, or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to human CEACAM6 and Macaca fascicularis CEACAM6, and which therefore do not significantly cross-react with the closely related human CEACAM1, human CEACAM3, and human CEACAM5.

Antibodies of this invention, or antigen-binding antibody fragments thereof, or variants thereof bind specifically to the mature extracellular domain of CEACAM6 and the mature extracellular domain of Macaca fascicularis CEACAM6, and do not significantly cross-react with the closely related mature extracellular domains of human CEACAM1, of human CEACAM3, and of human CEACAM5. The mature extracellular domains might be part of the full length proteins expressed on the cell surface as well as soluble proteins (naturally occurring or recombinantly expressed).

Antibodies of this invention, or antigen-binding antibody fragments thereof, or variants thereof bind specifically to proteins comprising the mature extracellular domain of human CEACAM6 and / or the mature extracellular domain of Macaca fascicularis CEACAM6, and do not significantly cross-react with proteins comprising only the closely related mature extracellular domains of human CEACAM1 and / or of human CEACAM3, and / or of human CEACAM5.

It is an embodiment of this invention to provide antibodies or antigen-binding antibody fragments thereof, or variants thereof which are specific for human and Macaca fascilularis CEACAM6, which means, the antibodies are cross-reactive to human and Macaca fascilularis CEACAM6.

It is an embodiment of this invention to provide antibodies or antigen-binding antibody fragments thereof, or a variants thereof which are selective for CEACAM6,

which means these do not significantly cross-react with the closely related CEACAM1, CEACAM3, and CEACAM5.

It is another embodiment of the invention to provide antibodies, or antigen-binding antibody fragments thereof, or variants thereof, which bind to human CEACAM6 and are cross-reactive to CEACAM6 of another species including, but not limited to, monkey with similar affinity. Preferably, said other species is a non-human primate, such as for example Macaca fascicularis, Macaca mulatta, orang-utang, gorilla, and chimpanzee. Most preferably, the antibodies, or antigen-binding antibody fragments thereof, or variants thereof bind to human CEACAM6 and are cross-reactive to cynomolgus CEACAM6.

A monoclonal antibody binding to antigen 1 (Ag1) is "cross-reactive" to antigen 2 (Ag2) when the EC_{50} and / or K_D values are in a similar range for both antigens. In the present disclosure, a monoclonal antibody binding to Ag1 is cross-reactive to Ag2 when the ratio of affinity for Ag1 to affinity for Ag2 is equal or less 10 (≤ 10) and equal or greater than 0.1 (≥ 0.1), which means that the affinities for Ag1 and Ag2 do not differ more than a factor of 10 (the affinities are within one order of magnitude of monovalent K_D), on condition that affinities are measured with the same method in the same experimental setting for both antigens.

Accordingly, the antibody according to the invention has a ratio of affinity for human CEACAM6 to the affinity for Macaca fascicularis CEACAM6 which is equal or less 10 (≤ 10) and equal or greater than 0.1 (≥ 0.1), which means that the affinities for human and Macaca fascicularis CEACAM6 do not differ more than a factor of 10 (the affinities are within one order of magnitude of monovalent K_D). Thus, the antibody of this invention, or antigen-binding antibody fragment thereof, or variant thereof 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.

A monoclonal antibody binding to antigen 1 (Ag1) is "not significantly cross-reactive" to antigen 3 (Ag3) when the affinities are very different for the two antigens. Affinity for Ag3 may not be measurable if the binding response (the measured binding signal in an assay) is too low. In the present application, a monoclonal antibody binding to Ag1 is "not significantly cross-reactive" to Ag3, when the binding response (the measured binding signal in an assay) of the monoclonal antibody to Ag3 is less than 5%, preferably less than 2% 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 K_D or the concentration required to reach the saturation plateau obtained with Ag1.

According to the invention the antibodies or antigen-binding antibody fragments thereof, or variants thereof do not significantly cross react with human CEACAM1, human CEACAM3, and human CEACAM5.

A preferred embodiment of the invention has an affinity for human CEACAM6 and Macaca fascicularis CEACAM6 which is ≤400 nM, preferably ≤ 200 nM, alternatively preferably ≤ 100 nM, determined as monovalent affinity to recombinant CEACAM6 (see Example 2) as shown in Table 13, Table 18 and Table 20.

According to the invention the antibodies or antigen-binding antibody fragments thereof, or variants thereof bind to human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and to Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177) (affinities are within one order of magnitude of monovalent K_D). The CEACAM6 domain 1 is also known as N domain.

It is an embodiment of the invention to provide antibodies or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and specifically to Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177) with affinities (monovalent K_D) which are within one order of magnitude. Highly preferred are antibodies or antigen-binding antibody fragments thereof, or variants thereof which have an affinity for both, human CEACAM6 domain 1 and Macaca fascicularis CEACAM6 domain 1 of K_D ≤ 100 nM.

Antibodies of this invention, or antigen-binding antibody fragments thereof, or variants thereof bind specifically to proteins comprising human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and / or Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177).

Antibodies of this invention, or antigen-binding antibody fragments thereof, or variants thereof bind specifically to proteins comprising human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and / or Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177) and do

not significantly cross-react with the closely related human CEACAM1, human CEACAM3, and human CEACAM5.

Antibodies of this invention, or antigen-binding antibody fragments thereof, or variants thereof bind specifically to proteins comprising human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and / or Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177) and do not significantly cross-react with proteins comprising only the closely related mature extracellular domains of human CEACAM1, and / or of human CEACAM3, and / or of human CEACAM5.

It is an embodiment of the invention to provide antibodies, or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to the mature extracellular domain of CEACAM6 and the mature extracellular domain of Macaca fascicularis CEACAM6, and compete for binding to the 9A6 antibody (Genovac/Aldevron) on human CEACAM6 and do not significantly cross-react with the closely related mature extracellular domains of human CEACAM1, of human CEACAM3, and of human CEACAM5.

It is an embodiment of the invention to provide antibodies, or antigen-binding antibody fragments thereof, or a variants thereof which bind specifically to human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and to Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177), and compete for binding to the 9A6 antibody (Genovac/Aldevron) on human CEACAM6.

It is an embodiment of the invention to provide antibodies or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to human CEACAM6 and Macaca fascicularis CEACAM6, and which interfere with CEACAM6 and CEACAM1 interaction. An antibody interferes with the CEACAM6 and CEACAM1 interaction, when the binding signal of a preformed antibody-CEACAM6-complex is more than 20%, preferably more than 50% reduced compared to that of the CEACAM6 protein alone in a typical binding assay with CEACAM1 which is provided in the examples. Interference with CEACAM6 and CEACAM1 interaction might be a mechanism for the modulation of innate and adaptive immune responses.

It is an embodiment of the invention to provide antibodies or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to human

CEACAM6 and Macaca fascicularis CEACAM6, and which have an immunomodulatory activity. “Immunomodulation” is the adjustment of the immune response to a desired level as in immunopotention, immunosuppression or induction of immunologic tolerance. An “immunomodulatory antibody” drug is an immune response-modifying agent that stimulates or suppresses the immune response for the treatment of a disease e.g. cancer or anti-inflammation. The invention provides an anti-CEACAM6 immunomodulatory antibody, as shown in Example 11, which blocks CEACAM6 which is an immune cell suppressive ligand on cancer cells and potentially other cells including components of the immune system which results into a change of the immune marker expression profile and activation status of T cells towards an anti-tumor T cell re-activation and an effective anti-cancer immune response. An antibody binding to CEACAM6 domain 1 is preferred.

It is an embodiment of the invention to provide antibodies or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to human CEACAM6 and Macaca fascicularis CEACAM6, and which are able to relieve CEACAM6 mediated immunosuppression of tumor antigen specific T cells as measured by either IFN-gamma secretion of tumor antigen specific T cells or the number of IFN-gamma secreting activated T cells. An anti-CEACAM6 antibody is able to relieve CEACAM6 mediated immunosuppression of tumor antigen specific T cells if an antibody in the co-culture of tumor specific T cells with tumor cells yields a >1.2, preferably >1.5 times increase in IFN-gamma secretion compared to the control samples. Preferably the tumor antigen specific T cells are $CD8^+$ T cells. Preferred is an antibody which does not significantly cross-react with the closely related CEACAM1, CEACAM3, and CEACAM5 and which binds to CEACAM6 domain 1. This is exemplary shown by blockade of CEACAM6 by antibodies of the invention in the co-culture of survivin-peptide specific $CD8^+$ T cells with KS tumor cells, which yields a >1.5 times increase in IFN-gamma secretion compared to the control samples that were treated with the isotype-matched control (Figure 5 and Figure 6).

It is an embodiment of the invention to provide antibodies or antigen-binding antibody fragments thereof, or variants thereof which bind specifically to human CEACAM6 and Macaca fascicularis CEACAM6, and which are able to change the cytokine profile of tumor antigen specific T cells towards a more cytotoxic and / or activated phenotype characterized by increased IFN-gamma and / or IL-2 and / or TNF-alpha secretion. Preferably the tumor antigen specific T cells are $CD8^+$ T cells and the phenotype is an increased IFN-gamma and IL-2 and TNF-alpha secretion. An anti-

CEACAM6 antibody is able to change the cytokine profile of tumor antigen specific T cells towards a more cytotoxic and / or activated phenotype if the antibody in the co-culture of tumor specific $CD8^+$ T cells with tumor cells yields a >1.2, preferably >1.5 times increase in IFN-gamma and / or IL-2 and / or TNF-alpha secretion compared to the control samples that were treated with the isotype-matched control. Blockade of CEACAM6 by antibodies of the invention in the co-culture of survivin-peptide specific T cells with KS tumor cells yields a >1.5 times increase in IFN-gamma, IL-2 and TNF-alpha secretion compared to the control samples that were treated with the isotype-matched control (Figure 6).

It is an embodiment of the invention to provide antibodies, or antigen-binding antibody fragments thereof, or variants thereof, which bind to a broad range of different CEACAM6 expressing cell lines including, but not limited to the ones shown in the examples. These examples include human cell lines from many tumor origins (e.g. NSCLC, SCLC, CRC, PancCA, BreastCA, GastricCA, multiple myeloma, cervix, skin cancer which represent cancer indications previously described in the literature to be CEACAM6 positive (see introduction or review Beauchimen and Arabzadeh, Cancer Metastasis Rev. 2013 Dec;32(3-4):643-71).

It is an embodiment of the invention to provide antibodies, or antigen-binding antibody fragments thereof, or variants thereof that are safe for human administration. Preferably the antibodies are chimeric, humanized or human. Highly preferred are humanized or human antibodies.

Nevertheless in certain assays an expression of the antibodies of this invention as murine IgG is preferred; immunohistochemistry with human samples for example can be analyzed more easily by using murine antibodies or human-mouse chimeric antibodies.

It is another embodiment of the invention to provide antibodies which constitute a tool for diagnosis of malignant or dysplastic conditions in which CEACAM6 expression is elevated compared to normal tissue or where CEACAM6 is shed from the cell surface and becoming detectable in serum. Provided are anti-CEACAM6 antibodies conjugated to a detectable marker. Preferred markers are a radiolabel, an enzyme, a chromophore or a fluorophore.

Throughout this document, reference is made to the following preferred anti-CEACAM6 antibodies of the invention as depicted in Table 1.

		SEQ ID NO: VH Protein	SEQ ID NO: H-CDR1	SEQ ID NO: H-CDR2	SEQ ID NO: H-CDR3	SEQ ID NO: VL Protein	SEQ ID NO: L-CDR1	SEQ ID NO: L-CDR2	SEQ ID NO: L-CDR3	SEQ ID NO: IgG Heavy Chain	SEQ ID NO: IgG Light Chain
TPP-2971	mIgG1	3	4	5	6	7	8	9	10		
TPP-3308	hIgG2 - chim	33	34	35	36	37	38	39	40	43	44
TPP-3310	hIgG2	47	48	49	50	51	52	53	54	57	58
TPP-3714	hIgG2	119	120	121	122	123	124	125	126	129	130
TPP-3187	mIgG1	23	24	25	26	27	28	29	30		
TPP-3323	hIgG2 - chim	75	76	77	78	79	80	81	82	85	86
TPP-3820	hIgG2	133	134	135	136	137	138	139	140	143	144
TPP-3821	hIgG2	147	148	149	150	151	152	153	154	157	158
TPP-3186	mIgG1	13	14	15	16	17	18	19	20		
TPP-3322	hIgG2 - chim	61	62	63	64	65	66	67	68	71	72
TPP-3707	hIgG2	105	106	107	108	109	110	111	112	115	116
TPP-3705	hIgG2	91	92	93	94	95	96	97	98	101	102

Table 1: Protein sequences of preferred antibodies of this invention

The sequences of preferred antibodies of this invention or antigen-binding fragments thereof depicted in Table 1 are further provided and explained in Figure 8.

TPP-3308 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 43 and a light chain region corresponding to SEQ ID NO: 44.

TPP-3310 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 57 and a light chain region corresponding to SEQ ID NO: 58.

TPP-3714 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 129 and a light chain region corresponding to SEQ ID NO: 130.

TPP-3323 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 85 and a light chain region corresponding to SEQ ID NO: 86.

TPP-3820 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 143 and a light chain region corresponding to SEQ ID NO: 144.

TPP-3821 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 157 and a light chain region corresponding to SEQ ID NO: 158.

TPP-3322 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 71 and a light chain region corresponding to SEQ ID NO: 72.

TPP-3707 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 115 and a light chain region corresponding to SEQ ID NO: 116.

TPP-3705 represents an antibody comprising a heavy chain region corresponding to SEQ ID NO: 101 and a light chain region corresponding to SEQ ID NO: 102.

In a further preferred embodiment the antibodies or antigen-binding fragments comprise heavy or light chain CDR sequences which are at least 50%, 55%, 60% 70%, 80%, 90, or 95% identical to at least one, preferably corresponding, CDR sequence of the antibodies "TPP-2971", "TPP-3186", "TPP-3187", "TPP-3308", "TPP-3310", "TPP-3322", "TPP-3323", "TPP-3705", "TPP-3707", "TPP-3714", "TPP-3820", "TPP-3821" or at least 50%, 60%, 70%, 80%, 90%, 92% or 95% identical to the VH or VL sequence of "TPP-2971", "TPP-3186", "TPP-3187", "TPP-3308", "TPP-3310", "TPP-3322", "TPP-3323", "TPP-3705", "TPP-3707", "TPP-3714", "TPP-3820", "TPP-3821", respectively.

In a further preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises at least one CDR sequence or at least one variable heavy chain or variable light chain sequence as depicted in Table 1.

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:4 (H-CDR1), SEQ ID NO:5 (H-CDR2) and SEQ ID NO:6 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:8 (L-CDR1), SEQ ID NO:9 (L-CDR2) and SEQ ID NO:10 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:34 (H-CDR1), SEQ ID NO:35 (H-CDR2) and SEQ ID NO:36 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:38 (L-CDR1), SEQ ID NO:39 (L-CDR2) and SEQ ID NO:40 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:48 (H-CDR1), SEQ ID NO:49 (H-CDR2) and SEQ ID NO:50 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:52 (L-CDR1), SEQ ID NO:53 (L-CDR2) and SEQ ID NO:54 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:120 (H-CDR1), SEQ ID NO:121 (H-CDR2) and SEQ ID NO:122 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:124 (L-CDR1), SEQ ID NO:125 (L-CDR2) and SEQ ID NO:126 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:24 (H-CDR1), SEQ ID NO:25 (H-CDR2) and SEQ ID NO:26 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:28 (L-CDR1), SEQ ID NO:29 (L-CDR2) and SEQ ID NO:30 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:76 (H-CDR1), SEQ ID NO:77 (H-CDR2) and SEQ ID NO:78 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:80 (L-CDR1), SEQ ID NO:81 (L-CDR2) and SEQ ID NO:82 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:134 (H-CDR1), SEQ ID NO:135 (H-CDR2) and SEQ ID NO:136 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:138 (L-CDR1), SEQ ID NO:139 (L-CDR2) and SEQ ID NO:140 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:148 (H-CDR1), SEQ ID NO:149 (H-CDR2) and SEQ ID NO:150 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:152 (L-CDR1), SEQ ID NO:153 (L-CDR2) and SEQ ID NO:154 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:62 (H-CDR1), SEQ ID NO:63 (H-CDR2) and SEQ ID NO:64 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:66 (L-CDR1), SEQ ID NO:67 (L-CDR2) and SEQ ID NO:68 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:14 (H-CDR1), SEQ ID NO:15 (H-CDR2) and SEQ ID NO:16 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:18 (L-CDR1), SEQ ID NO:19 (L-CDR2) and SEQ ID NO:20 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:106 (H-CDR1), SEQ ID NO:107 (H-CDR2) and SEQ ID NO:108 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:110 (L-CDR1), SEQ ID NO:111 (L-CDR2) and SEQ ID NO:112 (L-CDR3).

In a preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a heavy chain antigen-binding region that comprises SEQ ID NO:92 (H-CDR1), SEQ ID NO:93 (H-CDR2) and SEQ ID NO:94 (H-CDR3) and comprises a light chain antigen-binding region that comprises SEQ ID NO:96 (L-CDR1), SEQ ID NO:97 (L-CDR2) and SEQ ID NO:98 (L-CDR3).

Antibodies differ in sequence, not only within their complementarity determining regions (CDRs), but also in the framework (FR). These sequence differences are encoded in the different V-genes. The human antibody germline repertoire has been completely sequenced. There are about 50 functional VH germline genes which can be grouped into six subfamilies according to sequence homology VH1, VH2, VH3, VH4, VH5 and VH6 (Tomlinson et al., 1992, J. Mol. Biol. 227, 776-798; Matsuda & Honjo, 1996, Advan. Immunol. 62, 1-29). About 40 functional VL kappa genes comprising seven subfamilies are known (Cox et al., 1994, Eur. J. Immunol. 24, 827-836; Barbie & Lefranc, 1998, Exp. Clin. Immunogenet. 15, 171-183): Vkappa1, Vkappa2, Vkappa3, Vkappa4, Vkappa5, Vkappa6 and Vkappa7. Disclosed herein are heavy chains of antibodies of this invention that belong to the human VH2 subfamily and the light chains of antibodies of this invention that belong to the human Vkappa1 subfamily, respectively. It is known that framework sequences of antibodies belonging to the same subfamily are closely related, e.g. antibodies comprising a human VH3 subfamily member all share comparable stability (Honegger et al., 2009, Protein Eng Des Sel. 22(3):121-134). It is well known in the art that CDRs from antibodies can be grafted on different frameworks while maintaining special features of the corresponding origin antibody. CDRs have been successfully grafted on frameworks belonging to a different species as well as on frameworks of the same species belonging to a different subfamily. In a further embodiment the antibody or antigen-binding fragment of the invention comprises at least one CDR sequence of antibody of the invention as depicted in Table 1 and a human variable chain framework sequence.

In a preferred embodiment the antibody or antigen-binding fragment of the invention comprises a variable light chain or light chain antigen-binding region comprising the L-CDR1, L-CDR2 and L-CDR3 sequence of the variable light chain and a variable heavy chain or heavy chain antigen-binding region comprising the H-CDR1, H-CDR2 and H-CDR3 sequence of the variable heavy chain antibody of the invention as depicted in Table 1 and a human variable light and human variable heavy chain framework sequence.

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:3 (VH) and a variable light chain sequences as presented by SEQ ID NO:7 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:33 (VH) and a variable light chain sequences as presented by SEQ ID NO:37 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:119 (VH) and a variable light chain sequences as presented by SEQ ID NO:123 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:23 (VH) and a variable light chain sequences as presented by SEQ ID NO:27 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:75 (VH) and a variable light chain sequences as presented by SEQ ID NO:79 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:133 (VH) and a variable light chain sequences as presented by SEQ ID NO:137 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:147 (VH) and a variable light chain sequences as presented by SEQ ID NO:151 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:13 (VH) and a variable light chain sequences as presented by SEQ ID NO:17 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:61 (VH) and a variable light chain sequences as presented by SEQ ID NO:65 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:105 (VH) and a variable light chain sequences as presented by SEQ ID NO:109 (VL).

In a highly preferred embodiment the antibody of the invention or antigen-binding fragment thereof comprises a variable heavy chain sequence as presented by SEQ ID NO:91 (VH) and a variable light chain sequences as presented by SEQ ID NO:95 (VL).

In some embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof binds to an epitope of human CEACAM6, wherein said epitope comprises one or more amino acid residues selected from the group consisting of Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In certain embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof binds to an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In some embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises one, two, three four, five, eight, ten, fifteen or more amino acid residues selected from the group consisting of Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In certain embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

In some embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof binds to an epitope of human CEACAM6, wherein said epitope comprises one or more amino acid residues selected from the group consisting of Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In certain embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof binds to an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In some embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises one, two, three four, five, eight, ten, fifteen or more amino acid residues selected from the group consisting of Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In certain embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In some embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof binds to an epitope of human CEACAM6, wherein said epitope comprises one or more amino acid residues selected from the group consisting of Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL).

In certain embodiments, the anti-CEACAM6 antibody of the invention binds to an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an

antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL).

In some embodiments, the anti-CEACAM6 antibody of the invention interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises one, two, three four, five, eight, ten, fifteen or more amino acid residues selected from the group consisting of Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL).

In certain embodiments, the anti-CEACAM6 antibody of the invention interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL).

In some embodiments, the anti-CEACAM6 antibody of the invention or an antigen-binding antibody fragment thereof, or a variant thereof binds to an epitope of human CEACAM6, wherein said epitope comprises one or more amino acid residues selected from the group consisting of Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL), and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In certain embodiments, the anti-CEACAM6 antibody of the invention binds to an epitope of human CEACAM6, wherein said epitope comprises the amino acid

residues Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL) and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In some embodiments, the anti-CEACAM6 antibody of the invention interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises one, two, three four, five, eight, ten, fifteen or more amino acid residues selected from the group consisting of Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL) and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

In certain embodiments, the anti-CEACAM6 antibody of the invention interacts with, e.g. binds to, an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 of SEQ ID NO: 179, and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof competes for binding to CECEAM6 with an antibody comprising a variable heavy chain sequence as presented by SEQ ID NO:47 (VH) and a variable light chain sequences as presented by SEQ ID NO:51 (VL) and wherein said antibody or antigen-binding antibody fragment thereof, or variant thereof binds to a human CEACAM6 protein comprising an Ile63Leu mutation and does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation (numbering according to SEQ-ID:179).

An antibody of the invention may be an IgG (immunoglobulin G e.g. IgG1 IgG2, IgG3, IgG4) or IgA, IgD, IgE, IgM, while an antibody fragment may be a Fab, Fab', $F(ab')_2$, Fab'-SH or scFv, for example. An inventive antibody fragment, accordingly, may be, or may contain, an antigen-binding region that behaves in one or more ways as described herein.

In a preferred embodiment the antibodies or antigen-binding antibody fragments of the invention are monoclonal.

In some embodiments antibodies of the invention or antigen-binding fragments thereof, or nucleic acids encoding the same are isolated. An isolated biological component (such as a nucleic acid molecule or protein such as an antibody) is one that has been substantially separated or purified away from other biological components in the cell of the organism in which the component naturally occurs, e.g., other chromosomal and extra-chromosomal DNA and RNA, proteins and organelles. The term also embraces nucleic acids and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

Antibody Generation

An antibody of the invention may be derived from a recombinant antibody library that is based on amino acid sequences that have been isolated from the antibodies of a large number of healthy volunteers e.g. using the n-CoDeR® technology the fully human CDRs are recombined into new antibody molecules (Carlson & Söderlind, Expert Rev Mol Diagn. 2001 May;1(1):102-8). Or alternatively for example antibody libraries as the fully human antibody phage display library described in Hoet RM et al., Nat Biotechnol 2005;23(3):344-8) can be used to isolate CEACAM6-specific antibodies. Antibodies or antibody fragments isolated from human antibody libraries are considered human antibodies or human antibody fragments herein.

Human antibodies may be further prepared by administering an immunogen to a transgenic animal that has been modified to produce intact human antibodies or intact antibodies with human variable regions in response to antigenic challenge. Such animals typically contain all or a portion of the human immunoglobulin loci, which replace the endogenous immunoglobulin loci, or which are present extrachromosomally or integrated randomly into the animal's chromosomes. For example immunization of

genetically engineered mice inter alia immunization of hMAb mice (e.g. VelocImmune mouse® or XENOMOUSE®) may be performed.

Further antibodies may be generated using the hybridoma technology (for example see Köhler and Milstein Nature. 1975 Aug 7;256(5517):495-7), resulting in for example murine, rat, or rabbit antibodies which can be converted into chimeric or humanized antibodies. Humanized antibodies and methods of making them are reviewed, e.g., in Almagro and Fransson, Front. Biosci. 13:1619-1633 (2008), and are further described, e.g., in Riechmann et al., Nature 332:323-329 (1988); Queen et al., Proc. Natl Acad. Sci. USA 86:10029-10033 (1989); US Patent Nos. 5,821,337, 7,527,791, 6,982,321, and 7,087,409; Kashmiri et al., Methods 36:25-34 (2005) (describing specificity determining region (SDR) grafting); Padlan, Mol. Immunol. 28:489-498 (1991) (describing "resurfacing"); Dall' Acqua et al., Methods 36:43-60 (2005) (describing "FR shuffling"); and Osboum et al., Methods 36:61-68 (2005) and Klimka et al., Br. J. Cancer, 83:252-260 (2000) (describing the "guided selection" approach to FR shuffling).

Examples are provided for the generation of antibodies using a recombinant antibody library and immunization of mice combined with subsequent humanization.

It is a further aspect of the invention to provide a method to generate antibodies specifically binding to human CEACAM6 and to Macaca fascicularis CEACAM6, which do not significantly cross-react with human CEACAM1, human CEACAM3, and human CEACAM5. It is an embodiment of the invention to provide a method for generation of anti-CEACAM6 antibodies characterized by comprising the steps of immunization of an animal, preferentially a mouse, with cynomolgus CECAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177), determining the amino acid sequence of antibodies specifically binding to human CEACAM6 and to cynomolgus CEACAM6, followed optionally by humanization or generation of a chimeric antibody, and expression of said antibodies. The expression system can be a recombinant or a cell free expression system. Suitable host cells for recombinant expression are prokaryotic and eukaryotic cells. Preferred are mammalian expression systems.

Peptide Variants

Antibodies or antigen-binding fragments of the invention are not limited to the specific peptide sequences provided herein. Rather, the invention also embodies

variants of these polypeptides. With reference to the instant disclosure and conventionally available technologies and references, the skilled worker will be able to prepare, test and utilize functional variants of the antibodies disclosed herein, while appreciating these variants having the ability to bind to CEACAM6 fall within the scope of the present invention.

A variant can include, for example, an antibody that has at least one altered complementary determining region (CDR) (hyper-variable) and/or framework (FR) (variable) domain/position, vis-à-vis a peptide sequence disclosed herein.

By altering one or more amino acid residues in a CDR or FR region, the skilled worker routinely can generate mutated or diversified antibody sequences, which can be screened against the antigen, for new or improved properties, for example.

A further preferred embodiment of the invention is an antibody or antigen-binding fragment in which the VH and VL sequences are selected as shown in Table 1. The skilled worker can use the data in Table 1 to design peptide variants that are within the scope of the present invention. It is preferred that variants are constructed by changing amino acids within one or more CDR regions; a variant might also have one or more altered framework regions. Alterations also may be made in the framework regions. For example, a peptide FR domain might be altered where there is a deviation in a residue compared to a germline sequence.

Alternatively, the skilled worker could make the same analysis by comparing the amino acid sequences disclosed herein to known sequences of the same class of such antibodies, using, for example, the procedure described by Knappik A., et al., JMB 2000, 296:57-86.

Furthermore, variants may be obtained by using one antibody as starting point for further optimization by diversifying one or more amino acid residues in the antibody, preferably amino acid residues in one or more CDRs, and by screening the resulting collection of antibody variants for variants with improved properties. Particularly preferred is diversification of one or more amino acid residues in CDR3 of VL and/or VH. Diversification can be done e.g. by synthesizing a collection of DNA molecules using trinucleotide mutagenesis (TRIM) technology (Virnekäs B. et al., Nucl. Acids Res. 1994, 22: 5600.). Antibodies or antigen-binding fragments thereof include molecules with modifications/variations including but not limited to e.g. modifications leading to altered half-life (e.g. modification of the Fc part or attachment of further molecules such as PEG), altered binding affinity or altered ADCC or CDC activity.

Conservative Amino Acid Variants

Polypeptide variants may be made that conserve the overall molecular structure of an antibody peptide sequence described herein. Given the properties of the individual amino acids, some rational substitutions will be recognized by the skilled worker. Amino acid substitutions, *i.e.*, "conservative substitutions," may be made, for instance, on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

For example, (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophane, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α-helices. Similarly, certain amino acids, such as alanine, cysteine, leucine, methionine, glutamic acid, glutamine, histidine and lysine are more commonly found in α-helices, while valine, isoleucine, phenylalanine, tyrosine, tryptophan and threonine are more commonly found in β-pleated sheets. Glycine, serine, aspartic acid, asparagine, and proline are commonly found in turns. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative amino acid variants.

Glycosylation Variants

Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. Native antibodies produced by mammalian cells typically comprise a branched, biantennary oligosaccharide that is generally attached by an N-linkage to Asn297 using Kabat EU numbering of the CH2 domain of the Fc region; see, e.g., Wright et al. Trends Biotechnol. 15: 26-32 (1997).

In certain embodiments, an antibody provided herein is altered to increase or decrease the extent to which the antibody is glycosylated. Addition or deletion of glycosylation sites to an antibody may be conveniently accomplished by altering the

expression system (e.g. host cell) and / or by altering the amino acid sequence such that one or more glycosylation sites is created or removed.

In one embodiment of this invention, aglycosyl antibodies having decreased effector function or antibody derivatives are prepared by expression in a prokaryotic host. Suitable prokaryotic hosts for include but are not limited to *E. coli, Bacillus subtilis, Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus.

In one embodiment, antibody variants are provided having decreased effector function, which are characterized by a modification at the conserved N-linked site in the CH2 domains of the Fc portion of said antibody. In one embodiment of present invention, the modification comprises a mutation at the heavy chain glycosylation site to prevent glycosylation at the site. Thus, in one preferred embodiment of this invention, the aglycosyl antibodies or antibody derivatives are prepared by mutation of the heavy chain glycosylation site, - i.e., mutation of N297 using Kabat EU numbering and expressed in an appropriate host cell.

In another embodiment of the present invention, aglycosyl antibodies or antibody derivatives have decreased effector function, wherein the modification at the conserved N-linked site in the CH2 domains of the Fc portion of said antibody or antibody derivative comprises the removal of the CH2 domain glycans, - i.e., deglycosylation. These aglycosyl antibodies may be generated by conventional methods and then deglycosylated enzymatically. Methods for enzymatic deglycosylation of antibodies are well known in the art (e.g. Winkelhake & Nicolson (1976), J Biol Chem. 251(4):1074-80).

In another embodiment of this invention, deglycosylation may be achieved using the glycosylation inhibitor tunicamycin (Nose & Wigzell (1983), Proc Natl Acad Sci USA, 80(21):6632-6). That is, the modification is the prevention of glycosylation at the conserved N-linked site in the CH2 domains of the Fc portion of said antibody.

In one embodiment, antibody variants are provided having a carbohydrate structure that lacks fucose attached (directly or indirectly) to an Fc region. For example, the amount of fucose in such antibody may be from 1% to 80%, from 1% to 65%, from 5% to 65% or from 20% to 40%. The amount of fucose is determined by calculating the average amount of fucose within the sugar chain at Asn297, relative to the sum of all glycostructures attached to Asn 297 (e.g. complex, hybrid and high mannose structures) as measured by MALDI-TOF mass spectrometry, as described in WO

2008/077546, for example. Asn297 refers to the asparagine residue located at about position 297 in the Fc region (Eu numbering of Fc region residues); however, Asn297 may also be located about ± 3 amino acids upstream or downstream of position 297, i.e., between positions 294 and 300, due to minor sequence variations in antibodies. Such fucosylation variants may have improved ADCC function.

Examples of publications related to "defucosylated" or "fucose-deficient" antibody variants include: Okazaki et al. J Mol. Biol. 336: 1239-1249 (2004); Yamane-Ohnuki et al. Biotech. Bioeng. 87: 614 (2004).

Examples of cell lines capable of producing defucosylated antibodies include Lec13 CHO cells deficient in protein fucosylation (Ripka et al. Arch. Biochem. Biophys. 249:533-545 (1986); and WO 2004/056312), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene, FUT8, knockout CHO cells (see, e.g., Yamane-Ohnuki et al. Biotech. Bioeng. 87: 614 (2004); Kanda, Y. et al., Biotechnol. Bioeng., 94(4):680-688 (2006)).

Antibody variants are further provided with bisected oligosaccharides, e.g., in which a biantennary oligosaccharide attached to the Fc region of the antibody is bisected by GlcNAc. Such antibody variants may have reduced fucosylation and/or improved ADCC function. Examples of such antibody variants are described, e.g., in WO 2003/011878; US Patent No. 6,602,684; and US 2005/0123546.

Antibody variants with at least one galactose residue in the oligosaccharide attached to the Fc region are also provided. Such antibody variants may have improved CDC function. Such antibody variants are described, e.g., in WO1997/30087; WO1998/58964; and WO1999/22764.

Fc Region Variants

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

In certain embodiments, the invention contemplates an antibody variant that possesses some but not all effector functions, which make it a desirable candidate for applications in which the half-life of the antibody in vivo is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious. In vitro

and/or in vivo cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity), but retains FcRn binding ability. In some embodiments, alterations are made in the Fc region that result in altered (i.e., either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC).

In certain embodiments, the invention contemplates an antibody variant that possesses an increased or decreased half-live. Antibodies with increased half-lives and improved binding to the neonatal Fc receptor (FcRn), which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J Immunol. 117:587 (1976) and Kim et al., J Immunol. 24:249 (1994)), are described in US2005/0014934 (Hinton et al.). Those antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn.

Antibody-Drug Conjugates (ADC)

The invention also provides antibody-drug conjugates (ADC, immunoconjugates) comprising an anti-CEACAM6 antibody conjugated to one or more cytotoxic agents, such as chemotherapeutic agents or drugs, growth inhibitory agents, toxins (e.g., protein toxins, enzymatically active toxins of bacterial, fungal, plant, human or animal origin, or fragments thereof), or radioactive isotopes.

In one embodiment, an immunoconjugate is an antibody-drug conjugate (ADC) in which an antibody is conjugated to one or more drugs, including but not limited to a maytansinoid (see U.S. Patent Nos. 5,208,020, 5,416,064 and European Patent EP0425235); an auristatin such as monomethylauristatin drug moieties DE and DF (MMAE and MMAF) (see U.S. Patent Nos. 5,635,483 and 5,780,588, and 7,498,298); a dolastatin; a calicheamicin or derivative thereof; an anthracycline such as daunomycin or doxorubicin; methotrexate; vindesine; a taxane such as docetaxel, paclitaxel, larotaxel, tesetaxel, and ortataxel; a trichothecene; and CC1065.

In another embodiment, an immunoconjugate comprises an antibody as described herein conjugated to an enzymatically active toxin or fragment thereof, including but not limited to diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alphasarcin, Aleurites fordii proteins, dianthin proteins,

Phytolaca americana proteins (P API, P APII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

In another embodiment, an immunoconjugate comprises an antibody as described herein conjugated to a radioactive atom to form a radioconjugate. A variety of radioactive isotopes are available for the production of radioconjugates. Examples include ^{227}Th, ^{225}Ac, ^{211}At, ^{131}I, ^{125}I, ^{90}Y, ^{186}Re, ^{188}Re, ^{153}Sm, ^{212}Bi, ^{32}P, ^{212}Pb and radioactive isotopes of Lu. When the radioconjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example Tc99m, or a spin label for nuclear magnetic resonance (NMR) imaging, such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

Conjugates of an antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene).

The linker may be a "cleavable linker" facilitating release of a cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Res. 52: 12 7-131 (1992).

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

DNA molecules of the invention

The present invention also relates to the DNA molecules that encode an antibody of the invention or antigen-binding fragment thereof. The DNA sequences used for the antibodies expressed are given in Table 32. These sequences are optimized in certain cases for mammalian expression. DNA molecules of the invention are not limited to the sequences disclosed herein, but also include variants thereof. DNA variants within the invention may be described by reference to their physical properties in hybridization. The skilled worker will recognize that DNA can be used to identify its complement and, since DNA is double stranded, its equivalent or homolog, using nucleic acid hybridization techniques. It also will be recognized that hybridization can occur with less than 100% complementarity. However, given appropriate choice of conditions, hybridization techniques can be used to differentiate among DNA sequences based on their structural relatedness to a particular probe. For guidance regarding such conditions see, Sambrook et al., 1989 *supra* and Ausubel et al., 1995 (Ausubel, F. M., Brent, R., Kingston, R. E., Moore, D. D., Sedman, J. G., Smith, J. A., & Struhl, K. eds. (1995). Current Protocols in Molecular Biology. New York: John Wiley and Sons).

Structural similarity between two polynucleotide sequences can be expressed as a function of "stringency" of the conditions under which the two sequences will hybridize with one another. As used herein, the term "stringency" refers to the extent that the conditions disfavor hybridization. Stringent conditions strongly disfavor hybridization, and only the most structurally related molecules will hybridize to one another under such conditions. Conversely, non-stringent conditions favor hybridization of molecules displaying a lesser degree of structural relatedness. Hybridization stringency, therefore, directly correlates with the structural relationships of two nucleic acid sequences.

Hybridization stringency is a function of many factors, including overall DNA concentration, ionic strength, temperature, probe size and the presence of agents which disrupt hydrogen bonding. Factors promoting hybridization include high DNA concentrations, high ionic strengths, low temperatures, longer probe size and the absence of agents that disrupt hydrogen bonding. Hybridization typically is performed in two phases: the “binding” phase and the “washing” phase.

Functionally Equivalent DNA Variants

Yet another class of DNA variants within the scope of the invention may be described with reference to the product they encode. These functionally equivalent polynucleotides are characterized by the fact that they encode the same peptide sequences due to the degeneracy of the genetic code.

It is recognized that variants of DNA molecules provided herein can be constructed in several different ways. For example, they may be constructed as completely synthetic DNAs. Methods of efficiently synthesizing oligonucleotides are widely available. *See* Ausubel *et al.*, section 2.11, Supplement 21 (1993). Overlapping oligonucleotides may be synthesized and assembled in a fashion first reported by Khorana *et al.*, J. Mol. Biol. 72:209-217 (1971); *see also* Ausubel *et al.*, *supra*, Section 8.2. Synthetic DNAs preferably are designed with convenient restriction sites engineered at the 5' and 3' ends of the gene to facilitate cloning into an appropriate vector.

As indicated, a method of generating variants is to start with one of the DNAs disclosed herein and then to conduct site-directed mutagenesis. *See* Ausubel et al., *supra,* chapter 8, Supplement 37 (1997). In a typical method, a target DNA is cloned into a single-stranded DNA bacteriophage vehicle. Single-stranded DNA is isolated and hybridized with an oligonucleotide containing the desired nucleotide alteration(s). The complementary strand is synthesized and the double stranded phage is introduced into a host. Some of the resulting progeny will contain the desired mutant, which can be confirmed using DNA sequencing. In addition, various methods are available that increase the probability that the progeny phage will be the desired mutant. These methods are well known to those in the field and kits are commercially available for generating such mutants.

Recombinant DNA constructs and expression

The present invention further provides recombinant DNA constructs comprising one or more of the nucleotide sequences of the present invention (see Table 32). The recombinant constructs of the present invention can be used in connection with a vector, such as a plasmid, phagemid, phage or viral vector, into which a DNA molecule encoding an antibody of the invention or antigen-binding fragment thereof or variant thereof is inserted.

An antibody, antigen binding portion, or variant thereof provided herein can be prepared by recombinant expression of nucleic acid sequences encoding light and heavy chains or portions thereof in a host cell. To express an antibody, antigen binding portion, or variant thereof recombinantly a host cell can be transfected with one or more recombinant expression vectors carrying DNA fragments encoding the light and/or heavy chains or portions thereof such that the light and heavy chains are expressed in the host cell. Standard recombinant DNA methodologies are used to prepare and/or obtain nucleic acids encoding the heavy and light chains, incorporate these nucleic acids into recombinant expression vectors and introduce the vectors into host cells, such as those described in Sambrook, Fritsch and Maniatis (eds.), Molecular Cloning; A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), Ausubel, F. M. et al. (eds.) Current Protocols in Molecular Biology, Greene Publishing Associates, (1989) and in U.S. Pat. No. 4,816,397 by Boss et al..

In addition, the nucleic acid sequences encoding variable regions of the heavy and/or light chains can be converted, for example, to nucleic acid sequences encoding full-length antibody chains, Fab fragments, or to scFv. The VL- or VH-encoding DNA fragment can be operatively linked, (such that the amino acid sequences encoded by the two DNA fragments are in-frame) to another DNA fragment encoding, for example, an antibody constant region or a flexible linker. The sequences of human heavy chain and light chain constant regions are known in the art (see e.g., Kabat, E. A., el al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification.

To create a polynucleotide sequence that encodes a scFv, the VH- and VL-encoding nucleic acids can be operatively linked to another fragment encoding a flexible linker such that the VH and VL sequences can be expressed as a contiguous single-chain protein, with the VL and VH regions joined by the flexible linker (see e.g., Bird et al. (1988) Science 242:423-426; Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883; McCafferty et al., Nature (1990) 348:552-554).

To express the antibodies, antigen binding fragments thereof or variants thereof standard recombinant DNA expression methods can be used (see, for example, Goeddel; Gene Expression Technology. Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990)). For example, DNA encoding the desired polypeptide can be

inserted into an expression vector which is then transfected into a suitable host cell. Suitable host cells are prokaryotic and eukaryotic cells. Examples for prokaryotic host cells are e.g. bacteria, examples for eukaryotic hosts cells are yeasts, insects and insect cells, plants and plant cells, transgenic animals, or mammalian cells. In some embodiments, the DNAs encoding the heavy and light chains are inserted into separate vectors. In other embodiments, the DNA encoding the heavy and light chains is inserted into the same vector. It is understood that the design of the expression vector, including the selection of regulatory sequences is affected by factors such as the choice of the host cell, the level of expression of protein desired and whether expression is constitutive or inducible.

Therefore, an embodiment of the present invention are also host cells comprising the vector or a nucleic acid molecule, whereby the host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, and may be a prokaryotic cell, such as a bacterial cell.

Another embodiment of the present invention is a method of using the host cell to produce an antibody and antigen binding fragments, comprising culturing the host cell under suitable conditions and recovering said antibody.

Therefore another embodiment of the present invention is the production of the antibodies according to this invention with the host cells of the present invention and purification of these antibodies to at least 95% homogeneity by weight.

Bacterial Expression

Useful expression vectors for bacterial use are constructed by inserting a DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, if desirable, to provide amplification within the host. Suitable prokaryotic hosts for transformation include but are not limited to *E. coli, Bacillus subtilis, Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus.

Bacterial vectors may be, for example, bacteriophage-, plasmid- or phagemid-based. These vectors can contain a selectable marker and a bacterial origin of replication derived from commercially available plasmids typically containing elements

of the well-known cloning vector pBR322 (ATCC 37017). Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is de-repressed/induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the protein being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of antibodies or to screen peptide libraries, for example, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable.

Therefore, an embodiment of the present invention is an expression vector comprising a nucleic acid sequence encoding for the novel antibodies of the present invention.

Antibodies of the present invention or antigen-binding fragments thereof or variants thereof include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic host, including, for example, *E. coli*, *Bacillus subtilis, Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, preferably, from *E. coli* cells.

Mammalian Expression

Preferred regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV) (such as the CMV promoter/enhancer), Simian Virus 40 (SV40) (such as the SV40 promoter/enhancer), adenovirus, (e.g., the adenovirus major late promoter (AdMLP)) and polyoma. Expression of the antibodies may be constitutive or regulated (e.g. inducible by addition or removal of small molecule inductors such as Tetracyclin in conjunction with Tet system). For further description of viral regulatory elements, and sequences thereof, see e.g., U.S. 5,168,062 by Stinski, U.S. 4,510,245 by Bell et al. and U.S. 4,968,615 by Schaffner et al.. The recombinant expression vectors can also include origins of

replication and selectable markers (see e.g., U.S. 4,399,216, 4,634,665 and U.S. 5,179,017). Suitable selectable markers include genes that confer resistance to drugs such as G418, puromycin, hygromycin, blasticidin, zeocin/bleomycin or methotrexate or selectable marker that exploit auxotrophies such as Glutamine Synthetase (Bebbington et al., Biotechnology (N Y). 1992 Feb;10(2):169-75), on a host cell into which the vector has been introduced. For example, the dihydrofolate reductase (DHFR) gene confers resistance to methotrexate, neo gene confers resistance to G418, the bsd gene from Aspergillus terreus confers resistance to blasticidin, puromycin N-acetyl-transferase confers resistance to puromycin, the Sh ble gene product confers resitance to zeocin, and resistance to hygromycin is conferred by the E. coli hygromycin resistance gene (hyg or hph). Selectable markers like DHFR or Glutamine Synthetase are also useful for amplification techniques in conjunction with MTX and MSX.

Transfection of the expression vector into a host cell can be carried out using standard techniques such as electroporation, nucleofection, calcium-phosphate precipitation, lipofection, polycation-based transfection such as polyethlylenimine (PEI)-based transfection and DEAE-dextran transfection.

Suitable mammalian host cells for expressing the antibodies, antigen binding fragments thereof or variants thereof provided herein include Chinese Hamster Ovary (CHO cells) such as CHO-K1, CHO-S, CHO-K1SV [including dhfr- CHO cells, described in Urlaub and Chasin, (1980) Proc. Natl. Acad. Sci. USA 77:4216-4220 and Urlaub et al., Cell. 1983 Jun;33(2):405-12, used with a DHFR selectable marker, e.g., as described in R. J. Kaufman and P. A. Sharp (1982) Mol. Biol. 159:601-621; and other knockout cells exemplified in Fan et al., Biotechnol Bioeng. 2012 Apr;109(4):1007-15], NS0 myeloma cells, COS cells, HEK293 cells, HKB11 cells, BHK21 cells, CAP cells, EB66 cells, and SP2 cells.

Expression might also be transient or semi-stable in expression systems such as HEK293, HEK293T, HEK293-EBNA, HEK293E, HEK293-6E, HEK293-Freestyle, HKB11, Expi293F, 293EBNALT75, CHO Freestyle, CHO-S, CHO-K1, CHO-K1SV, CHOEBNALT85, CHOS-XE, CHO-3E7 or CAP-T cells (for instance Durocher et al., Nucleic Acids Res. 2002 Jan 15;30(2):E9).

In some embodiments, the expression vector is designed such that the expressed protein is secreted into the culture medium in which the host cells are grown. The antibodies, antigen binding fragments thereof or variants thereof can be recovered from the culture medium using standard protein purification methods.

Purification

Antibodies of the invention or antigen-binding fragments thereof or variants thereof can be recovered and purified from recombinant cell cultures by well-known methods including, but not limited to ammonium sulfate or ethanol precipitation, acid extraction, Protein A chromatography, Protein G chromatography, anion or cation exchange chromatography, phospho-cellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. High performance liquid chromatography ("HPLC") can also be employed for purification. See, e.g., Colligan, Current Protocols in Immunology, or Current Protocols in Protein Science, John Wiley & Sons, NY, N.Y., (1997-2001), e.g., Chapters 1, 4, 6, 8, 9, 10, each entirely incorporated herein by reference.

Antibodies of the present invention or antigen-binding fragments thereof or variants thereof include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from an eukaryotic host, including, for example, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the antibody of the present invention can be glycosylated or can be non-glycosylated. Such methods are described in many standard laboratory manuals, such as Sambrook, supra, Sections 17.37-17.42; Ausubel, supra, Chapters 10, 12, 13, 16, 18 and 20.

In preferred embodiments, the antibody is purified (1) to greater than 95% by weight of antibody as determined e.g. by the Lowry method, UV-Vis spectroscopy or by by SDS-Capillary Gel electrophoresis (for example on a Caliper LabChip GXII, GX 90 or Biorad Bioanalyzer device), and in further preferred embodiments more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence, or (3) to homogeneity by SDS-PAGE under reducing or non-reducing conditions using Coomassie blue or, preferably, silver stain. Isolated naturally occurring antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

Therapeutic Methods

Therapeutic methods involve administering to a subject in need of treatment a therapeutically effective amount of an antibody or an antigen-binding fragment thereof

or a variant thereof contemplated by the invention. A "therapeutically effective" amount hereby is defined as the amount of an antibody or antigen-binding fragment that is of sufficient quantity to reduce proliferation of CEACAM6 positive cell or to reduce size of a CEACAM6 expressing tumor in a treated area of a subject - either as a single dose or according to a multiple dose regimen, alone or in combination with other agents, which leads to the alleviation of an adverse condition, yet which amount is toxicologically tolerable. The subject may be a human or non-human animal (*e.g.*, rabbit, rat, mouse, dog, monkey or other lower-order primate).

It is an embodiment of the invention to provide an antibody or antigen-binding fragment thereof for use as medicament.

It is an embodiment of the invention to provide an antibody or antigen-binding fragment thereof for use as a medicament for the treatment of cancer. In a preferred embodiment the cancer is a tumor and in a highly preferred embodiment the cancer is a solid tumor.

It is an embodiment of the invention to use the antibody or antigen-binding fragment thereof in the manufacture of a medicament for the treatment of a disease.

It is an embodiment of the invention to use the antibody or antigen-binding fragment thereof in the manufacture of a medicament for the treatment of cancer. In a preferred embodiment the cancer is a tumor and in a highly preferred embodiment the cancer is a solid tumor.

The inventive antibodies or antigen-binding fragments thereof can be used as a therapeutic or a diagnostic tool in a variety of situations with aberrant CEACAM6-signaling, e.g. cell proliferative disorders such as cancer or fibrotic diseases. Disorders and conditions particularly suitable for treatment with an antibody of the inventions are solid tumors, such as cancers of the breast, respiratory tract, brain, reproductive organs, digestive tract, urinary tract, eye, liver, skin, head and neck, thyroid, parathyroid, and their distant metastases. Those disorders also include lymphomas, sarcomas and leukemias.

Tumors of the digestive tract include, but are not limited to anal, colon, colorectal, esophageal, gallbladder, gastric, pancreatic, rectal, small-intestine, and salivary gland cancers.

Examples of esophageal cancer include, but are not limited to esophageal cell carcinomas and adenocarcinomas, as well as squamous cell carcinomas, leiomyosarcoma, malignant melanoma, rhabdomyosarcoma and lymphoma,.

Examples of gastric cancer include, but are not limited to intestinal type and diffuse type gastric adenocarcinoma.

Examples of pancreatic cancer include, but are not limited to ductal adenocarcinoma, adenosquamous carcinomas and pancreatic endocrine tumors.

Examples of breast cancer include, but are not limited to triple negative breast cancer, invasive ductal carcinoma, invasive lobular carcinoma, ductal carcinoma *in situ*, and lobular carcinoma *in situ*.

Examples of cancers of the respiratory tract include, but are not limited to small-cell and non-small-cell lung carcinoma, as well as bronchial adenoma and pleuropulmonary blastoma.

Examples of brain cancers include, but are not limited to brain stem and hypophtalmic glioma, cerebellar and cerebral astrocytoma, glioblastoma, medulloblastoma, ependymoma, as well as neuroectodermal and pineal tumor.

Tumors of the male reproductive organs include, but are not limited to prostate and testicular cancer. Tumors of the female reproductive organs include, but are not limited to endometrial, cervical, ovarian, vaginal and vulvar cancer, as well as sarcoma of the uterus.

Examples of ovarian cancer include, but are not limited to serous tumour, endometrioid tumor, mucinous cystadenocarcinoma, granulosa cell tumor, Sertoli-Leydig cell tumor and arrhenoblastoma

Examples of cervical cancer include, but are not limited to squamous cell carcinoma, adenocarcinoma, adenosquamous carcinoma, small cell carcinoma, neuroendocrine tumour, glassy cell carcinoma and villoglandular adenocarcinoma.

Tumors of the urinary tract include, but are not limited to bladder, penile, kidney, renal pelvis, ureter, urethral, and hereditary and sporadic papillary renal cancers.

Examples of kidney cancer include, but are not limited to renal cell carcinoma, urothelial cell carcinoma, juxtaglomerular cell tumor (reninoma), angiomyolipoma, renal oncocytoma, Bellini duct carcinoma, clear-cell sarcoma of the kidney, mesoblastic nephroma and Wilms' tumor.

Examples of bladder cancer include, but are not limited to transitional cell carcinoma, squamous cell carcinoma, adenocarcinoma, sarcoma and small cell carcinoma.

Eye cancers include, but are not limited to intraocular melanoma and retinoblastoma.

Examples of liver cancers include, but are not limited to hepatocellular carcinoma (liver cell carcinomas with or without fibrolamellar variant), cholangiocarcinoma (intrahepatic bile duct carcinoma), and mixed hepatocellular cholangiocarcinoma.

Skin cancers include, but are not limited to squamous cell carcinoma, Kaposi's sarcoma, malignant melanoma, Merkel cell skin cancer, and non-melanoma skin cancer.

Head-and-neck cancers include, but are not limited to squamous cell cancer of the head and neck, laryngeal, hypopharyngeal, nasopharyngeal, oropharyngeal cancer, salivary gland cancer, lip and oral cavity cancer, and squamous cell cancer.

Lymphomas include, but are not limited to AIDS-related lymphoma, non-Hodgkin's lymphoma, cutaneous T-cell lymphoma, Burkitt lymphoma, Hodgkin's disease, and lymphoma of the central nervous system.

Sarcomas include, but are not limited to sarcoma of the soft tissue, osteosarcoma, malignant fibrous histiocytoma, lymphosarcoma, and rhabdomyosarcoma.

Leukemias include, but are not limited to acute myeloid leukemia, acute lymphoblastic leukemia, chronic lymphocytic leukemia, chronic myelogenous leukemia, and hairy cell leukemia.

In a preferred embodiment, the antibodies of the invention or antigen-binding fragments thereof are suitable for a therapeutic or diagnostic method for the treatment or diagnosis of a cancer disease comprised in a group consisting of colorectal cancer, non-small-cell lung cancer (NSCLC), small cell lung cancer (SCLC), pancreatic cancer, gastric cancer, breast cancer and multiple myeloma.

In addition, the inventive antibodies or antigen-binding fragments thereof can also be used as a therapeutic or a diagnostic tool in a variety of other disorders wherein CEACAM6 is involved such as, but not limited to lung infection e.g. influenza,

Crohns disease, inflammatory bowel disease, psoriasis, lung cystic fibrosis, prevention of bacterial docking to GI-intract, trauma, bleeding burn, surgery, stroke, myocardial infarction, sepsis, pneumonia, vaccination for infection & cancer, chronic virus infection.

The disorders mentioned above have been well characterized in humans, but also exist with a similar etiology in other animals, including mammals, and can be treated by administering pharmaceutical compositions of the present invention.

An antibody of the invention or an antigen-binding fragment thereof or a variant thereof might be co-administered with known medicaments, and in some instances the antibody might itself be modified. For example, an antibody or an antigen-binding fragment thereof or a variant thereof could be conjugated to a cytotoxic agent or radioisotope to potentially further increase efficacy.

Antibodies of the present invention or antigen-binding fragments thereof or variants thereof may be administered as the sole pharmaceutical agent or in combination with one or more additional therapeutic agents where the combination causes no unacceptable adverse effects. This combination therapy includes administration of a single pharmaceutical dosage formulation which contains an antibody of the invention or an antigen-binding fragment thereof or a variants thereof and one or more additional therapeutic agents, as well as administration of an antibody of the invention and each additional therapeutic agent in its own separate pharmaceutical dosage formulation. For example, an antibody of the invention or an antigen-binding fragment thereof or a variant thereof and a therapeutic agent may be administered to the patient together in a single liquid composition, or each agent may be administered in separate dosage formulation.

Where separate dosage formulations are used, an antibody of the invention or an antigen-binding fragment thereof or a variants thereof and one or more additional therapeutic agents may be administered at essentially the same time (*e.g.*, concurrently) or at separately staggered times (*e.g.*, sequentially).

In particular, antibodies of the present invention or antigen-binding fragments thereof or variants thereof may be used in fixed or separate combination with other anti-tumor agents such as alkylating agents, anti-metabolites, plant-derived anti-tumor agents, hormonal therapy agents, topoisomerase inhibitors, immunologicals,

antibodies, antibody drugs, biological response modifiers, anti-angiogenic compounds, cell therapies, and other anti-tumor drugs including but not limited to camptothecin derivatives, kinase inhibitors, targeted drugs.

In this regard, the following is a non-limiting list of examples of secondary agents that may be used in combination with the antibodies of the present invention:

Alkylating agents include, but are not limited to, nitrogen mustard N-oxide, cyclophosphamide, ifosfamide, thiotepa, ranimustine, nimustine, temozolomide, altretamine, apaziquone, brostallicin, bendamustine, carmustine, estramustine, fotemustine, glufosfamide, mafosfamide, bendamustin, and mitolactol; platinum-coordinated alkylating compounds include, but are not limited to, cisplatin, carboplatin, eptaplatin, lobaplatin, nedaplatin, oxaliplatin, and satraplatin;

Anti-metabolites include, but are not limited to, methotrexate, 6-mercaptopurine riboside, mercaptopurine, 5-fluorouracil alone or in combination with leucovorin, tegafur, doxifluridine, carmofur, cytarabine, cytarabine ocfosfate, enocitabine, gemcitabine, fludarabin, 5-azacitidine, capecitabine, cladribine, clofarabine, decitabine, eflornithine, ethynylcytidine, cytosine arabinoside, hydroxyurea, melphalan, nelarabine, nolatrexed, ocfosfite, disodium premetrexed, pentostatin, pelitrexol, raltitrexed, triapine, trimetrexate, vidarabine, vincristine, and vinorelbine;

Hormonal therapy agents include, but are not limited to, exemestane, Lupron, anastrozole, doxercalciferol, fadrozole, formestane, 11-beta hydroxysteroid dehydrogenase 1 inhibitors, 17-alpha hydroxylase/17,20 lyase inhibitors such as abiraterone acetate, 5-alpha reductase inhibitors such as finasteride and epristeride, anti-estrogens such as tamoxifen citrate and fulvestrant, Trelstar, toremifene, raloxifene, lasofoxifene, letrozole, anti-androgens such as bicalutamide, flutamide, mifepristone, nilutamide, Casodex, and anti-progesterones and combinations thereof;

Plant-derived anti-tumor substances include, e.g., those selected from mitotic inhibitors, for example epothilones such as sagopilone, ixabepilone and epothilone B, vinblastine, vinflunine, docetaxel, and Paclitaxel;

Cytotoxic topoisomerase inhibiting agents include, but are not limited to, aclarubicin, doxorubicin, amonafide, belotecan, camptothecin, 10-hydroxycamptothecin, 9-aminocamptothecin, diflomotecan, Irinotecan, topotecan, edotecarin, epimbicin, etoposide, exatecan, gimatecan, lurtotecan, mitoxantrone, pirambicin, pixantrone, rubitecan, sobuzoxane, tafluposide, and combinations thereof;

Immunologicals include interferons such as interferon alpha, interferon alpha-2a, interferon alpha-2b, interferon beta, interferon gamma-1a and interferon gamma-n1, GM-CSF and other immune enhancing agents such as L19-IL2 and other IL2 derivatives, filgrastim, lentinan, sizofilan, TheraCys, ubenimex, aldesleukin, alemtuzumab, BAM-002, dacarbazine, daclizumab, denileukin, gemtuzumab, ozogamicin, ibritumomab, imiquimod, lenograstim, lentinan, melanoma vaccine (Corixa), molgramostim, sargramostim, tasonermin, tecleukin, thymalasin, tositumomab, Vimlizin, epratuzumab, mitumomab, oregovomab, pemtumomab, and Provenge; ALNX6000, Urelumab, PF-005082566, Galunisertib, AZ10606120, NF340, BMS-777607;

Immunologicals also include drugs directed towards immune checkpoint modulators or co-inhibitory receptors including but not limited to CTLA-4, PD1, PD-L1, B7-H3 receptor, B7-H4 receptor, BTLA, TIM3, LAG3, KIRDL, 2B4, VISTA, CD244, CD160, TIGIT, CEACAM1, CEACAM5, HHLA2. Specifically some of these drugs are Ipilimumab, Tremelimumab, Nivolumab, Pembrolizumab, Pidilizumab, AMP-224, AMP-514, PDR001, MDX1105, BMS-936,559, Atezolizumab, Medi4736, Avelumab, MSB0010718C, MGA271, IMP321, BMS-986,016, Bavituximab, MNRP1685A, Celecoxib, PF-04418948, RQ-15986;

Immunologicals also include activators of co-stimulatory receptors including drugs directed towards but not limited to CD28, ICOS, 4-1BB, OX40, CD27, KIRDS, GITR, HVEM, TNFRSF25, CD40L. TMIGD2, TIM-1, CEACAM1, CEACAM5. Among those drugs are CP-870893, Lucatumumab, Dacetuzumab, Anti-OX40, MEDI0562, MEDI6469, MEDI6383, CDX-1127, TRX518, Varlilumab;

Immunologicals also include agents that modulate Treg activity including those directed but not limited to FOXP3, CD25, CCR4. Among those agents is daclizumab;

Immunologicals also include agents that modulate the activity of myeloid derived suppressor cells including those directed but not limited to CSF1R. An example is emactuzumab, Taladafil;

Immunologicals also include agents which modulate the innate immune cell response including agents directed to Toll-like receptors including but not limited to TLR3, TLR4, TLR7, TLR8, TLR9, NGK2A, NKG2D. These drugs are for example Imiquimod, CPG7909 (PF-3512676, CPG2006); MGN1703, SD-101, hiltonol (Poly ICLC), Anti-NGK2A (IPH2201), OM-174, 852A, VTX-2337, IMO-2055;

Immunologicals also include drugs which modulate the innate immune cell response including drugs directed but not limited to CSF-1, CSF1R, KIR, ILTs, LIRs, MICA, MICB, CD244, CCL2, CD47. Specifically some of these drugs are Anti-KIR (IHP2101; IPH2101; 1-7F9); Lirilumab (IPH2012; BMS-986,015); Carlumab (CNTO888), IMC-CS4, FPA008, PLX3397, ARRY-382, CC-90002, Anti-CD47 (Hu5F9-G4), BLZ945;

Immunologicals also include agents for immune cell retargeting including but not limited to bispecific antibodies, Darts e.g. against B7-H3, Bites e.g CD19xCD3; e.g. Removab anti-EPCAMxCD3xFC, NK cell targeting agents;

Immunologicals also include agents which modulate the tumor microenvironment and improve immune cell infiltration and response including Vaccines and Adjuvants and which are not limited to GVAX, FVAX;

In this regard Vaccines comprise dendritic cell-based vaccines, viral vaccines, mRNA based vaxxines, multipeptide based vaccines;

Immunologicals also include agents for improved immune cell infiltration including but not limited to IFN-g, IL15, IL21, IL2, CXCR4, CXCl12, Some of these drugs are Denenicokin (BMS982, 470), ALT-803, hetIL15, Ulocuplumab, BKT140, CXCR2-specific mab, AD3100, Maravirox, PF-4136309;

Immunologicals also include agents or modalities which improve the priming and activation of APCs and T cells including drugs directed to but not limited to m-TOR GSK3beta inhibitors, loaded DCs (e.g. Provenge), Radiation therapy, external beam radiation;

Immunologicals also include Kynurenine pathway modulators including drugs directed to but not limited to IDO1, IDO2, TDO. Among those drugs are INCB024360, Indoximod (NLG8189; 1-methyl-D-tryptophan, D-1MT), GDC-0919, NLG919, LM10;

Immunologicals also include Adenosine Pathway modulators including drugs directed to but not limited to CD39, CD73, A2A receptor, A2B receptor. Such drugs include Compound9, NCX-4016, AT38, SCH58261, SCH420814, PSB1115, ARL67176, AMPCP;

Immunologicals also include TGFbeta/ALK5 pathway modulator. Such drugs include OY2157299, EW-7187;

Immunologicals also include Sting activators;

Biological response modifiers are agents that modify defense mechanisms of living organisms or biological responses such as survival, growth or differentiation of tissue cells to direct them to have anti-tumor activity; such agents include, e.g., krestin, lentinan, sizofiran, picibanil, ProMune, and ubenimex;

Anti-angiogenic compounds include, but are not limited to, acitretin, aflibercept, angiostatin, aplidine, asentar, axitinib, bevacizumab, brivanib alaninat, cilengtide, combretastatin, endostatin, fenretinide, halofuginone, pazopanib, ranibizumab, rebimastat, recentin, regorafenib, removab, revlimid, sorafenib, squalamine, sunitinib, telatinib, thalidomide, ukrain, vatalanib, and vitaxin;

Antiangiogenic agents also include VEGF inhibitors including but not limited to sorafenib, regorafenib, bevacizumab, sunitinib, recentin, axitinib, aflibercept, telatinib, brivanib alaninate, vatalanib, pazopanib, and ranibizumab;

Antibody drugs include, but are not limited to, trastuzumab, cetuximab, bevacizumab, rituximab, ticilimumab, ipilimumab, tremelimumab, pembrolizumab, nivolumab, Pidilizumab, RG-7446/ MPDL3280A, BMS-936559 (MDX1105), Durvalumab (Medi-4736), MSB-0010718C, lumiliximab, catumaxomab, atacicept, oregovomab, panitumumab and alemtuzumab;

Antibody drugs also include antibody drug conjugates including but not limited to those targeting Mesothelin, C4.4A, FGFR2, HER2, PSMA;

Antibody drugs also include Thorium targeted conjugates but not limited to those targeting Mesothelin, C4.4A, FGFR2, HER2, PSMA, CEACAM6;

Antibody drugs also include bispecific (or multispecific) antibody formats including but not limited to bispecific (or multispecific) IgGs and bispecific (or multispecific) antibody fragments as well as protein fusions and conjugates thereof (e.g. CrossMab, DAF(2in1), DAF(4in1), DutaMab, DT-IgG, KiHassembled IgG, charge pair assembled IgG, KiH-commonLC, Fab-arm exchange, SEEDbody, Triomab, LUZ-Y, Fcab, κλ-mAb, orthogonal Fab, DVD-IgG, IgG(H)-scFv, scFv-(H)IgG, IgG(L)-scFv, scFv-(L)IgG, IgG(L,H)-Fv, IgG(H)-V, V(H)-IgG, IgG(L)-V, V(L)-IgG, KIH-IgG-scFab, 2scFv-IgG, IgG-2scFv, scFv4-Ig, Zybody, DVI-IgG (4in1), di-nanobody, BiTE, Diabody, DART, DART-Fc, TandAb, scDiabody, scDIabody-CH3, Diabody-CH3, Triple Body, Miniantibody, Minibody, TriBi minibody, scFv-CH3 KIH, Fab-scFv, scFv-CH-CL-scFv, F(ab')2, F(ab')2-scFv2, scFv- KIH, Fab-scFv-Fc, Tetravalent HCAb, scDiabody-Fc, Diabody-Fc, Tandem scFv-Fc, Intrabody, Dock and Lock fusion, ImmTAC, HSAbody,

scDiabody-HAS, Tandem scFv-toxin, IgG-IgG, Cov-X-Body, scFv1-PEG-scFv2 and others);

Antibody drugs also include recombinant proteins generated by recombinant technologies with antibody-like binding properties such as but not limited to DARPIN molecules;

Cell therapies include, but are not limited to tumor infiltrating lymphocyte isolated from cancer patients such as Ex vivo stimulated T cells e.g. Sipuleucel-T;

Cell therapies include, but are not limited to tumor infiltrating lymphocyte isolated from cancer patients such as Sipuleucel-T and genetically engineered T cells bearing chimeric antigen receptors (CARs) such as e.g. CD19-CAR-T cells; CAR-Her2-T-cells;

Other anti-cancer agents including, e.g., alitretinoin, ampligen, atrasentan bexarotene, bortezomib, bosentan, calcitriol, exisulind, fotemustine, ibandronic acid, miltefosine, mitoxantrone, l-asparaginase, procarbazine, dacarbazine, hydroxycarbamide, pegaspargase, pentostatin, tazaroten, velcade, gallium nitrate, canfosfamide, darinaparsin, and tretinoin, PI3065, TG100-115;

EGFR (HER1) inhibitors such as, e.g., cetuximab, panitumumab, vectibix, gefitinib, erlotinib, and Zactima;

HER2 inhibitors such as, e.g., lapatinib, tratuzumab, and pertuzumab;

mTOR inhibitors such as, e.g., temsirolimus, sirolimus/Rapamycin, and everolimus;

c-Met inhibitors;

PI3K inhibitors such as PI3K inhibitor 1 (2-amino-N-[7-methoxy-8-(3-morpholin-4-ylpropoxy)-2,3-dihydroimidazo[1,2-c]quinazolin-5-yl]pyrimidine-5-carboxamide dihydrochloride (see compound of Examples 1 and 2 WO 2012/136553)

and AKT inhibitors;

CDK inhibitors such as roscovitine and flavopiridol;

Spindle assembly checkpoints inhibitors and targeted anti-mitotic agents such as PLK inhibitors, Aurora inhibitors (e.g. Hesperadin), checkpoint kinase inhibitors, and KSP inhibitors;

BRAFV600E inhibitors such as Vemurafenib, Dabrafenib;

HDAC inhibitors such as, e.g., panobinostat, vorinostat, MS275, belinostat, and LBH589;

HSP90 and HSP70 inhibitors;

Proteasome inhibitors such as bortezomib and carfilzomib;

Serine/threonine kinase inhibitors including MEK inhibitors and Raf inhibitors such as sorafenib;

Farnesyl transferase inhibitors such as, e.g., tipifarnib;

Tyrosine kinase inhibitors including, e.g., dasatinib, nilotibib, regorafenib, bosutinib, sorafenib, bevacizumab, sunitinib, cediranib, axitinib, aflibercept, telatinib, imatinib mesylate, brivanib alaninate, pazopanib, ranibizumab, vatalanib, cetuximab, panitumumab, vectibix, gefitinib, erlotinib, lapatinib, tratuzumab, pertuzumab, and c-Kit inhibitors;

Vitamin D receptor agonists;

Bcl-2 protein inhibitors such as obatoclax, oblimersen sodium, and gossypol;

Cluster of differentiation 20 receptor antagonists such as, e.g., rituximab;

Ribonucleotide reductase inhibitors such as, e.g., gemcitabine;

Tumor necrosis factor related apoptosis inducing ligand receptor 1 agonists such as, e.g., mapatumumab;

Tumor necrosis factor related apoptosis inducing ligand receptor 2 agonists such as e.g., lexatumumab, conatumumab, CS-1008, PRO95780;

5-Hydroxytryptamine receptor antagonists such as, e.g., rEV598, xaliprode, palonosetron hydrochloride, granisetron, Zindol, and AB-1001;

Integrin inhibitors including alpha5-beta1 integrin inhibitors such as, e.g., E7820, JSM 6425, volociximab, and endostatin;

Androgen receptor antagonists including, e.g., nandrolone decanoate, fluoxymesterone, Android, Prost-aid, andromustine, bicalutamide, flutamide, apo-cyproterone, apo-flutamide, chlormadinone acetate, Androcur, Tabi, cyproterone acetate, and nilutamide;

Aromatase inhibitors such as, e.g., anastrozole, letrozole, testolactone, exemestane, aminoglutethimide, and formestane;

Matrix metalloproteinase inhibitors;

In addition, the antibodies of the invention can be combined with modalities which cause immunogenic cell death including but not limited to ultraviolet light, oxidizing treatments, heat shock, targeted and untargeted radiotherapy, shikonin, high-hydrostatic pressure, oncolytic viruses, and photodynamic therapy;

In addition, the antibodies of the invention can be combined with agents which cause immunogenic cell death including but not limited to sunitinib, JAK2 inhibitors, anthracyclincs, doxorubicin, mitoxantrone, oxaliplatin, and cyclophosphamide, targeted and untargeted microtubule-destabilizing drugs (like e.g. auristatins and maytansinoids);

The compounds of the present invention may also be employed in cancer treatment in conjunction with radiation therapy and/or surgical intervention;

Furthermore, the antibodies of the invention may be utilized, as such or in compositions, in research and diagnostics, or as analytical reference standards, and the like, which are well known in the art;

Diagnostic Methods

Anti-CEACAM6 antibodies or antigen-binding fragments thereof can be used for detecting the presence of CEACAM6-expressing tumors. The presence of CEACAM6-containing cells or shed CEACAM6 within various biological samples, including serum, and tissue biopsy specimens, may be detected with anti-CEACAM6 antibodies. In addition, anti-CEACAM6 antibodies may be used in various imaging methodologies such as immunoscintigraphy with a ^{99}Tc (or other isotope) conjugated antibody. For example, an imaging protocol similar to the one described using a ^{111}In conjugated anti-PSMA antibody may be used to detect pancreatic or ovarian carcinomas (Sodee et al., Clin. Nuc. Med. 21: 759-766, 1997). Another method of detection that can be used is positron emitting tomography by conjugating the antibodies of the invention with a suitable isotope (see Herzog et al., J. Nucl. Med. 34:2222-2226, 1993).

Pharmaceutical Compositions and Administration

To treat any of the foregoing disorders, pharmaceutical compositions for use in accordance with the present invention may be formulated in a conventional manner using one or more physiologically acceptable carriers or excipients. An antibody of the

invention or antigen-binding fragment thereof can be administered by any suitable means, which can vary, depending on the type of disorder being treated. Possible administration routes include parenteral (*e.g.*, intramuscular, intravenous, intra-arterial, intraperitoneal, or subcutaneous), intrapulmonary and intranasal, and, if desired for local immunosuppressive treatment, intralesional administration. In addition, an antibody of the invention or an antigen-binding fragment thereof or a variant thereof might be administered by pulse infusion, with, *e.g.,* declining doses of the antibody. Preferably, the dosing is given by injections, most preferably intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. The amount to be administered will depend on a variety of factors such as the clinical symptoms, weight of the individual, whether other drugs are administered. The skilled artisan will recognize that the route of administration will vary depending on the disorder or condition to be treated.

An embodiment of the present invention are pharmaceutical compositions which comprise anti-CEACAM6 antibodies or antigen-binding fragments thereof or variants thereof, alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. A further embodiment are pharmaceutical compositions comprising a CEACAM6 binding antibody or antigen-binding fragment thereof and a further pharmaceutically active compound that is suitable to treat CEACAM6 related diseases such as cancer. Any of these molecules can be administered to a patient alone, or in combination with other agents, drugs or hormones, in pharmaceutical compositions where it is mixed with excipient(s) or pharmaceutically acceptable carriers. In one embodiment of the present invention, the pharmaceutically acceptable carrier is pharmaceutically inert.

The present invention also relates to the administration of pharmaceutical compositions. Such administration is accomplished orally or parenterally. Methods of parenteral delivery include topical, intra-arterial (directly to the tumor), intramuscular, subcutaneous, intramedullary, intrathecal, intraventricular, intravenous, intraperitoneal, or intranasal administration. In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Ed. Maack Publishing Co, Easton, Pa.).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as methyl-cellulose, hydroxypropylmethylcellulose, or sodium carboxymethyl cellulose; and gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores can be provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e. dosage.

Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations for parenteral administration include aqueous solutions of active compounds. For injection, the pharmaceutical compositions of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances that increase viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or

dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with acids, including but not limited to hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents that are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder in 1 mM - 50 mM histidine or phosphate or Tris, 0.1%-2% sucrose and / or 2%-7% mannitol at a pH range of 4.5 to 7.5 optionally comprising additional substances like polysorbate that is combined with buffer prior to use.

After pharmaceutical compositions comprising a compound of the invention formulated in an acceptable carrier have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of anti-CEACAM6 antibodies or antigen-binding fragment thereof, such labeling would include amount, frequency and method of administration.

Kits

The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

Therapeutically Effective Dose

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose, i.e. treatment of a particular disease state characterized by CEACAM6 expression.

The determination of an effective dose is well within the capability of those skilled in the art.

Determining a therapeutically effective amount of the novel antibody of this invention or an antigen-binding fragment thereof or a variant thereof, largely will depend on particular patient characteristics, route of administration, and the nature of the disorder being treated. General guidance can be found, for example, in the publications of the International Conference on Harmonization and in REMINGTON'S PHARMACEUTICAL SCIENCES, chapters 27 and 28, pp. 484-528 (18th ed., Alfonso R. Gennaro, Ed., Easton, Pa.: Mack Pub. Co., 1990). More specifically, determining a therapeutically effective amount will depend on such factors as toxicity and efficacy of the medicament. Toxicity may be determined using methods well known in the art and found in the foregoing references. Efficacy may be determined utilizing the same guidance in conjunction with the methods described below in the Examples.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., neoplastic cells, or in animal models, usually mice, rabbits, dogs, pigs or monkeys. The animal model is also used to achieve a desirable concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of antibody or antigen-binding fragment thereof, that ameliorate the symptoms or condition. Therapeutic efficacy and toxicity of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ED_{50} (the dose therapeutically effective in 50% of the population) and LD_{50} (the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic index, and it can be expressed as the ratio, ED_{50}/LD_{50}. Pharmaceutical compositions that exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used in formulating a range of dosage for human use. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage

varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage is chosen by the individual physician in view of the patient to be treated. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Additional factors that may be taken into account include the severity of the disease state, e.g., tumor size and location; age, weight and gender of the patient; diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long acting pharmaceutical compositions might be administered for example every 3 to 4 days, every week, once every two weeks, or once every three weeks, depending on half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 10 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature. See U.S. Pat. No. 4,657,760; 5,206,344; or 5,225,212. Those skilled in the art will employ different formulations for polynucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc. Preferred specific activities for a radiolabelled antibody may range from 0.1 to 10 mCi/mg of protein (Riva et al., Clin. Cancer Res. 5:3275-3280, 1999; Ulaner et al., 2008 Radiology 246(3):895-902)

A further preferred embodiment of the invention is:

1. An isolated antibody or antigen-binding fragment thereof specifically binding to human CEACAM6 and to Macaca fascicularis CEACAM6.

2. An isolated antibody or antigen-binding fragment thereof specifically binding to the mature extracellular domain of human CEACAM6 (represented by amino acids at position 35-320 of SEQ-ID No: 179) and to the mature extracellular domain of Macaca fascicularis CEACAM6 (represented by amino acids at position 35-320 of SEQ-ID No: 177).

3. An isolated antibody or antigen-binding fragment thereof specifically binding to human CEACAM6 domain 1 (represented by amino acids 35 – 142 of

SEQ-ID NO:179) and to Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177).

4. An isolated antibody or antigen-binding fragment thereof specifically binding to a protein comprising human CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:179) and to a protein comprising Macaca fascicularis CEACAM6 domain 1 (represented by amino acids 35 – 142 of SEQ-ID NO:177).

5. The antibody or antigen-binding fragment thereof according to any one of embodiments 1 to 4, which does not significantly cross-react with human CEACAM1, human CEACAM3, and human CEACAM5.

6. The antibody or antigen-binding fragment thereof according to any one of embodiments 1 to 5 able to bind to human and Macaca fascicularis CEACAM6, or the mature extracellular domain thereof, or the domain 1 thereof and the affinities are within one order of magnitude of monovalent K_D.

7. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which competes for binding to the 9A6 antibody (Genovac/Aldevron) on human CEACAM6.

8. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which interferes with the CEACAM6 and CEACAM1 interaction.

9. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which is able to change the cytokine profile of tumor antigen specific T cells towards a more activated phenotype characterized by an IFN-gamma secretion increase, preferably by a ≥ 1.5 times (1.5 times or higher) increase compared to control samples.

10. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which is able to induce immunomodulation.

11. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which is able to relieve CEACAM6 mediated immunosuppression of tumor antigen specific T cells as measured by either

IFN-gamma secretion of tumor antigen specific T cells or the number of IFN-gamma secreting activated T cells.

12. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which is able to change the cytokine profile of tumor antigen specific T cells towards a more cytotoxic and / or activated phenotype characterized by an IFN-gamma and / or IL-2 and / or TNF-alpha secretion increase, preferably by a ≥ 1.5 times (1.5 times or higher) increase of IFN-gamma and / or IL-2 and / or TNF-alpha secretion compared to control samples.

13. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments which binds to an epitope of human CEACAM6, wherein said epitope comprises one or more amino acid residues selected from the group consisting of Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

14. The antibody or antigen-binding fragment thereof according to embodiment 13 which binds to an epitope of human CEACAM6, wherein said epitope comprises the amino acid residues Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 of SEQ ID NO: 179.

15. The antibody or antigen-binding fragment thereof according to embodiment 13 or 14 which binds to a human CEACAM6 protein comprising an Ile63Leu mutation and which does not bind to a human CEACAM6 protein comprising an Ile63Phe mutation according to SEQ ID NO: 179 numbering.

16. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments comprising:

i. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:48, an H-CDR2 comprising SEQ ID NO:49, and an H-CDR3 comprising SEQ ID NO:50 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:52, a L-CDR2 comprising SEQ ID NO:53, and a L-CDR3 comprising SEQ ID NO:54, or

ii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:106, an H-CDR2 comprising SEQ ID NO:107, and an H-CDR3 comprising SEQ ID NO:108 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:110, a L-CDR2 comprising SEQ ID NO:111, and a L-CDR3 comprising SEQ ID NO:112, or

iii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:4, an H-CDR2 comprising SEQ ID NO:5, and an H-CDR3 comprising SEQ ID NO:6 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:8, a L-CDR2 comprising SEQ ID NO:9, and a L-CDR3 comprising SEQ ID NO:10, or

iv. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:34, an H-CDR2 comprising SEQ ID NO:35, and an H-CDR3 comprising SEQ ID NO:36 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:38, a L-CDR2 comprising SEQ ID NO:39, and a L-CDR3 comprising SEQ ID NO:40, or

v. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:120, an H-CDR2 comprising SEQ ID NO:121, and an H-CDR3 comprising SEQ ID NO:122 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:124, a L-CDR2 comprising SEQ ID NO:125, and a L-CDR3 comprising SEQ ID NO:126, or

vi. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:24, an H-CDR2 comprising SEQ ID NO:25, and an H-CDR3 comprising SEQ ID NO:26 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:28, a L-CDR2 comprising SEQ ID NO:29, and a L-CDR3 comprising SEQ ID NO:30, or

vii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:76, an H-CDR2 comprising SEQ

ID NO:77, and an H-CDR3 comprising SEQ ID NO:78 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:80, a L-CDR2 comprising SEQ ID NO:81, and a L-CDR3 comprising SEQ ID NO:82, or

viii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:134, an H-CDR2 comprising SEQ ID NO:135, and an H-CDR3 comprising SEQ ID NO:136 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:138, a L-CDR2 comprising SEQ ID NO:139, and a L-CDR3 comprising SEQ ID NO:140, or

ix. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:148, an H-CDR2 comprising SEQ ID NO:149, and an H-CDR3 comprising SEQ ID NO:150 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:152, a L-CDR2 comprising SEQ ID NO:153, and a L-CDR3 comprising SEQ ID NO:154, or

x. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:14, an H-CDR2 comprising SEQ ID NO:15, and an H-CDR3 comprising SEQ ID NO:16 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:18, a L-CDR2 comprising SEQ ID NO:19, and a L-CDR3 comprising SEQ ID NO:20, or

xi. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:62, an H-CDR2 comprising SEQ ID NO:63, and an H-CDR3 comprising SEQ ID NO:64 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:66, a L-CDR2 comprising SEQ ID NO:67, and a L-CDR3 comprising SEQ ID NO:68, or

xii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:92, an H-CDR2 comprising SEQ ID NO:93, and an H-CDR3 comprising SEQ ID NO:94 and a light chain antigen-binding region that comprises a L-CDR1

comprising SEQ ID NO:96, a L-CDR2 comprising SEQ ID NO:97, and a L-CDR3 comprising SEQ ID NO:98.

17. The antibody or antigen-binding fragment thereof according to any one of the preceding embodiments comprising:

i. a variable heavy chain sequence as presented by SEQ ID NO: 47 and a variable light chain sequence as presented by SEQ ID NO: 51, or

ii. a variable heavy chain sequence as presented by SEQ ID NO: 105 and a variable light chain sequence as presented by SEQ ID NO: 109, or

iii. a variable heavy chain sequence as presented by SEQ ID NO: 3 and a variable light chain sequence as presented by SEQ ID NO: 7, or

iv. a variable heavy chain sequence as presented by SEQ ID NO: 33 and a variable light chain sequence as presented by SEQ ID NO: 37, or

v. a variable heavy chain sequence as presented by SEQ ID NO: 119 and a variable light chain sequence as presented by SEQ ID NO: 123, or

vi. a variable heavy chain sequence as presented by SEQ ID NO: 23 and a variable light chain sequence as presented by SEQ ID NO: 27, or

vii. a variable heavy chain sequence as presented by SEQ ID NO: 75 and a variable light chain sequence as presented by SEQ ID NO: 79, or

viii. a variable heavy chain sequence as presented by SEQ ID NO: 133 and a variable light chain sequence as presented by SEQ ID NO: 137, or

ix. a variable heavy chain sequence as presented by SEQ ID NO: 147 and a variable light chain sequence as presented by SEQ ID NO: 151, or

x. a variable heavy chain sequence as presented by SEQ ID NO: 13 and a variable light chain sequence as presented by SEQ ID NO: 17, or

xi. a variable heavy chain sequence as presented by SEQ ID NO: 61 and a variable light chain sequence as presented by SEQ ID NO: 65, or

xii. a variable heavy chain sequence as presented by SEQ ID NO: 91 and a variable light chain sequence as presented by SEQ ID NO: 95.

18. The antibody according to any one of the preceding embodiments, which is an IgG antibody.

19. The antibody according to embodiment 18 comprising:

i. a heavy chain region corresponding to SEQ ID NO: 57 and a light chain region corresponding to SEQ ID NO: 58, or

ii. a heavy chain region corresponding to SEQ ID NO: 115 and a light chain region corresponding to SEQ ID NO: 116, or

iii. a heavy chain region corresponding to SEQ ID NO: 43 and a light chain region corresponding to SEQ ID NO: 44, or

iv. a heavy chain region corresponding to SEQ ID NO: 129 and a light chain region corresponding to SEQ ID NO: 130, or

v. a heavy chain region corresponding to SEQ ID NO: 85 and a light chain region corresponding to SEQ ID NO: 86, or

vi. a heavy chain region corresponding to SEQ ID NO: 143 and a light chain region corresponding to SEQ ID NO: 144, or

vii. a heavy chain region corresponding to SEQ ID NO: 157 and a light chain region corresponding to SEQ ID NO: 158, or

viii. a heavy chain region corresponding to SEQ ID NO: 71 and a light chain region corresponding to SEQ ID NO: 72, or

ix. a heavy chain region corresponding to SEQ ID NO: 101 and a light chain region corresponding to SEQ ID NO: 102.

20. The antigen-binding fragment according to embodiments 1 to 17, which is an scFv, Fab, Fab' fragment or a $F(ab')_2$ fragment.

21. The antibody or antigen-binding fragment according to any one of the preceding embodiments, which is a monoclonal antibody or antigen-binding fragment.

22. The antibody or antigen-binding fragment according to any one of the preceding embodiments, which is human, humanized or chimeric antibody or antigen-binding fragment.

23. An antibody-drug conjugate, comprising an antibody or antigen binding fragment thereof according to any one of the embodiments 1 to 22.

24. An isolated nucleic acid sequence that encodes the antibody or antigen-binding fragment according to any one of the embodiments 1 to 22.

25. A vector comprising a nucleic acid sequence according to embodiment 24.

26. An isolated cell expressing an antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 and / or comprising a nucleic acid according to embodiment 24 or a vector according to embodiment 25.

27. An isolated cell according to embodiment 26, wherein said cell is a prokaryotic or an eukaryotic cell.

28. A method of producing an antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 comprising culturing of a cell according to embodiment 27 and purification of the antibody or antigen-binding fragment.

29. An antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 or an antibody-drug conjugate according to embodiment 23 for use as a medicament.

30. An antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 or an antibody-drug conjugate according to embodiment 23 for use as a diagnostic agent.

31. An antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 or an antibody-drug conjugate according to embodiment 23 for use as a medicament for the treatment of cancer.

32. An antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 or an antibody-drug conjugate according to embodiment 23 in the manufacture of a medicament for the treatment of a disease.

33. An antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 or an antibody-drug conjugate according to embodiment 23 in the manufacture of a medicament for the treatment of cancer.

34. A pharmaceutical composition comprising an antibody or antigen-binding fragment according to any one of the embodiments 1 to 22 or an antibody-drug conjugate according to embodiment 23.

35. A combination of a pharmaceutical composition according to embodiment 34 and one or more therapeutically active compounds.

36. A method for treating a disorder or condition associated with the undesired presence of CEACAM6, comprising administering to a subject in need thereof an effective amount of the pharmaceutical composition according to embodiment 34 or a combination according to embodiment 35.

37. A process for the preparation of anti-CEACAM6 antibodies specifically binding to human CEACAM6 and Macaca fascicularis CEACAM6, which process comprises immunization of an animal, preferentially a mouse, with a protein comprising cynomolgus CECAM6 domain 1 represented by amino acids 35 – 142 of SEQ-ID NO:177, determining the amino acid sequence of

antibodies specifically binding to human CEACAM6 and to cynomolgus CEACAM6, followed optionally by humanization or generation of a chimeric antibody, and recombinant expression of said antibodies.

EXAMPLES

The present invention is further described by the following examples. The examples are provided solely to illustrate the invention by reference to specific embodiments. These exemplifications, while illustrating certain specific aspects of the invention, do not portray the limitations or circumscribe the scope of the disclosed invention.

All examples were carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. Routine molecular biology techniques of the following examples can be carried out as described in standard laboratory manuals, such as Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

Example 1: Monkey CEACAM6 Sequences & Tool Generation

An overview of protein sequences of antigens and reference compounds used is provided in Table 2:

Name	Protein-ID	Description	SEQ-ID
human CEACAM6	TPP-4639	full-length	SEQ-ID NO:179
Macaca fascicularis CEACAM6	TPP-4189	full-length	SEQ-ID NO:177
human CEACAM1	TPP-4185	full-length	SEQ-ID NO:173
human CEACAM3	TPP-4187	full-length	SEQ-ID NO:175
human CEACAM5	TPP-4188	full-length	SEQ-ID NO:176
human CEACAM8	TPP-4190	full-length	SEQ-ID NO:178
human CEACAM19	TPP-4186	full-length	SEQ-ID NO:174
human CEACAM6	TPP-1436	extracellular (mature form) (R&D Systems 3934-CM)	SEQ-ID NO:162
human CEACAM1	TPP-1437	extracellular (mature	SEQ-ID NO:163

Name	Protein-ID	Description	SEQ-ID
		form) (R&D Systems 2244-CM)	
human CEACAM3	TPP-2755	extracellular (mature form) (Sino Biological Inc. 11933-H08H)	SEQ-ID NO:172
human CEACAM5	TPP-1438	extracellular (mature form) (R&D Systems 4128-CM)	SEQ-ID NO:164
Macaca mulatta CEACAM6-Xa-Fc-His	TPP-1306	extracellular (mature form), fusion to Xa-Fc-His	SEQ-ID NO:161
Human CEACAM6-Xa-Fc-His	TPP-1790	extracellular (mature form), fusion to Xa-Fc-His	SEQ-ID NO:165
Human CEACAM6-Dom1-MacMul-Xa-Fc-His	TPP-1791	extracellular (mature form), fusion to Xa-Fc-His, Domain 1 replaced by corresponding Macaca mulatta domain	SEQ-ID NO:166
Human CEACAM6-Dom2-MacMul-Xa-Fc-His	TPP-1792	extracellular (mature form), fusion to Xa-Fc-His, Domain 2 replaced by corresponding Macaca mulatta domain	SEQ-ID NO:167
Human CEACAM6-Dom3-MacMul-Xa-Fc-His	TPP-1793	extracellular (mature form), fusion to Xa-Fc-His, Domain 3 replaced by corresponding Macaca mulatta domain	SEQ-ID NO:168

Name	Protein-ID	Description	SEQ-ID
Human CEACAM6	APP-320	Extracellular (mature form), obtained by cleavage with Factor Xa of TPP-1790	
Human CEACAM6-Domain 1-His	TPP-1794	Domain 1, fusion to His (expressed in E. coli)	SEQ-ID NO:169
Macaca fascicularis CEACAM6-Xa-Fc-His	TPP-2443	extracellular (mature form), fusion to Xa-Fc-His	SEQ-ID NO:170
Macaca fascicularis CEACAM6	APP-319	extracellular (mature form), obtained by Factor Xa cleavage of TPP-2443	
Macaca fascicularis CEACAM6-Domain 1-Xa-Fc-His	TPP-2452	Domain 1, fusion to Xa-Fc-His	SEQ-ID NO:171
Macaca fascicularis CEACAM6-Domain 1	APP-325	Domain 1, obtained by Factor Xa cleavage of TPP-2452	
Neo201 (human IgG1)	TPP-1173	based on US20130189268	SEQ-ID NO:1 & SEQ-ID NO:2
Neo201 (human IgG2)	TPP-3688	based on US20130189268	SEQ-ID NO:89 & SEQ-ID:90
9A6 (mouse IgG1)	TPP-1744	Based on Genovac/Aldevron (GM-0509)	
9A6 (chimeric hIgG1)	TPP-1745	Based on Genovac/Aldevron (GM-0509)	
9A6 (chimeric hIgG2)	TPP-3470	Based on Genovac/Aldevron (GM-0509)	

Table 2: Name, Protein-IDs and SEQ-IDs used in this study

Protein sequences for human CEACAMs were obtained from UniProtKB/TrEMBL database: human CEACAM6 (P40199), human CEACAM1 (P13688), human CEACAM3 (P40198), human CEACAM5 (P06731), human CEACAM8 (P31997), human CEACAM19 (Q7Z692). The Macaca mulatta (rhesus monkey) protein sequence of CEACAM6 was also available (F6YVW1). The Macaca fascicularis (cynomolgus monkey) protein sequence of CEACAM6 was deduced from publicly available nucleotide sequences by a) applying common intron/exon splicing rules b) comparison to different monkey/primate protein sequences and c) conservation of genomic structure between human/primate/monkey. Cynomolgus CEACAM6 is represented by TPP-4189.

Recombinant extracellular domains of CEACAMs were obtained from commercial sources or produced in-house. To this end, the extracellular domains were C-terminally appended with a Factor Xa cleavage site, a human IgG1 Fc fragment as well as a His Tag and expressed in HEK293 cells using standard transient transfection procedures. Proteins were purified from the cell culture supernatant via Protein-A and size exclusion chromatography. In cases, in which the Fc-part needed to be removed, proteins were cleaved with Factor Xa according to the manufacturer's recommendations (e.g. Factor Xa Protease from Hematologic Technologies Inc. HTI No. HCXA-0060) and subsequently purified by Protein-A and size exclusion chromatography. In cases in which biotinylated proteins were needed, commercial biotinylation kits were used (e.g. EZ-Link Amine-PEG3-Biotin from Pierce #21347) and degree of biotinylation was characterized by commercial kits (e.g. Biotin Quantitation Kit from Pierce #28005).

The single N-terminal domain 1 of human CEACAM6 was produced as 6x His fused protein construct in E.coli BL21 DE3 using pET28a vector (Novagen). After overnight induction with IPTG at 37 °C, recombinant protein was isolated and refolded from inclusion bodies. Prior to refolding, inclusion bodies were washed in Tris buffer pH 8.5 containing 150 mM NaCl, 1 mM EDTA, 0.1% Tween20 and solubilized in the same buffer containing 8 M urea and no detergent. The solution was diluted (1:10) slowly into 50 mM CHES pH 9.2 containing 500 mM arginine and incubated at 4 °C for 16 h. Purification was achieved performing standard Nickel-NTA chromatography and size exclusion chromatography in 30 mM Tris buffer pH 8.5, 150 mM NaCl on Superdex 75.

The 9A6 murine IgG1 antibody (GM-0509) was obtained from Genovac and chimerized to human IgG1 and human IgG2. The basis of Neo201 protein sequence as either human IgG1 or human IgG2 was US20130189268. All antibodies were expressed in HEK293 cells using standard transient transfection procedures and purified from the cell culture supernatant via Protein-A and size exclusion chromatography.

Stable HeLa cell lines expressing different full-length human CEACAM-receptors were generated. Therefore sequences of the following receptors were transfected: human CEACAM1 (TPP-4185), human CEACAM3 (TPP-4187), human CEACAM5 (TPP-4188), human CEACAM6 (TPP-4639), human CEACAM8 (TPP-4190), human CEACEAM19 (TPP-4186) or cynomolgus CEACAM6 (TPP-4189). The HeLa cell line does not endogenously express any of these receptors on the surface as was confirmed by FACS analysis, and surface expression could only be detected after transfection of the respective CEACAM-receptor. Briefly, expression constructs were cloned into UCOE-based vectors (EMD Millipore Corporation) and transfected in HeLa cells. After selection with hygromycin, suitable stable clones were screened by Western blotting of total cell lysate as well as FACS staining of cellular surface using suitable antibodies (human CEACAM1: #MAB22441 from R&D Systems; human CEACAM5: #MAB41281 from R&D Systems; human CEACAM6: #MAB3934 from R&D Systems; human CEACAM8: ab90294 from abcam; human CEACAM19: #NBP1-70494 from Novus; human CEACAM3: AF4166 from R&D Systems; cynomolgus CEACAM6: Neo201-hIgG1).

Example 2: Characterization of immunomodulating 9A6-mIgG1 antibody

9A6 antibody has been described in the literature as being immunomodulatory (Witzens-Harig et al., Blood 2013 May 30;121(22):4493-503). This antibody was characterized with regards to its affinity, its selectivity towards other human CEACAMs, its cross-reactivity to monkey CEACAM6, its specific binding to a certain domain on CEACAM6, and its selectivity towards other human CEACAMs.

Affinity measurements using Surface Plasmon Resonance (SPR)

Surface plasmon resonance (SPR) experiments for quantitative binding analyses were performed either using a Biacore T100, Biacore T200 or a Biacore 4000 instrument (GE Healthcare Biacore, Inc.) equipped with Series S Sensor Chips CM5 (GE Healthcare Biacore, Inc.). Binding assays were carried out at 25 °C with assay buffer HBS-EP+ (10 mM HEPES pH 7.4, 150 mM NaCl, 3 mM EDTA, 0.05 % Surfactant P20). Antibodies were captured with an anti-hIgG capture antibody covalently immobilized to the chip surface via amine coupling chemistry. Reagents for amine coupling (1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride (EDC), N-hydroxysuccinimide (NHS), ethanolamine-HCl pH 8.5) were used from the Amine Coupling Kit (GE Healthcare, product code BR-1000-50). Anti-hIgG, anti-mIgG capture antibodies and immobilization buffer (10 mM sodium acetate pH 5.0) were used from the Human Antibody Capture Kit (GE Healthcare, BR-1008-39) and the Mouse Antibody Capture Kit (GE Healthcare, BR-1008-38), respectively. The sensor chip surface was activated with a freshly prepared solution of 0.2 M EDC and 0.05 M NHS passed over the chip surface for 420 s at a flow rate of 10 µl/min, followed by an injection of anti-hIgG or anti-mIgG capture antibody (dissolved to 25 µg/ml in immobilization buffer) for 180 s at a flow rate of 5 µl/min. Excess of activated groups were blocked with a 1 molar solution of ethanolamine injected at a flow rate of 10 µl/min for 420 s.

CEACAM antigens were used as analyte to determine K_D values. Antibodies were captured for 20 s at a flow rate of 10 µl/min prior to each analyte injection. For kinetic affinity determination various concentrations between 1.56 and 200 nM of human CEACAM1, human CEACAM3, human CEACAM5, human CEACAM6, cynomolgus CEACAM6, cynomolgus CEACAM6-domain 1 protein in assay buffer (see above) were injected over the captured antibodies at a flow rate of 60 µl/min for 3 minutes and the dissociation was monitored for 10 minutes.

Obtained sensorgrams were double-referenced, i.e. in-line reference cell correction followed by buffer sample subtraction. K_D values were calculated based on the ratio of dissociation (k_d) and association (k_a) rate constants which were obtained by globally fitting sensorgrams with a first order 1:1 Langmuir binding model, implemented in the Biacore Evaluation Software Package (Biacore T100/T200/4000 Evaluation Software, GE Healthcare Biacore, Inc.).

Sandwich competition experiments by SPR

Sandwich competition experiments by SPR were performed in a similar manner as outlined above with minor modifications. First, each antibody to be analyzed was covalently immobilized on the sensor surface via amine coupling (for details see above). To check whether a different antibody competes for binding to a certain CEACAM antigen, the respective antigen was captured by injection over the immobilized antibody and the second antibody to be tested for competition was immediately injected subsequently. If the second antibody binds to the antigen bound by the first antibody (+), both antibodies do not show competition and vice versa, if no binding is observed by injection of the second antibody (-), both antibodies compete for a similar epitope.

Domain mapping studies using ELISA

To elucidate specific epitope information, several chimeric domain constructs were designed, expressed and purified. Briefly, the wild type human CEACAM6 sequence was C-terminally fused with a human IgG1 Fc fragment, expressed in HEK293 cells and purified from the supernatant via Protein-A and size exclusion chromatography (TPP-1790). In order to create different domain chimeras, the human sequence of one single domain was consequently replaced by the corresponding Macaca mulatta sequence (F6YVW1) in the Fc-fused human CEACAM6. This created three different domain chimeras hDom1-hDom2-mDom3 (TPP-1793), hDom1-mDom2-hDom3 (TPP-1792), and mDom1-hDom2-hDom3 (TPP-1791), together with the wild-type Macaca mulatta Fc fusion construct as control (TPP-1306). In addition to the chimeras, the single domain 1 of human CEACAM6 was produced as described above from E. coli (TPP-1794).

Mapping of the domain specificity of the antibodies was carried out using an ELISA assay:

For ELISA analysis, the Fc-fused domain chimeras and the single domain 1 were coated on Nunc MaxiSorb plates and blocked with SmartBlock solution. After incubation with an IgG-concentration series (1 nM – 1000 nM) for 1 h, plates were washed with PBS/T. Analysis of the bound IgGs to the CEACAM6 domain constructs was achieved over detection via Anti-Human IgG (Fab specific)–Peroxidase antibody

(A0293, Sigma). Fluorescence detection was performed with AmplexRed (A12222, Invitrogen) following standard protocols.

ELISA-based binding analysis

ELISAs were used to characterize the binding of antibodies to various CEACAM paralogs and orthologs. Black 384-well plates were coated with 25 µl/well of various CEACAM protein preparations at 2 µg/ml in coating buffer (Candor) for 1 h at 37 °C. After one wash with PBS/0.05% Tween-20, wells were blocked with 100% Smart Block (Candor) for one hour at 37 °C. After three washes with PBS/0.05% Tween-20, dilution series of the antibodies in PBS/0.05% Tween-20/10% Smart Block ranging from 2 µg/ml to 2 ng/ml were added and the plates were incubated for 1 h at room temperature. After three washes with PBS/0.05% Tween-20, an appropriate secondary antibody was added. For detection of proteins with a human Fc such as TPP-1173, an anti-human IgG HRP (Sigma A0170) was used at 1:10.000 dilution. For detection of proteins with a mouse Fc such as TPP-1744 an anti-mouse IgG HRP (ThermoScientific 31432) was used at 1:10.000 dilution. PBS/0.05% Tween-20/10%Smart Block was used as dilution buffer. The plates were incubated for 1 hour at room temperature. After three washes, the plates were developed with Amplex Red (Life Technologies) and fluorescence was read at an emission wavelength of 590 nm. GraphPad Prism 6.0 software was used to calculate EC_{50} values using four-parameter non-linear curve fit.

Results

To measure the monovalent affinity of 9A6 to human CEACAM6 and to assess its cross-reactivity towards monkey CEACAM6, SPR experiments were conducted as outlined above. Results are shown in Table 3:

	Alias	Recombinant human CEACAM6 (R&D Systems; TPP-1436)	Recombinant macaca mulatta CEACAM6 (TPP-1306)
9A6-mIgG1	TPP-1744	22	-
Neo201-hIgG1	TPP-1173	10	23

"-": no binding detected

Table 3: SPR analysis: monovalent K_D (in nM)

As shown, 9A6-mIgG1 can bind with high affinity (22 nM) to recombinant human CEACAM6. However, no binding to Macaca mulatta CEACAM6 was detected. For comparison, Neo201—hIgG1 was also tested. This antibody displayed high affinity binding to both human and monkey CEACAM6. In summary, 9A6 displays high affinity binding to human CEACAM6 but it is not cross-reactive to monkey CEACAM6.

To map the binding domain of 9A6 on CEACAM6, binding on different human/monkey chimera was assessed by ELISA as outlined above. To be able to compare to Neo201-hIgG1 (TPP-1173), 9A6 was chimerized to a human IgG1 (TPP-1745). Results are shown in Table 4:

	TPP-#	Origin of domain 1	Origin of domain 2	Origin of domain 3	9A6-hIgG1 (TPP-1745)	Neo201-hIgG1 (TPP-1173)
hWT	1790	human	human	human	+	+
DOM1 MM	1791	M. mulatta	human	human	-	+
DOM2 MM	1792	human	M. mulatta	human	+	+
DOM3 MM	1793	human	human	M. mulatta	+	+
hDOM1	1794	human	-	-	+	-
MM WT	1306	M. mulatta	M. mulatta	M. mulatta	-	+

"+" denotes binding detected; "-"denotes no binding detected

Table 4: Domain mapping analysis by ELISA binding assay

9A6 is able to bind to wildytpe human CEACAM6, and to chimeras employing Domain 2 or 3 of Macaca mulatta CEACAM6. However, it fails to bind to a chimera employing Domain 1 of Macaca mulatta CEACAM6 or to wildtype Macaca mulatta CEACAM6. Consistent with this, it is able to bind to the single domain 1 of human CEACAM6. In contrast, Neo201-hIgG1 binds to all forms tested except for single domain 1 of human CEACAM6. In conclusion, 9A6 binds to the N-terminal Domain 1 of human CEACAM6.

To substantiate the results, a competition experiment was performed as outlined above. Results are shown in Table 5.

	9A6-mIgG1 (TPP-1744)	Neo201-hIgG1 (TPP-1173)
9A6-mIgG1 (TPP-1744)	-	+
Neo201-hIgG1 (TPP-1173)	+	-

If the second antibody binds to the antigen bound by the first antibody (+), both antibodies do not show competition and vice versa, if no binding is observed by injection of the second antibody (-), both antibodies compete for a similar epitope

Table 5: Sandwich competition experiments by SPR on recombinant human CEACAM6 (R&D Systems, TPP-1436)

As evident from Table 5, 9A6-mIgG1 and Neo201-hIgG1 do not compete with each other for binding to human CEACAM6. This is consistent with the published epitope of Neo201 residing outside domain 1.

To analyze the selectivity of 9A6 towards different CEACAM6 orthologs and to allow comparison to Neo201-hIgG1, 9A6 was chimerized to hIgG1 (TPP-1745). In ELISA binding experiment conducted as outlined above, the EC_{50} values listed in Table 6 have been obtained:

	TPP-	Human CEACAM6 (TPP-1436)	Human CEACAM3 (TPP-2755)	Human CEACAM5 (TPP-1438)	Cynomolgus CEACAM6 (APP-319)
9A6-hIgG1	TPP-1745	0.09	-	-	-
Neo201-hIgG1	TPP-1173	0.11	-	0.09	1.35

"-" denotes EC_{50} > 10 nM

Table 6: Selectivity/cross-reactivity analysis by binding ELISA - EC_{50} values in nM

High affinity binding of 9A6 to human CEACAM6 was confirmed. Consistent with SPR experiments using rhesus monkey CEACAM6, 9A6 also fails to bind to cynomolgus monkey CEACAM6. It is, however, selective for CEACAM6 since no binding to human CEACAM3 or CEACAM5 was observed.

In contrast, Neo201-hIgG1 displays similar high affinity binding to human CEACAM6 and is even cross-reactive to cynomolgus CEACAM6. This comes at a reduced selectivity, since it displays also high affinity binding to human CEACAM5.

Example 3: Protein Sequence Alignment of CEACAMs

The mature extracellular form of human CEACAM6 (amino acids 35-320 of UniProtKB/Swiss-Prot: P40199.3) consists of different domains: N-terminal domain 1 (according to www.uniprot.org amino acids 35-142 of UniProtKB/Swiss-Prot: P40199.3), domain 2 (according to www.uniprot.org amino acids 145-232 of UniProtKB/Swiss-Prot: P40199.3), and domain 3 (according to www.uniprot.org amino acids 237-314 of UniProtKB/Swiss-Prot: P40199.3). Since the goal was to identify a selective, high affinity antibody to N-terminal domain 1 of CEACAM6, yet being cross-reactive to cynomolgus monkey CEACAM6, the probability of combining the desired properties in one molecule was assessed.

To this end, the protein sequence of N-terminal domain 1 of human CEACAM6 was compared to other proteins using Blastp algorithm (NCBI) using standard settings to identify most relevant CEACAM6 homologs. (Partial) mature extracellular domains of human CEACAM6 (amino acids 35-320 of UniProtKB/Swiss-Prot: P40199.3), human CEACAM1 (amino acids 35-428 of UniProtKB/Swiss-Prot: P13688.2), human CEACAM3 (amino acids 35-155 of UniProtKB/Swiss-Prot: P40198.2), human CEACAM5 (amino acids 35-417 of UniProtKB/Swiss-Prot: P06731.3) and cynomolgus (macaca fascicularis) CEACAM6 (amino acids 35-320 of TPP-4189) were aligned using “Global Alignment – Wilbur and Lipman (fast)” in Phylosopher software (Genedata). The alignment is shown in Figure 1. The percentage sequence identities of N-terminal domain1 of human CEACAM6 to other N-terminal domains (according to alignment) were determined using Vector NTI Software (Life Technologies). Those results are shown in Table 7.

	Sequence identity of N-terminal domains to N-terminal domain 1 of human CEACAM6
Human CEACAM6	(100%)
Human CEACAM3	90%
Human CEACAM1	90%
Human CEACAM5	89%
Cynomolgus CEACAM6	81%

Table 7: Percentage of protein sequence identities of N-terminal domains of different CEACAMs to N-terminal domain 1 of human CEACAM6.

The sequence alignment in Figure 1 shows a very high degree of similarity of protein sequences of human CEACM6 and human CEACAM3, human CEACAM5 and human CEACAM1 throughout the entire extracellular region. The target region (domain 1 of human CEACAM6) is especially similar to other CEACAMs, which is also reflected in Table 7. The paralogs of human CEACAM6 are much more similar to human CEACAM6 than the cynomolgus ortholog. In fact, there are only 2 positions in N-terminal region in the primary sequence that are identical in human and cynomolgus CEACAM6 but different from amino acids in this position in the other human paralogs (marked in Figure 1 with asterisks).

To conclude: it is highly challenging to identify a high affinity antibody to the N-terminal domain 1 of human CEACAM6 that is selective but still cross-reactive to monkey CEACAM6.

Example 4: Antibody generation by Phage Display

To identify human anti-CEACAM6 antibodies, various selections with the human Fab-phage library FAB-300 from DYAX were performed, essentially as described earlier (Hoet et al., 2005; Huang et al., 2006). As summarized in Table 8, different strategies with up to 4 rounds of phage selection were employed using biotinylated Fc-tagged recombinant CEACAM6 from human and cynomolgus monkey (TPP-1436 & TPP-2443), coated on strepavidin-beads, and the human tumor cell line KPL-4 (Kurebayashi et al., Br J Cancer. 1999 Feb;79 (5-6):707-17), which is expressing high

amounts of endogenous target protein on the cell surface. In addition, depletion for binder against CEACAM5 (TPP-1438; hC5) and CEACAM1 (TPP-1437; hC1) (off-targets) or recombinant human IgG1-Fc (Fc) was included as indicated prior to each selection on protein targets. For example, in strategy A after depletion on human CEACAM1-coated beads (hC1), the first round of panning was done on human CEACAM6 (hC6). The resulting output was divided and one part was used for a second and a third round of selection on human CEACAM6. The other part was used for second round of panning on KPL-4 cells, a third round on human CEACAM6 and a final fourth panning round on KLP-4 cells. In strategy C, a specific elution step was performed, using the mouse mAb 9A6-mIgG1 (TPP-1744).

Strategy:	A		B		C		D
Round 1	hC6		hC6		hC6		cynoC6
Round 2	hC6	KPL-4	hC6	KPL-4	hC6	KPL-4	hC6
Round 3	hC6	hC6	hC6	hC6	hC6	hC6	cynoC6
Round 4	-	KPL-4	-	KPL-4	-	KPL-4	hC6
Depletion	hC1		hC1 and hC5		hC1		Fc
Specific elution	-		-		9A6		-

Table 8: Phage selection strategies: human hC6 = TPP-1790; cynomolgus cynoC6 = TPP-2443, hC1 = TPP-1438, hC5 = TPP-1437, Fc = Recombinant Human IgG1 Fc (R&D Systems #110-HG-100)

Phage pools enriched from different rounds of selections were screened for binders to target and off-target by Fab-phage ELISA as described (Hoet et al., Nat Biotechnol. 2005 Mar;23(3):344-8) or by FACS-analysis on CEACAM6-expressing cells. Phage pools with a favorable profile were selected for geneIII-removal and subsequent ELISA-screening of soluble Fabs in an ELISA. DNA of resulting sFab-hits was sequenced and unique representatives characterized for cell-binding by FACS-analysis on KPL-4 cells (Table 9). In some strategies phage binder according to the invention were directly re-cloned into IgG.

Protein-ID (as hIgG1)	FACS-titration as sFab on KPL-4 cells
TPP-1667	++
TPP-1668	+
TPP-1669	+
TPP-1670	+
TPP-1672	+
TPP-1673	+
TPP-1674	+
TPP-1676	+
TPP-1677	0
TPP-1678	0
TPP-1679	+++
TPP-1680	+
TPP-1684	0
TPP-1686	+

+++: >1000 events @ ~2.2 µg/ml sFab
++: >100 events @ ~2.2 µg/ml sFab
+: >100 events @ ~6.7 µg/ml sFab
0: below threshold

Table 9: FACS-titration of unique sFab-hits:

Binding of phage display selected, purified Fab fragments (see list in Table 9) to biotinylated variants of human CEACAM1 (TPP-1437), human CEACAM5 (TPP-1438) and human CEACAM6 (TPP-1436) was analyzed by biolayer interferometry using an Octet RED384 instrument (Pall ForteBio Corp.). Biotinylated antigens were loaded onto Streptavidin (SA) Biosensors (ForteBio Part number 18-5019) and after a baseline equilibrium step in assay buffer (PBS supplemented with 0.1% (w/v) BSA, 0.02% (v/v) Tween20 and 0.05% (v/v) sodium azide; ForteBio Part number 18-5032), binding of Fabs diluted in assay buffer to a final concentration of 200 nM was monitored for 300 seconds followed by a dissociation phase of 300 seconds.

The corresponding purified Fab fragments from Table 9 also displayed binding to human CEACAM6 but not to human CEACAM5 or human CEACAM1.

In order to analyze whether the Fabs compete with 9A6 for binding to human CEACAM6, a competition experiment was carried out. Here, biotinylated human CEACAM6 (TPP-1436) was loaded onto SA Biosensors and binding responses of Fabs were compared to binding responses of Fabs obtained with loaded CEACAM6 saturated with 9A6-mIgG1 (TPP-1744) (as outlined in Example 1). If the binding

response in presence of 9A6 is significantly reduced or abolished this is a strong indication that a tested Fab binds to an epitope similar to that of 9A6.

Surprisingly, all Fabs tested were able to compete with 9A6 for binding to human CEACAM6.

The Fab sequences were reformatted into human IgG1 format for further characterization.

Affinities (monovalent K_D) of reformatted antibodies towards recombinant human CEACAM6 (TPP-1436) were determined by SPR analogously to experimental procedures described in Example 2. Sensorgrams were either evaluated by globally fitting sensorgrams with a first order 1:1 Langmuir binding model or with a steady-state affinity analysis implemented in the Biacore Evaluation Software (Biacore T200/4000 Evaluation Software) Package. Results are shown in Table 10:

Protein-ID	K_D (in nM)
TPP-1667	(750)
TPP-1668	(550)
TPP-1669	(185)
TPP-1670	(340)
TPP-1672	(580)
TPP-1673	(515)
TPP-1674	(600)
TPP-1676	(1980)
TPP-1677	(580)
TPP-1678	(300)
TPP-1679	76
TPP-1680	(870)
TPP-1684	(480)
TPP-1686	(310)
TPP-2968	weak

values in brackets: not accurately determined under present experimental conditions but are sufficient for comparison among each other

Table 10: SPR analysis: monovalent K_D (in nM)

As evident from Table 10, the antibodies displayed rather low monovalent affinities, the lowest value (highest affinity) being 76 nM for TPP-1679. Three IgGs displaying the highest monovalent affinities were analyzed with regards to their

selectivity and cross-reactivity to cynomolgus CEACAM6 in an ELISA binding experiment (carried out in analogy to the protocol given in Example 2)

TPP-	Human CEACAM6 (TPP-1436)	Human CEACAM3 (TPP-2755)	Human CEACAM5 (TPP-1438)	Cynomolgus CEACAM6 (APP-319)
TPP-1679	0.16	2.24	0.86	-
TPP-1669	0.22	-	1.01	-
TPP-1678	0.19	-	-	42.74

"-" denotes EC_{50} > 10 nM (in the case of cynomolgus CEACAM6 > 100 nM)

Table 11: Selectivity/cross-reactivity analysis by binding ELISA: EC_{50} values in nM

To summarize, antibodies with rather poor monovalent affinities have been obtained. This might be a trade-off due to avoiding binding to other paralogs. Still, selectivity profile is often insufficient (see TPP-1679 & TPP-1669 in Table 11). From all antibodies tested, TPP-1678 is the only one with a very marginal cross-reactivity to recombinant cynomolgus CEACAM6 (see Table 11).

In conclusion, no therapeutically useful anti-CEACAM6 antibodies have been obtained using phage display without further maturation.

Example 5: Antibody maturation of phage display-derived antibodies

To obtain antibodies with desirable affinity, selectivity and cross-reactivity profiles, some phage display-derived antibodies were affinity-matured.

Therefore, all CDR amino acid positions of TPP-1669, TPP-1678 and TPP-1679 were randomized individually. The resulting variants were expressed and assessed for binding to multiple CEACAM family members (human CEACAM6, cynomolgus CEACAM6, human CEACAM3 and human CEACAM5) by binding ELISA in cell supernatants.

For TPP-1669, individual mutations enhancing binding to cynomolgus CEACAM6 without at the same time enhancing binding to other human CEACAM family members as well could not be identified.

For TPP-1679, several individual mutations were identified, which enhanced binding to human CEACAM6 without concomitant enhanced binding to other human CEACAM family members, and a recombination library containing all possible permutations was generated. The corresponding variants were expressed as human IgG2 isotypes, purified and assessed for binding to multiple CEACAM family members by SPR analogously to experimental procedures described in Example 2. Table 12 summarizes the properties of selected antibodies obtained by this process.

	Human CEACAM6 (R&D Systems; TPP-1436)	Cynomolgus CEACAM6 (APP-319; (TPP-2443 cleaved)	Human CEACAM5 (R&D Systems; TPP-1438)	Human CEACAM3 (Sino Biological; TPP-2755)	Human CEACAM1 (R&D Systems; TPP-1437)
TPP-3399	9	-	weak	weak	-
TPP-3400	6	weak	weak	-	-
TPP-3401	16	-	(94)	-	-
TPP-3402	18	-	(172)	-	-
TPP-3403	13	weak	(144)	-	-
TPP-3404	11	(363)	(138)	-	-
TPP-3405	14	(522)	(126)	weak	-
TPP-3406	(15)	-	-	-	-
TPP-3407	(12)	-	-	weak	-
TPP-3408	(27)	-	-	-	-

values in brackets: not accurately determined under present experimental conditions
"-": no binding detected under current experimental conditions
"weak": if at most the two highest analyte concentrations analyzed (i.e. 100 and 200 nM) resulted in a binding signal that is between three times the signal to noise ratio and 20 percent of the theoretical maximum binding response ($Rmax_{theoretical}$)

Table 12: SPR analysis: monovalent K_D (in nM)

The results obtained in Table 12 indicate that affinity and selectivity enhancement is very well possible. However, it also underscores the challenge to

obtain cynomolgus CEACAM6 cross-reactive binders, which are at least within one order of magnitude close to the monovalent affinity towards human CEACAM6.

For TPP-1678, several individual mutations were identified, which enhanced binding to human CEACAM6 and cynomolgus CEACAM6 without greater concomitant enhanced binding to other human CEACAM family members, and a recombination library containing several permutations was generated. The corresponding variants were expressed as human IgG2 isotypes, purified and assessed for binding to multiple CEACAM family members by SPR analogously to experimental procedures described in Example 2 (summarized in Table 13).

The binding characteristics of these antibodies were also determined by a binding ELISA (monovalent binding, biotinylated CEACAM proteins): A 1:440 dilution of of an anti-human IgG (Sigma, I2136) in Coating buffer (Candor) was used to coat black 384-well Maxisorp plates (Nunc) for 1 hour at 37 °C. After one wash with PBS/0.05% Tween-20 the plates were blocked with 100% SmartBlock (Candor) for 1 hour at 37 °C. After three washes, 2 µg/ml of the relevant antibodies were added to the plate in PBS/0.05% Tween-20/10% SmartBlock. The plates were incubated for 1 hour at room temperature. After three washes dilution series of the relevant biotinylated CEACAM proteins in PBS/0.05% Tween-20/10% SmartBlock were added and the plates were incubated for one hour at room temperature. After three washes 1 µg/ml of Streptavidin-Peroxidase (Sigma, S5512) in PBS/0.05% Tween-20/10% SmartBlock was added and the plates were incubated for 30 minutes at room temperature. After three washes, the plates were developed with Amplex Red (Life Technologies) and fluorescence was read at an emission wavelength of 590 nm. GraphPad Prism 6.0 software was used to calculate EC_{50} values using four-parameter non-linear curve fit.

Variants with a substantially improved affinity, selectivity and cross-reactivity profile were identified as summarized in Table 13 and Table 14 for selected antibodies obtained by this process.

	Human CEACAM6 (R&D Systems; TPP-1436)	Cynomolgus CEACAM6 (APP-319; (TPP-2443 cleaved)	Human CEACAM5 (R&D Systems; TPP-1438)	Human CEACAM3 (Sino Biological; TPP-2755)	Human CEACAM1 (R&D Systems; TPP-1437)
TPP-3705	28	32	-	-	-
TPP-3707	28	32	-	-	-
TPP-3708	3	5	-	weak	(158)
TPP-3709	8	20	-	-	(408)

values in brackets: not accurately determined under present experimental conditions
"-": no binding detected under current experimental conditions

"weak": if at most the two highest analyte concentrations analyzed (i.e. 100 and 200 nM) resulted in a binding signal that is between three times the signal to noise ratio and 20 percent of the theoretical maximum binding response ($Rmax_{theoretical}$)

Table 13: SPR analysis: monovalent K_D (in nM)

TPP-	Human CEACAM6 (R&D Systems TPP-1436 biotinylated)	Cynomolgus CEACAM6 (APP-319-biotinylated)	Human CEACAM1 (R&D Systems TPP-1437 biotinylated)	Human CEACAM3 (Sino Biological Inc. TPP-2755 biotinylated)	Human CEACAM 5 (R&D Systems TPP-1438 biotinylated)
TPP-3705	0.18	0.12	~ 3.82 x 10^6 (ambiguous fit)	113.04	-
TPP-3707	0.19	0.11	~ 8.94 x 10^5 (ambiguous fit)	139.18	-
TPP-3708	0.02	0.03	9.64	1.04	-
TPP-3709	0.04	0.07	36.53	4.68	-
TPP-3470 (9A6-hIgG2)	0.08	-	-	-	-

"-" denotes no binding detectable up to highest concentrations tested (150 ng/ml for human and cynomolgus CEACAM6; 2000 ng/ml for human CEACAM1, human CEACAM3, human CEACAM5)

Table 14: Selectivity/cross-reactivity analysis by binding ELISA: EC_{50} values in nM

In conclusion, using the TPP-1678 precursor, it was possible to obtain few high affinity human antibodies to human CECACAM6 that are truly cross-reactive to cynomolgus CEACAM6 and that are selective to CEACAM6: binding of TPP-3707 to human CEACAM6 is about 730-fold better than to human CEACAM3 (620-fold for TPP-3705) as judged by comparing their corresponding EC_{50} values.

Example 6: Antibody generation by mouse immunization

To generate mouse monoclonal antibodies against CEACAM6, two different immunization strategies were performed based on the sequence of immunogens applied to the Balb/c mice (strategy A and B in Table 15). Within each strategy, mice were immunized either via footpad or intraperitoneal application of antigens over 5 rounds of injection, as depicted in Table 15. Strategy A was focusing on the immunization with cynomolgus CEACAM6-Domain1, whereas Strategy B was based on the combination of full-length extracellular CEACAM6 from human and cynomolgus monkey as immunogens.

Immunisations by footpad were based on 5 injections of 1 µg antigen once weekly. Immunizations by intra-peritoneal route were based on 4 IP injections biweekly (10 µg of antigen) followed by one boost by intravenous injection.

	Strategy A		Stategy B	
	Footpad immunization	Intraperitoneal immunization	Footpad immunization	Intraperitoneal immunization
1st injection	cynoC6-D1 (APP-325)	cynoC6-D1 (APP-325)	hC6 (APP-320)	hC6 (APP-320)
2nd injection	cynoC6-D1 (APP-325)	cynoC6-D1 (APP-325)	CynoC6 (APP-319)	CynoC6 (APP-319)
3rd injection	cynoC6-D1 (APP-325)	cynoC6-D1 (APP-325)	hC6 (APP-320)	hC6 (APP-320)
4th injection	cynoC6-D1 (APP-325)	cynoC6-D1 (APP-325)	CynoC6 (APP-319)	CynoC6 (APP-319)
5th injection	cynoC6-D1 (APP-325)	cynoC6-D1*(APP-325)	hC6 (APP-320) + CynoC6 (APP-319)	hC6 (APP-320) + CynoC6 (APP-319)*

***: i.v. boost**

Table 15: Immunization schedule

Four days after the last injection, lymph nodes or spleen cells of mice were fused according to standard methods (e.g. Köhler and Milstein Nature. 1975 Aug 7;256(5517):495-7). Screening of resulting hybridoma-clones was done in an ELISA using biotinylated antigens and off-target proteins (as listed in Table 16). In more detail, microtiter-plates were coated with goat anti-mouse antibodies overnight at 4 °C. The following day plates were washed and blocked with 5% BSA for 2 h at room temperature, followed by another washing step. 20 µl of hybridoma supernatants were incubated with biotinylated antigens for 1 h at room temperature and the mixtures transferred to the coated wells followed by an incubation step (1 h at room temperature). After washing the plates, anti-streptavidin-HRP conjugates were added for 30 min at room temperature. Finally, wells were washed, and the color reaction was developed by addition of 50 µl TMB and recorded in a plate reader.

Target (all biotinylated)	Off-target (all biotinylated)
Human CEACAM-6 (TPP-1436)	hCEACAM1 (TPP-1437)
Cynomolgus CEACAM6-Fc (TPP-2443)	hCEACAM5 (TPP-1438)
Cynomolgus CEACAM6 (APP-319) Fc cleaved	

Table 16: List of proteins used in ELISA-screening of hybridomas (target and off-targets)

Surprisingly, only Strategy A resulted in clones showing a favorable profile with regards to human & cynomolgus CEACAM6 cross-reactivity as well as selectivity. In addition, some species specific clones were obtained from both strategies.

Candidates selected positively by ELISA were subcloned over at least 3 cloning rounds and produced at larger amounts from ascites fluid by protein A chromatography.

Antibodies from mouse immunizations were also characterized for binding to CEACAM6 in a cellular context. HeLa-cells overexpressing human or cynomolgus CEACAM6 were employed in FACS experiments with either supernatants from hybridoma or purified mIgs (see Example 1). Non-transfected HeLa-cells served as negative control. Table 17 summarizes the profile of identified candidates from ELISA and FACS-analysis:

Protein-ID	Human CEACAM6	Cynomolgus CEACAM6
TPP-2969	no binding detectable	binding
TPP-2970	no binding detectable	binding
TPP-2971	binding	binding
TPP-3100	binding	binding
TPP-3187	binding	binding
TPP-3101	binding	binding
TPP-3186	binding	binding

Table 17: Summary of qualitative results for binding of murine hybridoma-derived antibodies to human and cynomolgus CEACAM6 from ELISA (using biotinylated TPP-1436, TPP-2443 and APP-319) and FACS-analysis (using transfected HeLa cells see Example 1: TPP-4639 and TPP-4189)

The murine antibodies obtained were characterized more closely with regards to their monovalent affinities (K_D), their selectivity towards other human paralogs and their degree of cross-reactivity to cynomolgus CEACAM6 by SPR analysis as purified mIgGs.

SPR was conducted analogously to experimental procedures described in Example 2.

Results are summarized in Table 18:

	Human CEACAM6 (R&D Systems; TPP-1436)	Cynomolgus CEACAM6 (APP-319; (TPP-2443 cleaved)	Cynomolgus CEACAM6 Domain 1 (APP-325; TPP-2452 cleaved)	Human CEACAM5 (R&D Systems; TPP-1438)	Human CEACAM3 (Sino Biological; TPP-2755)	Human CEACAM1 (R&D Systems; TPP-1437)
TPP-2969	72	(109)	51	-	-	-
TPP-2970	72	56	47	-	-	-
TPP-2971	61	25	30	-	-	-
TPP-3100	79	n.t.	52	-	-	n.t.
TPP-3101	69	n.t.	13	(300)	weak	n.t.
TPP-3186	74	n.t.	53	-	-	n.t.
TPP-3187	68	n.t.	42	-	-	n.t.

values in brackets: not accurately determined under present experimental conditions

"-": no binding detected under current experimental conditions

"weak": if at most the two highest analyte concentrations analyzed (i.e. 100 and 200 nM) resulted in a binding signal that is between three times the signal to noise ratio and 20 percent of the theoretical maximum binding response ($Rmax_{theoretical}$)

n.t. – not tested

Table 18: SPR analysis: monovalent K_D (in nM)

There were unresolved discrepancies for TPP-2969 & TPP-2970 observed: in initial ELISA and FACS analysis they appeared cynomolgus CEACAM6 specific, whereas in later SPR experiment they exhibited also binding to recombinant human CEACAM6.

To summarize: immunization of mice with cynomolgus CEACAM6 N-terminal domain 1 (APP-325) suprisingly yielded some antibodies (e.g. TPP-3186, TPP-2971, TPP-3187) that are truly human – cynomolgus CEACAM6 cross-reactive and at the same time selective with regards to other human paralogs. The affinities are in an acceptable range for therapeutic puposes, yet their murine origine and associated immunogenicities preclude therapeutic applications in humans.

Example 7: Antibody humanization

To generate antibodies suitable for therapeutic applications in humans, selected murine antibodies were humanized.

Selected sequences of the murine hybridoma-derived antibodies were determined by sequencing the antibody cDNAs of the respective hybridoma cell lines (see Table 17). According to the sequencing results, TPP-3100 and TPP-3186 are identical. TPP-3101 yielded a single heavy chain but two light chain sequences. TPP-2971 and TPP-3187 were highly similar. They differed in four amino acids (see Figure 2).

The deciphered murine VH and VL sequences of the antibody TPP-2971 and TPP-3187 were humanized by grafting the CDRs according to the Kabat definition into human germline frameworks. As an exception, HCDR2 was partially grafted. Since this CDR is very long (16 amino acids) according to the Kabat definition, only the first 9 amino acids were grafted. These amino acids represent the part of HCDR2 which is identical to HCDR2 according to the Chothia definition (for CDR definitions according to Kabat and Chothia see: Andre C.R. Martin, “Protein sequence and structure analysis of antibody variable domains" in Antibody Engineering (Springer Lab Manuals), Eds.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg).

The human germline frameworks were chosen based on similarity searches of the murine framework pieces FW1, FW2, FW3, and FW4 with the set of human VH and

VL as well as J element germline sequences. The murine CDRs were grafted into the best matching germline sequences (excluding the CDRs), which were IGKV1-9*01 and IGKJ2*01 for VL (Identities 69.6%, FW1; 86.7%, FW2; 71.9%, FW3; 80.0%, FW4) and IGHV2-70*01 and IGHJ6*01 for VH ((Identities: 73.3% (TPP-2971) and 70.0% (TPP-3187), FW1; 85.7%, FW2; 71.9%, FW3; 90.9%, FW4)). Germline sequences applied in similarity searches were derived from the VBASE2 data set (Retter I, Althaus HH, Münch R, Müller W: VBASE2, an integrative V gene database. Nucleic Acids Res. 2005 Jan 1; 33(Database issue):D671-4). The names assigned to the most similar germline sequences were taken from the IMGT system (Lefranc, M.-P., Giudicelli, V., Ginestoux, C., Jabado-Michaloud, J., Folch, G., Bellahcene, F., Wu, Y., Gemrot, E., Brochet, X., Lane, J., Regnier, L., Ehrenmann, F., Lefranc, G. and Duroux, P. IMGT®, the international ImMunoGeneTics information system®. Nucl. Acids Res, 37, D1006-D1012 (2009); doi:10.1093/nar/gkn838)).

Two variants of humanized sequences derived from TPP-2971 have been generated: TPP-3310 and TPP-3714. In VH of TPP-3310 the J element was kept unchanged compared to the murine originator, whereas in VH of TPP-3714 the J element was made completely human germline-like (see Figure 3). No glycosylation sites or unpaired cysteines were found in the humanized sequences.

In addition, two variants of humanized sequences derived from TPP-3187 were generated: TPP-3820 and TPP-3821 (see Figure 4). In comparison to TPP-3714, VH of TPP-3820 contained threonine instead of serine at the position 30 in HFW1, and glycine instead of alanine at position 46 in HFW2, while VL contained two asparagine residues instead of two serine residues at positions 92 and 93 in LCDR3. These four amino acid exchanges reflect the differences between the murine originator sequences of TPP-3187 and TPP-2971.

The variable domain VH of TPP-3821 is identical to TPP-3714, while VL contained two asparagine residues instead of two serine residues at positions 92 and 93 in LCDR3 in comparison TPP-3714. These two amino acid exchanges reflect the differences in the CDRs between the murine originator sequences of TPP-3187 and TPP-2971. No glycosylation sites or unpaired cysteine residues were found in the sequences of TPP-3820 and TPP-3821.

Affinity determination and sandwich competition experiments of chimerized and humanized antibodies were performed by SPR analogously to experimental

procedures described in Example 2 and the results are summarized in Table 19 and Table 20:

	TPP-3308 (hIgG2 chimera of TPP-2971)	TPP-3322 (hIgG2 chimera of TPP-3186)	TPP-3323 (hIgG2 chimera of TPP-3187)	TPP-3470 (hIgG2 chimera of 9A6)
TPP-3308 (hIgG2 chimera of TPP-2971)	-	-	-	-
TPP-3322 (hIgG2 chimera of TPP-3186)	-	-	-	-
TPP-3323 (hIgG2 chimera of TPP-3187)	-	-	-	-
TPP-3470 (hIgG2 chimera of 9A6	-	-	-	-

If the second antibody binds to the antigen bound by the first antibody (+), both antibodies do not show competition and vice versa, if no binding is observed by injection of the second antibody (-), both antibodies compete for a similar epitope

Table 19: Sandwich competition experiments by SPR on recombinant human CEACAM6 (R&D Systems, TPP-1436)

	Human CEACAM6 (R&D Systems; TPP-1436)	Cynomolgus CEACAM6 (APP-319; (TPP-2443 cleaved)	Human CEACAM5 (R&D Systems; TPP-1438)	Human CEACAM3 (Sino Biological; TPP-2755)	Human CEACAM1 (R&D Systems; TPP-1437)
TPP-3310	13	31	-	-	-
TPP-3714	13	27	-	-	-
TPP-3820	27	54	-	-	-
TPP-3821	24	49	-	-	-

"-" denotes no binding detected under current experimental conditions

Table 20: SPR analysis: monovalent K_D (in nM)

Selectivity and cross-reactivity analysis was carried out by binding ELISA (monovalent, biotinylated CEACAM proteins) in analogy to the protocol provided in Example 5. Results obtained are summarized in Table 21.

TPP-	Human CEACAM6 (R&D Systems TPP-1436 biotinylated)	Cynomolgus CEACAM6 (APP-319-biotinylated)	Human CEACAM1 (R&D Systems TPP-1437 biotinylated)	Human CEACAM3 (Sino Biological Inc. TPP-2755 biotinylated)	Human CEACAM5 (R&D Systems TPP-1438 biotinylated)
TPP-3310	0.09	0.07	-	-	-
TPP-3714	0.09	0.07	-	-	-
TPP-3470 (hIgG2 chimera of 9A6	0.08	-	-	-	-

"-"denotes no binding detectable up to highest concentrations tested (150 ng/ml for human and cynomolgus CEACAM6; 2000 ng/ml for human CEACAM1, human CEACAM3, human CEACAM5)

Table 21: Selectivity/cross-reactivity analysis by binding ELISA: EC_{50} values in nM

The results in Table 19 indicate TPP-2971, TPP-3186 & TPP-3187 compete for the same or a similar epitope on human CEACAM6 as 9A6-hIgG2. The results in Table 20 and Table 21 underscore a high affinity binding to human & cynomolgus CEACAM6 with true crossreactivity while being selective to CEACAM6 and not binding to CEACAM6 paralogs.

In conclusion, humanization was fully successful, with antibodies exhibiting even higher affinities than their murine precursors, enabling a therapeutic application in humans.

Example 8: Selective CEACAM6 binding on cells

To demonstrate binding and selectivity of the anti-CEACAM6 antibodies to authentic antigens, the antibodies were tested for binding to native CEACAM6 on the cell surface of different cell lines by FACS experiments.

CEACAM6 selectivity was tested on a panel of HeLa-cells which have been transfected with different CEACAM-receptors (human CEACAM1, human CEACAM3, human CEACAM5, human CEACAM6, human CEACAM8, human CEACAM19 and cynomolgus CEACAM6 - see Example 1) in comparison to binding of HeLa wild type cells which were shown to be CEACAM6 negative. EC_{50} values were determined for

the binding to human and cynomolgus monkey CEACAM6 transfected HeLa cells. Results are shown in Table 22.

For FACS experiments HeLa wild type cells were cultured in RPMI-1640, 10% FCS, while CEACAM-receptor transfected HeLa cells received in addition 0.5% Gentamycin (stock 10 mg/ml, Fa. PAA) and 200 µg/ml Hygromycin B (stock 50 mg/ml, Invitrogen). Cells were washed 3 times with PBS w/o Ca^{2+}/Mg^{2+} and were detached from the culture plate non-enzymatically with EDTA dissociation buffer (Gibco). Cells were washed in cold FACS buffer (PBS w/o Ca^{2+}/Mg^{2+} and heat-inactivated 3% FCS) and were counted using a countess machine (Invitrogen). 10^5 cells per well were plated and incubated with the respective primary antibody (5 µg/ml) for 1 h at 4°C on a plate shaker. Then cells were washed (400 g, 5') with FACS buffer 2 times, were resuspended in 100 µl containing the secondary antibody (PE-anti-mouse or anti-human IgG, 1:150 dilution, Dianova #115-115-164, #109-115-098) and were incubated for another 1 h at 4 °C on a plate shaker. After 2 times washing the cells were resuspended in 100 µl FACS buffer and were analysed on a FACS Canto II machine (Beckton Dickinson) or a FACS Array (Beckton Dickinson).

For EC_{50} analysis, the primary antibodies were used at increasing concentrations in a range from 0.1 nM to 100 nM. Half maximal binding values (EC_{50}) were determined by plotting the median fluorescence intensity signal against the concentration (logarithmic scale). Curve fitting of data was performed using the Graph Pad prism analysis software.

Test antibody	Species, isotype	HeLa wild type	HeLa human CEA CAM1 TPP-4185	HeLa human CEA CAM3 TPP-4187	HeLa human CEA CAM5 TPP-4188	HeLa human CEA CAM6 TPP-4639	HeLa human CEA CAM8 TPP-4190	HeLa human CEA CAM 19 TPP-4186	HeLa Cyno-molgus CEA CAM6 TPP-4189
						EC_{50} [nM]			EC_{50} [nM]
TPP-2971	mIgG1		-	-	-	+ 0.5	-		++ 0.5
TPP-3100	mIgG1		-	-	-	++ 0.35	-		++ 3
TPP-3186	mIgG1		-	-	-	++ 0.5	-		++ 0.5
TPP-3187	mIgG1		-	-	-	++ 0.35	-		++ 4

Test antibody	Species, isotype	HeLa wild type	HeLa human CEA CAM1 TPP-4185	HeLa human CEA CAM3 TPP-4187	HeLa human CEA CAM5 TPP-4188	HeLa human CEA CAM6 TPP-4639	HeLa human CEA CAM8 TPP-4190	HeLa human CEA CAM 19 TPP-4186	HeLa Cyno-molgus CEA CAM6 TPP-4189
						EC_{50} [nM]			EC_{50} [nM]
TPP-3322	Hu/ mIgG1	-	-	-	-	+ 0.6	-		++ 0.8
TPP-3323	Hu/ mIgG1	-	-	-	-	+ 0.6	-		++ 0.8
TPP-3308	Hu/ mIgG1	-	-	-	-	+ 0.45	-		++ 0.6
TPP-3820	hIgG2	-	-	-	-	+++ (+) 1	-	-	1
TPP-3821	hIgG2	-	-	-	-	+++ (+) 1	-	-	1
TPP-3310	hIgG2	-	-	-	-	+++ (+) 0.6	-	-	1.5
TPP-3714	hIgG2	-	-	-	-	+++ (+) 1	-	-	1
TPP-3707	hIgG2	-	+	+	-	+++ 19	-	-	4
TPP-3470 (9A6-hIgG2)	hIgG2					1			>100
Anti-CEACAM 6 clone 9A6 (Genovac #GM0509)	mIgG1	-	-	-	-	+++	-	-	

Definition of -,+ ,++ , +++ as determined from FACS median fluorescence log shift: - = no shift; + = log shift as compared to control antibody, median 10-100; ++ = 2 log shift, median 100-1,000; +++ = 3 log shift, median 1,000-10,000

Table 22: Specific binding to CEACAM-receptor transfected HeLa cell line panel.

Anti-CEACAM6 antibodies were also tested for their binding to different cancer cell lines that endogenously express CEACAM6 by FACS analysis. Cell lines were cultured according to the protocols provided by the American tissue culture collection (ATCC). The observed binding signal was specific as the non-binding isotype control

did not result into a shift of the fluorescence signal. Half maximal binding (EC50) values are in the low nanomolar range (Table 23).

Cell line*	TPP-3310	TPP-3470 (9A6-hIgG2)
	EC50 [nM]	EC50 [nM]
PaTu-8902	0.15	0.2
SNU-C1	0.5	0.8
KS	0.8	1.0
NCI-H1993	0.8-1.6	1.6
T84	0.3	0.35

*All cell lines from public tissue bank such as the American tissue culture collection etc, except KS breast cancer cell line kindly provided by Dr. Brigitte Gückel (University of Tübingen).

Table 23: Binding of anti-CEACAM6 antibodies to endogenously CEACAM6 positive tumor cell lines (EC_{50} values)

In conclusion, for the murine TPP-2971, TPP-3100, TPP-3186 & TPP-3187 antibodies as well as the human TPP-3820, TPP-3821, TPP-3310, TPP-3714 & TPP-3707 antibodies, selective binding to human authentic cell-surface CEACAM6 was demonstrated (no binding to other human paralogs). The binding of these antibodies to human CEACAM6 is comparable to 9A6 on human CEACAM6 expressing cell lines. For TPP-3310, a similar binding as 9A6-hIgG2 to endogenously expressed CEACAM6 on human tumor cell lines was demonstrated.

Antibodies of the invention also bind to cynomolgus CEACAM6 with a comparable avidity as to the human receptor in the single-digit to subnanomolar binding EC_{50} range while no binding of 9A6 to the cynomolgus CEACAM6 on the cell surface was detected up to 100nM. This result indicates a true crossreactivity to human and cynomolgus CEACAM6 for the antibodies of the invention while 9A6 clearly binds preferentially to human CEACAM6.

Example 9: Thermal Stability Analysis

Thermal stability of IgGs was investigated using Differential Scanning Calorimetry (DSC) using a VP-Capillary DSC system (MicoCal Inc.) with a cell volume of 0.137 mL. All samples were diluted in DPBS pH.7.4 to a final concentration of 0.5 mg/mL and a buffer control without protein was used as a reference. The samples were scanned from 20 °C to 120 °C at a scan rate of 120 °C/h. Resulting thermograms were corrected by subtraction of buffer control scans and normalized for protein concentration using Origin 7.0 Data analysis (OriginLab Corp.). Melting temperatures were obtained by fitting the DSC data to a nonlinear regression routine ("Non-2-state: Cursor init") provided with Origin.

	Thermal Stability of Fab domain
TPP-3310	88.2 °C
TPP-3714	88.5 °C * / 95.1 °C *
TPP-3400	74.7 °C
TPP-3707	80.6 °C
TPP-3470 (9A6-hIgG2)	80.2 °C

* Fab unfolds non-cooperatively

Table 24: Thermal Stability of Fab domain

All of the IgGs measured display a high thermal stability within the Fab domain. The thermal stability of TPP-3310 and TPP-3714 is remarkably high and exceeding by far the thermal stability of TPP-3470 (9A6-hIgG2). This is surprising since high stability has been associated with antibodies possessing VH3 framework (Honegger et al., 2009, Protein Eng Des Sel. 22(3):121-134).

High thermal stability is indicative of a better pharmaceutical suitability of TPP-3310 and TPP-3174 as compared to TPP-3470 (9A6-hIgG2) (better stability, less propensity to aggregation, less risk of immunogenicity).

Example 10: Interference with interaction between CEACAM6 and CEACAM1

It has been hypothesized that CEACAM1 might be the binding partner for CEACAM6 *in trans* on activated T cells (Witzens-Harig et al., Blood 2013 May 30;121(22):4493-503): *trans* and *cis* homophilic and heterophilic interactions amongst CEACAMs have been described, for example between CEACAM1 and CEACAM5 or CEACAM6 and CEACAM8. CEACAM1 is displayed on activated T cells, CEACAM1 ligation and phosphorylation recruits SH2-domain-containing protein tyrosine phosphatase 1 (SHP1). SHP1 dephosphorylates ZAP70, which results in the inhibition of TCR signaling. Thereby, CEACAM1 ligation leads to an early inhibition of T-cell activation within 10 minutes after activation.

Moreover, a role for CEACAM5 in the inhibition of natural killer (NK) cell responses against colorectal cancer cells was reported (Zheng et al., PLoS One. 2011;6(6):e21146), which might be based on its heterophilic binding to inhibitory CEACAM1 expressed on the NK cells.

Therefore, a direct CEACAM6-CEACAM1 interaction was tested using recombinant proteins in a binding ELISA. After establishing in preliminary experiments that a moderate but specific interaction between CEACAM1 and CEACAM6 could be detected, the following protocol was used: Black 384-well Maxisorb plates (Nunc) were coated with 1 µg/ml CEACAM1 (R&D Systems, TPP-1437) in Coating Buffer (Candor) for 1 h at 37 °C or were left uncoated as a control. After one wash with PBS/0.05% Tween-20 the wells were blocked with 100% Smart Block (Candor) for 1 h at 37 °C. In separate plates, dilution series of antibodies of interest in PBS/0.05% Tween-20, 10% SmartBlock were incubated with 2 µg/ml CEACAM6-Fc (TPP-1790) for 1 h at RT. The blocked plates were washed three times and the preformed antibody-CEACAM6-complexes were added. The plates were incubated for 1 h at RT. After three washes an anti-human IgG HRP (Sigma A1070) was added at 1:10.000 and the plates were incubated for 1 h at RT. After three washes the plates were developed with Amplex Red (Life Technologies) and fluorescence was read at an emission wavelength of 590 nm.

	Competition with binding of human CEACAM6-Fc to human CEACAM1
TPP-3400	+
TPP-3310	+
TPP-3714	+
TPP-3323	+
TPP-3705	+
TPP-3707	+
TPP-3470 (9A6-hIgG2)	+
TPP-3688 (Neo201-hIgG2)	-

"+" denotes competition

"-" denotes no competition

Table 25: Competition ELISA for antibodies competing with binding of human CEACAM6-Fc (TPP-1790) to passively coated human CEACAM1 (TPP-1437).

As shown in Table 25, it was possible to compete the interaction of CEACAM6 with CEACAM1 with all antibodies tested except for TPP-3688 (Neo201-hIgG2).

In conclusion, this observation is consistent with the hypothesis of a) CEACAM1 on activated T cells being a possible interaction partner for CEACAM6 leading to inhibition of T cells, b) the N-terminal D1 domain of CEACAM6 being implicated in the interaction between CEACAM1 and CEACAM6, and c) antibodies of the invention being capable to interfere with CEACAM6-CEACAM1 interaction.

Example 11: Inhibition of immunosuppressive activity of CEACAM6 in vitro

The immunosuppressive function of CEACAM6 on tumor cells was studied recently in vitro (Witzens-Harig et al., Blood 2013 May 30;121(22):4493-503) and in vivo (Khandelwal et al., Poster Abstract 61, Meeting Abstract from 22nd Annual International Cancer Immunotherapy Symposium October 6-8, 2014, New York City, USA). Commercially available 9A6 antibody (Genovac/Aldevron) was shown to be able to inhibit immunosuppressive activity of CEACAM6, leading to enhanced cytokine secretion by T cells in vitro and anti-tumor efficacy in vivo.

To study the effect of the antibodies of the invention on the immunosuppressive activity of CEACAM6, co-culture experiments of a model tumor cell line with a model tumor antigen-specific T cell clone were conducted:

Tumor-antigen specific T cells were generated by a procedure described in Brackertz et al (Brackertz et al., Blood Cancer J. 2011 Mar;1(3):e11). Briefly, survivin specific $CD8^+$ T cells were isolated from peripheral mononuclear cells via CD8-specific magnetic-activated cell sorting. The isolated $HLA\text{-}A2^-CD8^+$ T cells were repetitively stimulated with allogenic $HLA\text{-}A2^+$ dendritic cells loaded with 10 µg of the HLA-restricted peptide epitope $Survivin_{95\text{-}104}$ (ELTLGEFLKL). After stimulation, the proliferating T cells were stained with HLA-A2/$Survivin_{95\text{-}104}$ multimers (A*02:01 391 LMLGEFLKL Survivin 96-104 labeled with APC, ProImmune Limited, #F391-4A-E), FACS sorted and cloned by limiting dilution in 96-well plates.

The T cell clone expansion was performed by culturing 2×10^5 T cell clones and feeder cells composed of 5×10^7 irradiated PBMCs (30 Gy) and 1×10^7 irradiated LCL (these B lymphoblastoid cell lines that were generated by EBV transduction of peripheral blood B cells from healthy donors with a EBV-infected monkey cell line (B95/8, ATTC), as described in Brackertz et al., Blood Cancer J. 2011 Mar;1(3):e11 and Dissertation Andreas Moosmann, Ludwig-Maximilians-University Munich, Germany, 2002) from different donors (100-150 Gy) in 40 ml of RPMI-1640 medium with glutamine (Sigma-Aldrich), 10% human serum (Human AB serum, Valley Biomedical, Inc, #HP1022), 1% Penicillin/Streptomycin (Life Technologies) at 37 °C and 5% CO_2. The expansion occurred in the presence of 50 U/ml IL-2 (Proleukin, Novartis, #1003780), 2.5 ng/ml IL-15 (rhIL-15-CF R&D #247_IL-025/CF) and 30 ng/ml anti-human CD3 antibody (OKT3 eBiosciences 16-0037-85) for 14 days. The KS human breast cancer cell line (obtained from Dr. Brigitte Gückel (University of Tübingen, Germany)) was cultured in DMEM (Sigma-Aldrich) with 10% FCS (FBS Superior, Biochrom) and 1% Penicillin/Streptomycin at 37 °C and 5% CO_2.

To analyze the modulatory activity of the anti-CEACAM6 antibodies on the immunosuppressive function of CEACAM6 in vitro, the survivin-peptide specific $CD8^+$ T cell clone was co-cultivated together with the $CEACAM6^+$, $HLA\text{-}A2^+$ and $survivin^+$ human breast cancer cell line KS and IFN-gamma secretion as readout for T cell activity was measured either by IFN-gamma ELISpot or IFN-gamma ELISA.

For the co-culture, KS tumor cells were detached non-enzymatically using PBS-EDTA for 5 min, centrifuged, washed and counted. Cell concentration was adjusted to

1 x 10^5 cells/ml in X-Vivo-20 (Lonza) and cells were pretreated with anti-CEACAM6 antibodies or isotype-matched control antibodies for 10 min on ice. After the incubation step, 10,000 KS target cells were seeded directly in triplicates to IFN-gamma-ELISpot or U-96-Well ELISA plates, respectively. In the meantime, survivin-peptide specific T cells were harvested, washed with X-Vivo-20 and seeded in the cell numbers indicated on the KS target cells. The co-culture of tumor cells, anti-CEACAM6 antibodies and T cells was incubated for 20 - 40 h at 37 °C. IFN-gamma ELISpot plates (MABTECH: ELISpot Assay for human Interferon gamma #3420-3PT, Antibodies mAB 1-D1K anti-IFNg, mAB 7-B6-1-Biotin, Steptavivin-ALP, BCIP/NBT plus substrate for ELISpot #3650-10) and IFN-gamma-ELISA (BD human IFN-gamma ELISA Set #555142) were developed according to the manufacturer´s instructions. ELISpot plates were counted with a C.T.L. ELISpot plate reader and optical density for ELISA plates was measured with a Tecan Infinite M200 plate reader. An experiment was considered as valid if the positive control TPP-3470 (9A6-hIgG2) was statistically significant compared to the isotype-matched antibody control.

Co-culture of KS tumor cells with survivin-peptide specific $CD8^+$ T cells in the presence of anti-CEACAM6 antibodies resulted in a statistically significant increase of IFN-gamma production by the T cells (Figure 5) compared to the samples not treated with anti-CEACAM6 antibody or treated with isotype-matched control antibody.

In conclusion, cynomolgus cross-reactive antibodies TPP-3310, TPP-3707, and TPP-3323 were able to relieve CEACAM6 mediated immunosuppression of tumor antigen specific T cells to the same extent as TPP-3470 (9A6-hIgG2) as measured by either IFN-gamma secretion of survivin-peptide specific $CD8^+$ T cells or number of IFN-gamma secreting activated T cells.

Example 12: Analysis of cytokine/chemokine profile secreted by T cells treated with anti-CEACAM6 antibodies

In order to study the effects of anti-CEACAM6 antibodies on the human T cell cytokine/chemokine profile towards an improved cytotoxicity and an effective anti-tumor immune response, Luminex-based multiplex cytokine analysis of co-culture

experiments of a model tumor cell line and a model tumor antigen specific T cell clone were performed.

A survivin-peptide specific $CD8^+$ T cell clone was generated and expanded in vitro as described in Example 11. Tumor cell culture and ELISA co-culture were performed as described in Example 11.

After 20 h of co-culture plates were centrifuged for 10 min at 1400 rpm and supernatant was collected. Multiplex analysis was performed using the MILLIPLEX Human Cytokine/Chemokine Magnetic Bead Panel - Premixed 38 Plex analytes (Merck Millipore #HCYTMAG-60K-PX38) on a BioPlex100 System (Bio-Rad) according to manufacturer´s instructions. Standard curves and concentrations were calculated with Bio-Plex Manager 6.0. An experiment was considered as valid if the positive control TPP-3470 (9A6-hIgG2) was >1.5x increased compared to the isotype-matched antibody control.

Blockade of CEACAM6 by antibodies of the invention in the co-culture of survivin-peptide specific T cells with KS tumor cells yields a >1.5 times increase in IFN-gamma, IL-2 and TNF-alpha secretion compared to the control samples that were treated with the isotype-matched control (Figure 6).

In conclusion, the cynomolgus cross-reactive antibodies TPP-3310 and TPP-3707 are able to change the cytokine profile of survivin-peptide specific $CD8^+$ T cells towards a more cytotoxic and activated phenotype characterized by increased IFN-gamma, IL-2 and TNF-alpha secretion as measured by Luminex-based multiplex analysis to the same extent as TPP-3470 (9A6-hIgG2).

Example 13: Anti-tumor efficacy in adoptive T cell transfer KS model

The anti-tumor efficacy of an anti-CEACAM6 antibody (9A6; Genovac/Aldevron) has been studied in vivo in adoptive human T cell transfer systems in which tumor-antigen specific human T cells are expanded in vitro and co-injected with an anti-CEACAM6 antibody into nude mice bearing human xenograft tumors (Khandelwal et al., Poster Abstract 61, Meeting Abstract from 22nd Annual International Cancer Immunotherapy Symposium October 6-8, 2014, New York City, USA).

To study the effect of antibodies of the invention on anti-tumor efficacy, the following adoptive T cell transfer experiment was conducted:

A survivin-peptide specific $CD8^+$ T cell clone was generated and expanded in vitro as described in Example 11.

Six to eight weeks old female NOD-Scid mice (NOD.CB17-$Prkdc^{scid}$/J; Charles River, France) were injected subcutaneously with 2 x 10^6 KS tumor cells (see Example 11). Randomization of mice was performed on day 16 and mice with a tumor surface lower than 40 mm^2 were excluded (= no tumor take). Mice (n = 8-10 mice per group) were treated on day 23 and 27 with i.v. adoptive transfer of 5 x 10^6 survivin-peptide specific T cell clone. 200 µg of the anti-CEACAM6 antibodies TPP-3740, TPP-3707, TPP-3310 or the respective isotype-matched control antibody were administered i.p. on days 22, 24, 26 and 28. The control group was injected with PBS instead of T cells and antibodies. Subcutaneously grown tumors were measured with a caliper and the surface was then calculated by using the formula "length x width". Only experiments were considered as valid, in which the vehicle-treated control group of mice exhibited a steady and significant increase of tumor surface and tumor volume throughout the entire duration of the study. The outcome of the experiment might be influenced by parameters that are difficult to control: not only the in vivo growth of KS cell lines proved to be variable but also survival of human T cells in mice as well T cell infiltration into tumors exhibited considerable variation.

Adoptive transfer of survivin-peptide specific T cells in combination with the anti-CEACAM6 antibodies tested resulted in a reduced tumor burden compared to T cells injected with the matched isotype control or the PBS control group (Figure 7). Similar efficacy was observed using TPP-3740 (9A6-hIgG2).

In conclusion, cynomolgus cross-reactive antibodies TPP-3310 and TPP-3707 exhibited anti-tumor efficacy to the same extent as TPP-3470 (9A6-hIgG2) in an adoptive T cell transfer model using survivin-peptide specific $CD8^+$ T cells and KS tumors.

Example 14: Tumor cell lines and tumor tissues that are CEACAM6 positive

CEACAM6 is expressed in various cancers which are potential target indications for treatment with CEACAM6 immunomodulating antibodies. Therefore cancer cell lines of different origin and which represent different cancers were tested for CEACAM6 expression by FACS analysis. The results are shown in Table 26.

Cancer cell lines which were acquired from public tissue banks such as the American tissue culture collection (ATCC) etc. were cultured according to the provider's instructions.

Cells were washed 3 times with PBS w/o Ca^{2+}/Mg^{2+} and were detached from the culture plate non-enzymatically with EDTA dissociation buffer (Gibco). Cells were washed in cold FACS buffer (PBS w/o Ca^{2+}/Mg^{2+} and heat-inactivated 3% FCS) and were counted using the cell counter countess machine (Invitrogen). 10^5 cells per well were plated and incubated with the mouse monoclonal antibody 9A6 (TPP-1744; 5 µg/ml) or the purified NA/LE Mouse IgG1 Isotype control antibody (BD Pharmingen #553447) for 1 h at 4 °C on a plate shaker. Then cells were washed (400 g, 5') with FACS buffer 2 times, were resuspended in 100 µl containing the PE-labeled anti-mouse secondary antibody (1:150 dilution, Dianova #115-115-164) and were incubated for another 1 h at 4 °C on a plate shaker. After 2 times washing the cells were resuspended in 100 µl FACS buffer and were analyzed on a FACS Canto II machine (Beckton Dickinson) or a FACS Array (Beckton Dickinson). The observed binding signal was specific as the non-binding isotype control did not result into a shift of the fluorescence signal (Table 26).

Cell line*	Cancer Origin	Type	CEACAM6 surface expression
MCF7	breast	adenocarcinoma	+
MCF7/AdrVp (MDR breast CA)	breast	adenocarcinoma	+
KS	breast	malignant effusion, breast cancer patient	+++
BT-20	breast	adenocarcinoma, ER negative	-
BT-474	breast	ductal carcinoma;	+++
HCC38	breast	primary ductal carcinoma	-
MDA-MB-361	breast	adenocarcinoma, derived from metastatic site: brain	+++
MDA-MB-453	breast	metastatic carcinoma, derived from metastatic site: pericardial effusion	-

Cell line*	Cancer Origin	Type	CEACAM6 surface expression
MFM-223	breast	epithelial-like, ductal carcinoma	+/-
MX-1	breast	infiltrating ductal carcinoma, ER-negative	-
SUM 149	breast	invasive ductal carcinoma, ER-PR- inflammatory breast cancer	-
SUM 159	breast	Er-, PR- anaplastic carcinoma of the breast	-
T-47D	breast	ductal carcinoma, from metastatic site: pleural effusion	+
ZR-75-1	breast	ductal carcinoma, from metastatic site: ascites	++
HPAC	pancreas	adenocarcinoma	++++
SW1990	pancreas	adenocarcinoma, from metastatic site: spleen	-
PaTu 8902	pancreas	adenocarcinoma	+-++
AsPC-1	pancreas	adenocarcinoma, from metastatic site: ascites	+++
DAN-G	pancreas	adenocarcinoma	+
MIA PaCa-2	pancreas		-
Panc1	pancreas	ductal, epithelioid pancreatic carcinoma	- -
BxPc3	pancreas	adenocarcinoma	+++
Capan-2	pancreas	adenocarcinoma	-
PC3.gd.neo (PaCa)	prostate	adenocarcinoma, from metastatic site: bone	-
HPAFII (PaCa)	pancreas	adenocarcinoma	+++
SW 1463	rectum	epithelials, Dukes' type C, colorectal adenocarcinoma	+/-
SNU-C1	colon	adencarcinoma, from metastatic site: peritoneum	++
HT55	colon	epithelial	+++

Cell line*	Cancer Origin	Type	CEACAM6 surface expression
Colo 201	colon	Dukes type D, adenocarcinoma, from metastatic site: ascites	-
Colo320DM	colon	Dukes type D, colorectal adenocarcinoma	-
CaCo-2	colon	adenocarcinoma	+-++
SW403	colon	Dukes type C adenocarcinoma	-
HCC2998	colon	adenocarcinoma	++
RKO	colon		-
KM-12	colon	adenocarcinoma	++
CL-34	large intestine	adenocarcinoma	+
COLO 205	colon	Dukes type D, adenocarcinoma	'+/-
HCT 116	colon		-
SW480	colon	Duke type B, colorectal adenocarcinoma	- -
WiDr	colon	adenocarcinoma	++
DLD-1	colon	Dukes Type C, adenocarcinoma	-
SW 620	colon	Dukes Type C, adenocarcinoma, from metastatic site: lymph node	-
SW1116	colon	adenocarcinoma	+++
T-84	colon	colon metatases from the lung	+ - ++
LoVo	colon	adenocarcinoma	++
HCT15	colon	Dukes type C, adenocarcinoma	-
HT29	colon	adenocarcinoma	++
LS174T	colon	Dukes type B, adenocarcinoma	+/-

Cell line*	Cancer Origin	Type	CEACAM6 surface expression
EKVX	lung	adenocarcinoma	-
A549	lung		+++
NCI-H1688	lung	SCLC	+
Calu-1	lung	epidermoid carcinoma, K-ras positive	-
Calu-3	lung	adenocarcinoma	+
HCC827	lung	adenocarcinoma	++
LXF-289	lung	adenocarcinoma	-
NCI-H1299	lung	from metastatic site: lymph node	-
NCI-H1437	lung	adenocarcinoma, from metastic site. pleural effusion	+++
NCI-H146 (SCLC)	lung	derived from metastatic site (bone marrow)	+/-
NCI-H1581	lung	Large cell NSCLC	-
NCI-H1975	lung	adenocarcinoma	-
NCI-H1993	lung	adenocarcinoma, from metastatic site: lymph node	+++
NCI-H2228	lung	adenocarcinoma	++
NCI-H226	lung	squamous cell carcinoma, mesothelioma, from metastatic site: pleural effusion	-
NCI-H23	lung	adenocarcinoma	-
NCI-H292	lung	mucoepidermoid pulmonary carcinoma	-
NCI-H322	lung	bronchioalveolar carcinoma	-
NCI-H358	lung	bronchioalveolar carcinoma, from metastatic site alveolus	-
NCI-H441	lung	papillary adenocarcinoma	++

Cell line*	Cancer Origin	Type	CEACAM6 surface expression
NCI-H460	lung	Large cell lung carcinoma, from metastatic site: pleural effusion	-
NCI-H520	lung	squamous cell carcinoma	-
NCI-H522	lung	adenocarcinoma K-ras, mutated p53	-
NCI-H661	lung	large cell lung carcinoma, from metastatic site: lymph node	-
NCI-H69 (SCLC)	lung		-
NCI-H82 (SCLC)	lung	from metastic sit:e pleural effusion	-
SW 900	lung	squamous cell carcinoma	-
HCC-2935	lung	adenocarcinoma	++++
HCC-1395	lung	primary ductal carcinoma	-
RPMI-8226	myeloma	plasmacytoma; multiple myeloma (IgG lambda-type) B lymphocyte; lymphoblast	+
SKMM2	myeloma		-
L-363	myeloma	plasma cell leukemia	-
JJN-3	myeloma	plasma cell leukemia	-
KMS-12-BM	myeloma		-
KMS-12-PE	myeloma		-
LP-1	myeloma		-
MOLP-2	myeloma		
MOLP-8	myeloma		-
SNU-1	gastric	from metastatic site : ascites	+++
Hela	cervix	adenocarcinoma	-

Cell line*	Cancer Origin	Type	CEACAM6 surface expression
DMS-153 (SCLC)	lung	from metastatic site : liver	-
MeWo	skin	fibroblast, malignant melanoma, from metastic site: lymph node	-

Definition of -,+ ,++ , +++ as determined from FACS median fluorescence log shift: - = no shift; + = log shift as compared to control antibody, median 10-100; ++ = 2 log shift, median 100-1,000; +++ = 3 log shift, median 1,000-10,000; ++++ = 4 log shif; median> 10000

*All cell lines from public tissue bank such as the American tissue culture collection etc, except KS breast cancer cell line which was kindly provided by Dr. Gückel (Tübingen); B.Gueckel, Cancer Cell International 2004, 4(Suppl 1):S38).

Table 26: Result of human cancer cell line screening by FACS for binding of CEACAM6 specific antibody 9A6 mIgG1 (TPP-1744) and thus CEACAM6 expression

In conclusion, CEACAM6 is expressed in cell lines which represent various cancers (e.g. colorectal cancer, non-small-cell lung cancer (NSCLC), small cell lung cancer (SCLC), pancreatic cancer, gastric cancer, breast cancer and multiple myeloma) which constitute potential target indications for treatment with CEACAM6 immunomodulating antibodies and other response modifiers (e.g. peptides, small molecules, artificial scaffold binders etc).

Example 15: Binding to single domain 1 of human and cynomolgus CEACAM6

To test whether antibodies of the invention can bind to the isolated single domain 1 of human and cynomolgus CEACAM6, SPR experiments were conducted as in Example 1.

The single N-terminal domain 1 of cynomolgus CEACAM6 (TPP-2453) was produced as described in Example 1 in analogy to TPP-1794:

Name	Protein-ID	Description	SEQ-ID
Macaca fascicularis CEACAM6-Domain 1-His	TPP-2453	Domain 1, fusion to His (expressed in E. coli)	SEQ-ID NO:180

SEQ-ID NO:180 (TPP-2453)

MQLTIESRPFNVAEGKEVLLLAHNLPQNTLGFNWYKGERVDAKRLIVAYVIGTQQTTPGPAHSGREMIYS
NASLLIQNVTQNDTGSYTLQAIKEDLVTEEATGRFWVYPELGSGSHHHHHHHH

Affinities (monovalent K_D) of antibodies of the invention towards recombinant single domain 1 of human and cynomolgus CEACAM6 were determined by SPR analogously to experimental procedures described in Example 1, and are shown in Table 27.

Test Antibody	Isotype	Recombinant single domain 1 of human CEACAM6 (TPP-1794) K_D [nM]	Recombinant single domain 1 of Macaca fascicularis CEACAM6 (TPP-2453) K_D [nM]
TPP-2971	Mouse IgG1	11	5.3
TPP-3186	Mouse IgG1	15	8.7
TPP-3187	Mouse IgG1	12	6.9
TPP-3308	Human IgG2 chimera	9.5	5.4
TPP-3310	Human IgG2	3.7	3.4
TPP-3322	Human IgG2 chimera	12	8.8
TPP-3323	Human IgG2 chimera	9	6.9
TPP-3705	Human IgG2	6.7	2.7
TPP-3707	Human IgG2	6.4	2.4
TPP-3714	Human IgG2	3.7	3.2
TPP-3820	Human IgG2	5.1	5.2
TPP-3821	Human IgG2	4.5	4.7
TPP-1745	Human IgG1	3.3	-

"-": no binding detected

Table 27: SPR analysis: monovalent K_D (in nM)

In conclusion, antibodies of the invention bind to both human and cynomolgus N-terminal domain 1 of CEACAM6 with comparable affinities.

Example 16: X-ray crystal structure of the human CEACAM6 single N-terminal domain1 in complex with Fab fragment APP-1574

The crystal structure of single N-terminal domain 1 of human CEACAM6 (TPP-1794; SEQ ID NO 169) bound to a Fab fragment related to TPP-3310 (called APP-1574) was determined.

To facilitate production of the Fab fragment TPP-3310 was produced as human IgG1 variant (called TPP-5468, see Table 28). Papain cleavage of TPP-5468 and subsequent purification results in APP-1574. This Fab fragment comprises the variable domains (VH and VL) of TPP-3310 (see Table 28).

Protein	Heavy Chain	Light Chain
TPP-5468	SEQ ID NO: 181	SEQ ID NO:182
APP-1574	SEQ ID NO: 183	SEQ ID NO: 184

Table 28: Amino acid sequences of IgG and Fab used for crystal structure determination

As detailed in Example 1, CEACAM6 domain 1 has been expressed and refolded from E. coli. The Fab-fragment has been generated by digestion of the antibody with Papain, followed by complex formation. Protein crystallography was then employed to generate atomic resolution for single N-terminal domain 1 of human CEACAM6 bound to APP-1574 Fab to define the epitope.

Protein Production

The single N-terminal domain 1 of human CEACAM6 (TPP-1794; SEQ-ID 169) was produced as 6x His fused protein construct as described in Example 1. The protein was concentrated to 6.7 mg/ml prior to complex formation.

The corresponding Fab-fragment of TPP-5468 (human IgG1) has been obtained by cleavage with the protease Papain. 1 mg of the antibody was mixed with 50 µl immobilized papain (ThermoFisher #20341) in digestion buffer (20 mM Na-Phosphate pH 7.0, 10 mM EDTA, 20 mM Cystein-HCl) and incubated for 4 h at 37 °C with continuous stirring. Immobilized papain was removed by centrifugation and resulting Fc-fragments and non-cleaved IgG were removed by passing over

MabSelectSURE (GE Healthcare, #11-0034-89 AC). The Fab-fragment in the flow-through was further purified via size exclusion chromatography in 30 mM Tris buffer pH 8.5, 150 mM NaCl on Superdex 75 and concentrated to 7.2 mg/ml.

For complex formation, purified Fab-fragment and human CEACAM6 N-terminal domain 1 were mixed in ratio 1 Fab to 1.4 human CEACAM6 N-terminal domain 1 for 1 human CEACAM6 N-terminal domain 1 h at 4 °C. The resulting protein complex was isolated by size exclusion chromatography in 30 mM Tris buffer pH 8.5, 150 mM NaCl on Superdex 75 and further concentrated to 21.2 mg/ml prior to crystallization.

Crystallization and structure determination

The complex of single N-terminal domain1 of human CEACAM6 and the Fab fragment APP-1574 was concentrated to 21.2 mg/ml, centrifuged at 20,000 g for 10 minutes and screened for crystallization. Crystals for data collection were grown by hanging drop vapor diffusion at 20 °C. In detail, 0.2 µl of the complex was mixed with 0.2 µl of reservoir solution containing 100 mM tri-sodium citrate pH 4.9, 19% (w/v) PEG 4000 and 10% (v/v) isopropanol. The drop was then equilibrated against 80 µl of the same reservoir solution. Before data collection, the crystals were flash cooled in liquid nitrogen.

Diffraction data were collected at beamline 14-1 at the BESSY II Synchrotron Source (Helmholtz Zentrum Berlin) and processed using XDS (Kabsch, W. XDS. Acta Cryst. D66, 125-132 (2010). The data of human CEACAM6 single N-terminal domain1-Fab fragment APP-1574 complex were processed to 2.7 Å in the space group P1 with cell dimensions a=64.7 Å, b=65.2 Å, c=78.6 Å, alpha=66.1°, beta=87.2° and gamma= 88.5°. The structure of the complex was solved by molecular replacement using PHASER (McCoy AJ et al, J Appl Cryst (2007). 40, 658-674). with in-house structures of the human CEACAM6 single N-terminal domain1 and a Fab as search models. The final model was built in COOT (Emsley, P. et al, Acta Cryst D66, 486-501 (2010)) and refined using CCP4 (Winn, M. D. et al. Acta. Cryst. D67, 235-242 (2011)).

The epitope was defined as residues of human CEACAM6 single N-terminal domain1 that contain atoms within 5 Å to any atom in Fab fragment APP-1574, identified by NCONT in the CCP4 program suite (Winn, M. D. et al. Acta. Cryst. D67, 235-242 (2011)) and listed in Table 29). There are two copies of human CEACAM6 single N-terminal domain1-Fab fragment APP-1574 complex in the asymmetric unit

(the smallest unique unit in the crystal). Only those antibody-contacting residues that are common in both copies are listed as epitope residues.

Epitope

The crystal structure of the human CEACAM6 single N-terminal domain1 -Fab fragment APP-1574 complex was used to identify the epitope of Fab fragment APP-1574 on CEACAM6. The interaction surface on human CEACAM6 single N-terminal domain1 by Fab fragment APP-1574 is formed by several continuous and discontinuous (i.e. noncontiguous) sequences; namely residues Pro59, Gln60, Asn61, Arg62, Ile63, Gly64, Val83, Ile84, Gly85, Thr86, Gln88, Thr90, Pro91, Ile125, Ser127, Asp128 and Leu129 (numbering according to SEQ-ID:179; TPP-4639) as detailed in Table 29.

In a very close direct contact are residues having at least one atom that is 3.6 Å or less away from the antibody. These residues are: Gln60, Asn61, Arg62, Ile63, Val83, Ile84, Gly85, Thr90, Ser127, Asp128 and Leu129 (numbering according to SEQ-ID:179; TPP-4639).

These residues form the exemplary three-dimensional conformational epitope that is recognized by the Fab fragment APP-1574 (Figures 9 and 10).

N-terminal domain 1 of human CEACAM6 (TPP-1794; SEQ-ID 169)		**Fab APP-1574**		
Amino Acid	**Number as in SEQ-ID 169 (number as in SEQ-ID NO: 179 in brackets)**	**Amino Acid**	**Number**	**Chain**
Pro	26 (59)	Tyr	32	H
Gln	27 (60)	Tyr	32	H
Asn	28 (61)	Trp	55	H
		Asn	56	H
		Tyr	32	H

		Asn	58	H
Arg	29 (62)	Trp	55	H
		Tyr	32	H
		Gly	33	H
Ile	30 (63)	Ser	101	H
		Gly	33	H
		Trp	54	H
		Leu	102	H
		Ser	101	H
		Pro	103	H
		Trp	55	H
Gly	31 (64)	Leu	102	H
Val	50 (83)	Ser	101	H
		Leu	102	H
		Tyr	104	H
Ile	51 (84)	Gly	33	H
		Tyr	32	H
Gly	52 (85)	Ile	34	H
		Gly	33	H
		Ser	101	H
		Tyr	32	H
		Thr	31	H
Thr	53 (86)	Ser	101	H
		Ile	34	H
		Arg	99	H
Gln	55 (88)	Tyr	49	L
Thr	57 (90)	Tyr	49	L
		Asn	53	L

Pro	58 (91)	Asn	53	L
Ile	92 (125)	Leu	102	H
Ser	94 (127)	Tyr	94	L
		Trp	54	H
		Tyr	60	H
		Trp	55	H
		Asn	56	H
		Asn	58	H
Asp	95 (128)	Tyr	94	L
		Tyr	60	H
Leu	96 (129)	Tyr	94	L
		Ser	92	L
		Ser	93	L
		Tyr	91	L
		Pro	103	H

Table 29: Interactions between single N-terminal domain 1 of human CEACAM6 and Fab APP-1574

CEACAM6 N-terminal domain1 residues numbered as in SEQ ID NO 169. The antibody residues are numbered based upon their linear amino acid sequence (SEQ ID NO: 183 and SEQ ID NO: 184) and corresponding chains are labeled ("H" for heavy chain, "L" for light chain). Human CEACAM6 single N-terminal domain1 residues shown here to have at least one atom with 5 Å to any atom in Fab fragment APP-1574, to account for potential water mediated interactions.

When carefully analyzing the epitope, it becomes apparent that Isoleucine-63 (according to SEQ-ID NO: 179) of human CEACAM6 is a central part of the epitope. The Isoleucine side-chain has good shape complementary with APP-1574. Modelling indicates that a Leucine at this position in cynomolgus CEACAM6 can be sterically accommodated and will not disrupt the interaction. This explains a retained binding

activity to cynomolgus CEACAM6 activity and is the basis for human-cynomolgus cross-reactivity. In contrast, a Phenylalanine at this position (as in human CEACAM1, human CEACAM3 and human CEACAM5) cannot be sterically accommodated and will lead to loss in binding activity. This is the basis for CEACAM6 selectivity.

Thereby, recognition of Isoleucine-63 (according to SEQ-ID NO: 179) represents the most significant "selectivity tuner" between target CEACAMs. The APP-1574 recognition mode of human CEACAM6 optimally exploits key residue difference between targets and off-targets. Previous analysis of a structure of the Fab fragment of TPP-1679 (which selectivity profile is insufficient, see Example 4) in complex with N-terminal domain 1 also identified Isoleucine-63 (according to SEQ-ID NO: 179) as potential selectivity switch (data not shown). However, since the molecular recognition mechanism by TPP-1679 is different, whereby Ileucine-63 (according to SEQ-ID NO: 179) is located at the binding site periphery, it was difficult to exploit.

In summary, binders that in addition to other residues forming the epitope (Table 29) also optimally exploit binding to the selectivity & cross-reactivity determining residue Isoleucine-63 (according to SEQ-ID O: 179) of CEACAM6 and still allowing the accommodation of a Leucine at that position, but not Phenylalanine, will be CEACAM6 selective, but at the same time human-cynomolgus CEACAM6 cross-reactive.

Mutagenesis

To substantiate the findings and predictions of structural analysis in binding studies, the following mutants of N-terminal domain 1 of human CEACAM6 were generated:

Protein	Protein-ID	Amino Acid Sequence
Human CEACAM6-Domain 1-His Wild-type	TPP-1794; SEQ-ID NO:169	MKLTIESTPF NVAEGKEVLL LAHNLPQNR**I** GYSWYKGERV DGNSLIVGYV IGTQQATPGP AYSGRETIYP NASLLIQNVT QNDTGFYTLQ VIKSDLVNEE ATGQFHVYPG SGSHHHHHHH H
Human CEACAM6-Domain 1-His -	TPP-8697 SEQ-ID	MKLTIESTPF NVAEGKEVLL LAHNLPQNR**L** GYSWYKGERV DGNSLIVGYV IGTQQATPGP AYSGRETIYP NASLLIQNVT QNDTGFYTLQ VIKSDLVNEE ATGQFHVYPG

I30L (I63L according to SEQ-ID NO: 179)	NO:185	SGSHHHHHHH H
Human CEACAM6-Domain 1-His - I30F (I63F according to SEQ-IDNO : 179)	TPP-8698 SEQ-ID NO:186	MKLTIESTPF NVAEGKEVLL LAHNLPQNR**F** GYSWYKGERV DGNSLIVGYV IGTQQATPGP AYSGRETIYP NASLLIQNVT QNDTGFYTLQ VIKSDLVNEE ATGQFHVYPG SGSHHHHHHH H

Table 30: Amino acid sequences of proteins used in mutational binding studies

The proteins were expressed in E. coli, refolded and purified as described in Example 1. Comparative binding activity to domain 1 wild-type protein and the two single mutations was determined by ELISA method. 1.5 ug/ml protein solutions in PBS were coated overnight to 384 Nunc MaxiSorp plates (Sigma, P6491). Plates were washed with PBS/T and blocked with Smart block (CANDOR Bioscience GmbH, 113125). Subsequently, dilution series of TPP-3310, TPP-1679 and an isotype control antibody were applied to the wells. After washing with PBS/T, bound antibodies were detected with Anti Human IgG Fc POD (Sigma, A0170) and 10 µM Amplex Red solution (Thermo, A12222). Positive binding signals were detected via Fluorescence (Ex. 535 nm / Em. 590 nm). Table 32 shows binding activity for TPP-3310 to the domain 1 wild-type protein and the mutation of Isoleucine 63 (as in SEQ-ID NO: 179) to Leucine (as in cynomolgus). The mutation of amino acid position 63 (as in SEQ-ID NO: 179) to Phenylalanine (as in human CEACAM1, human CEACAM3 and human CEACAM5) results in complete loss of binding ability. As a control for demonstration of efficient refolding of CEACAM6 N-terminal domain 1 proteins, TPP-1679 was employed (see Example 4), for which binding to a similar extent to all antigens tested in Table 31 was observed.

Antibody	**Human CEACAM6-Domain 1-His Wild-type** TPP-1794; SEQ-ID NO:169	**Human CEACAM6-Domain 1-His I30L** (I63L according to SEQ-ID NO: 179) TPP-8697; SEQ-ID NO:185	**Human CEACAM6-Domain 1-His I30F** (I63F according to SEQ-ID NO: 179) TPP-8698; SEQ-ID NO:186
TPP-3310	+	+	-
TPP-1679	+	+	+

Isotype control	-	-	-

"+" denotes binding detected; "-"denotes no binding detected

Table 31: Binding activity on CEACAM6 N-terminal domain 1 mutants.

In conclusion, the truly human – cynomolgus CEACAM6 cross-reactive antibody TPP-3310, which is at the same time selective with regards to other human paralogs, was able to tolerate an I63L substitution (according to SEQ-ID: 179) (corresponding to cynomolgus CEACAM6 residue) but not an I63F substitution (according to SEQ-ID: 179) (corresponding residue in human paralogs CEACAM1, CEACAM3, and CEACAM5) in the context of human CEACAM6 N-terminal domain 1 consistent with results obtained from X-ray crystallography and substantiating our prediction.

Example 17: Analysis of T cell mediated cytotoxicity in the presence of CEACAM6 antibodies

The effect of the anti-CEACAM6 antibodies on T cell mediated cytotoxicity was studied in cytotoxicity experiments with co-cultures of CEACAM6 positive tumor cells and T cells derived of different sources. These T cells were either $CD8^+$ survivin T cells or patient-derived T cells from a pancreatic cancer. For these tumor cell killing experiments an impedance based cytotoxicity assay (xCELLigence) system was used.

The survivin-peptide specific $CD8^+$ T cell clone was generated and expanded in vitro as described in Example 11. Pancreatic cancer tumor infiltrating lymphocyte cell lines (TILs) were isolated from fresh primary culture of tumor tissue from surgery. In brief, fresh primary tissue material was cut into small pieces and cultured in small dishes in X-Vivo-15 medium (Lonza) containing 2% human serum albumin, 2.5 µg/ml Fungizone, 20 µg/ml Gentamycin, 1% Penicillin/Streptomycin with 6000 IU/IL-2 for 10-18 days. Afterwards cells from the supernatant were harvested and either frozen or used directly for a "rapid expansion protocol" (REP). For rapid expansion of TILs, frozen TILs were gently thawed and cultured with $0.6*10^6$ cells/ml for 1 day in Complete Lymphocyte Medium CLM RPMI-1640 (Life Technologies #21875034), 10% human AB Serum (MILAN Analytica #000083), 1% Penicillin/Streptomycin (Life Technologies #15140122), 1% ml HEPES (Life Technolgies #15630056), 0.01% β-mercaptoethanol [stock 50 mM] (Life Technologies #31350010)) with 6000 IU/ml IL-2. TILs were

harvested and expanded at a 1:100 ratio with 60 Gy irradiated feeder PBMCs from 3 different donors in 400 ml REP medium (50% CLM mixed with 50% AIM-V serum free medium (Gibco #12055091) containing 3000 IU/ml IL-2 and 30 ng/ml OKT-3 antibody (eBioscience #16-0037-85)) in G-REX-100 Flasks (Wilson Wolf #80500S). Cells were cultured and splitted as described in Jin et al., J Immunother. 2012 Apr;35(3):283-92 . After 14 days cells were harvested and frozen in aliquots. Prior to co-culture cytotoxicity assays, individual aliquots of TILs were gently thawed and cultured with $0.6*10^6$ cells/ml for 2 days in CLM containing 6000 IU/ml IL-2 and 1 day in CLM without IL-2.

Tumor cells were cultivated according to standard protocols and provider's instructions

T cell mediated cytotoxity was analyzed in an impedance based cytotoxicity assay (xCELLigence) system. In this label free assay system cytotoxicity is measured directly and continuously over a long time period of around 100-150 h (real time). Adherent tumor cells are attached to microelectrodes at the bottom of a 96-Well E-plate (E-Plate VIEW 96 PET; ACEA Biosciences #ID:H000568) which changes the electrical impedance of these electrodes. This is monitored as an increase of the dimensionless "cell index". After adherence of the tumor cells (~24 h) antibodies and T cells are added to the wells which, if T cells exert cytotoxic activity, results in lysis of the tumor cells and detachment from the electrodes. This detachment changes the impedance of the wells and is measured as a decrease of the "cell index" or "normalized cell index" which is the "cell index" normalized to the time point of T cell addition. The T cells alone do not affect the electrical impedance of the electrodes and thus only the cytolysis of the tumor cells is measured. (Peper et al, J Immunol Methods. 2014 Mar;405:192-8)

In first experiments we established that tumor cell killing observed in this assay system is T cell dose dependent and works for different tumor cell:T cell ratios and different T cell sources (Survivin-peptide specific $CD8^+$ T cells, TILs from pancreatic cancer patients).

We then studied the effect of anti-CEACAM6 antibodies on the cytolytic efficacy of survivin T cells. Therefore, the CEACAM6 positive breast cancer KS or the CEACAM6 transfected colon cancer HCT-116 (HCT116-hC6) was added to 96-well plates for 24 h before survivin-peptide specific T cells were added at different cell ratios together with the anti-CEACAM6 mAbs. The coculture was followed for a time period ~100 h. In these experiments we observed an improved T cell dependent cytotoxicity in

the presence of the anti-CEACAM6 antibodies TPP-3310 and TPP-3470 of ~21% on both cell lines. The results are displayed in Figure 11 A and B) exemplarily for one cell ratio. Notably, the survivin-peptide specific $CD8^+$ T cells alone show already a high cytotoxic impact of 45-62%, which is most likely due to the preactivation of the cultured T cells and is thus considered as background cytolysis. In summary, the increase of IFN-gamma secretion observed in the previous ELISA assays translates into a cytotoxic effect within approximately 24 h of co-culture. We conclude that treatment of CEACAM6 positive tumor cells with anti-CEACAM6 antibodies leads to improved survivin-peptide specific $CD8^+$ T cell mediated killing of both tumor cell lines.

In subsequent experiments we tested the effect of the CEACAM6 antibodies on the cytolytic activity of patient-derived TILs cells of a pancreatic cancer. Therefore, the CEACAM6 positive lung cancer cell line HCC2935 was added to 96-well plates and cultivated for 24 h. Then, TILs were added at different ratios in the presence of the CEACAM6 antibody (30 µg/ml) and of a bispecific antibody anti-CD3 x anti-EPCAM IgG (0.25 ng/ml) (Marmé et al., Int J Cancer. 2002 Sep 10;101(2):183-9; Salnikov et al., J Cell Mol Med. 2009 Sep;13(9B):4023-33) to allow for HLA-independent T cell mediated tumor cell killing. In the presence of the anti-CEACAM6 antibodies TPP-3310 and TPP-3470 we observed a complete drop of impedance which was not observed in the presence of the isotype matched control antibody. The drop in impedance is interpreted as complete cytolytic kill of the target cell line HCC2935. In an additional experiment it could be demonstrated that the effect of the CEACAM6 antibody TPP-3310 is dose dependent and an IC_{50} value of 0.62-0.21 µg/ml was determined. Figure 12 shows exemplarily the results for TIL-12.

In summary these experiments show that the CEACAM6 antibodies of the invention have the potential to effectively block the immunosuppressive receptor CEACAM6 and improve the cytotoxic efficacy not only of model T cells but also of patient-derived Tumor infiltrating lymphocytes against CEACAM6 positive tumor cells.

Table of Sequences

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TPP-2971	792.15H12C9	HCDR1	PRT	SEQ ID NO:4
TPP-2971	792.15H12C9	HCDR2	PRT	SEQ ID NO:5
TPP-2971	792.15H12C9	HCDR3	PRT	SEQ ID NO:6
TPP-2971	792.15H12C9	VL	PRT	SEQ ID NO:7
TPP-2971	792.15H12C9	LCDR1	PRT	SEQ ID NO:8
TPP-2971	792.15H12C9	LCDR2	PRT	SEQ ID NO:9
TPP-2971	792.15H12C9	LCDR3	PRT	SEQ ID NO:10
TPP-3186	792.11G2D10	VH	PRT	SEQ ID NO:13
TPP-3186	792.11G2D10	HCDR1	PRT	SEQ ID NO:14
TPP-3186	792.11G2D10	HCDR2	PRT	SEQ ID NO:15
TPP-3186	792.11G2D10	HCDR3	PRT	SEQ ID NO:16
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TPP-3186	792.11G2D10	LCDR2	PRT	SEQ ID NO:19
TPP-3186	792.11G2D10	LCDR3	PRT	SEQ ID NO:20
TPP-3187	792.15C4F4	VH	PRT	SEQ ID NO:23
TPP-3187	792.15C4F4	HCDR1	PRT	SEQ ID NO:24
TPP-3187	792.15C4F4	HCDR2	PRT	SEQ ID NO:25
TPP-3187	792.15C4F4	HCDR3	PRT	SEQ ID NO:26
TPP-3187	792.15C4F4	VL	PRT	SEQ ID NO:27
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TPP-3308	TPP-2971X1-hIgG2Kappa	LCDR2	PRT	SEQ ID NO:39
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TPP-3714	TPP-2971HU2-hIgG2Kappa	Heavy Chain	DNA	SEQ ID NO:131
TPP-3714	TPP-2971HU2-hIgG2Kappa	Light Chain	DNA	SEQ ID NO:132
TPP-3820	3187HU1-hIgG2Kappa	VH	PRT	SEQ ID NO:133
TPP-3820	3187HU1-hIgG2Kappa	HCDR1	PRT	SEQ ID NO:134
TPP-3820	3187HU1-hIgG2Kappa	HCDR2	PRT	SEQ ID NO:135
TPP-3820	3187HU1-hIgG2Kappa	HCDR3	PRT	SEQ ID NO:136
TPP-3820	3187HU1-hIgG2Kappa	VL	PRT	SEQ ID NO:137
TPP-3820	3187HU1-hIgG2Kappa	LCDR1	PRT	SEQ ID NO:138
TPP-3820	3187HU1-hIgG2Kappa	LCDR2	PRT	SEQ ID NO:139
TPP-3820	3187HU1-hIgG2Kappa	LCDR3	PRT	SEQ ID NO:140
TPP-3820	3187HU1-hIgG2Kappa	VH	DNA	SEQ ID NO:141
TPP-3820	3187HU1-hIgG2Kappa	VL	DNA	SEQ ID NO:142
TPP-3820	3187HU1-hIgG2Kappa	Heavy Chain	PRT	SEQ ID NO:143
TPP-3820	3187HU1-hIgG2Kappa	Light Chain	PRT	SEQ ID NO:144
TPP-3820	3187HU1-hIgG2Kappa	Heavy Chain	DNA	SEQ ID NO:145
TPP-3820	3187HU1-	Light Chain	DNA	SEQ ID NO:146

"TPP ID"	"Sequence Name"	"Sequence Region"	"Sequence Type"	"SEQ ID"
	hIgG2Kappa			
TPP-3821	3187HU2-hIgG2Kappa	VH	PRT	SEQ ID NO:147
TPP-3821	3187HU2-hIgG2Kappa	HCDR1	PRT	SEQ ID NO:148
TPP-3821	3187HU2-hIgG2Kappa	HCDR2	PRT	SEQ ID NO:149
TPP-3821	3187HU2-hIgG2Kappa	HCDR3	PRT	SEQ ID NO:150
TPP-3821	3187HU2-hIgG2Kappa	VL	PRT	SEQ ID NO:151
TPP-3821	3187HU2-hIgG2Kappa	LCDR1	PRT	SEQ ID NO:152
TPP-3821	3187HU2-hIgG2Kappa	LCDR2	PRT	SEQ ID NO:153
TPP-3821	3187HU2-hIgG2Kappa	LCDR3	PRT	SEQ ID NO:154
TPP-3821	3187HU2-hIgG2Kappa	VH	DNA	SEQ ID NO:155
TPP-3821	3187HU2-hIgG2Kappa	VL	DNA	SEQ ID NO:156
TPP-3821	3187HU2-hIgG2Kappa	Heavy Chain	PRT	SEQ ID NO:157
TPP-3821	3187HU2-hIgG2Kappa	Light Chain	PRT	SEQ ID NO:158
TPP-3821	3187HU2-hIgG2Kappa	Heavy Chain	DNA	SEQ ID NO:159
TPP-3821	3187HU2-hIgG2Kappa	Light Chain	DNA	SEQ ID NO:160
TPP-1306	macaca mulatta CEACAM6-Xa-Fc-His	Chain 1	PRT	SEQ ID NO:161
TPP-1436	Ceacam6	Chain 1	PRT	SEQ ID NO:162
TPP-1437	Ceacam1	Chain 1	PRT	SEQ ID NO:163
TPP-1438	Ceacam5	Chain 1	PRT	SEQ ID NO:164
TPP-1790	hCeacam6-WT-Fc-6xHis	Chain 1	PRT	SEQ ID NO:165
TPP-1791	hCeacam6-Dom1-MacMul-Xa-Fc-His	Chain 1	PRT	SEQ ID NO:166
TPP-1792	hCeacam6-Dom2-MacMul-Xa-Fc-His	Chain 1	PRT	SEQ ID NO:167
TPP-1793	hCeacam6-Dom3-MacMul-Xa-Fc-His	Chain 1	PRT	SEQ ID NO:168
TPP-1794	hCeacam6-Dom1-8xHis (E.coli)	Chain 1	PRT	SEQ ID NO:169
TPP-2443	cyno CEACAM-6-Xa-Fc-His	Chain 1	PRT	SEQ ID NO:170
TPP-2452	cynomolgus Ceacam6-Dom1-Xa-Fc-His	Chain 1	PRT	SEQ ID NO:171
TPP-2755	human CEACAM3	Chain 1	PRT	SEQ ID NO:172
TPP-4185	CEACAM1	Chain 1	PRT	SEQ ID NO:173

"TPP ID"	"Sequence Name"	"Sequence Region"	"Sequence Type"	"SEQ ID"
TPP-4186	CEACAM19	Chain 1	PRT	SEQ ID NO:174
TPP-4187	CEACAM3	Chain 1	PRT	SEQ ID NO:175
TPP-4188	CEACAM5	Chain 1	PRT	SEQ ID NO:176
TPP-4189	CEACAM6_macfa	Chain 1	PRT	SEQ ID NO:177
TPP-4190	CEACAM8	Chain 1	PRT	SEQ ID NO:178
TPP-4639	CEACAM6	Chain 1	PRT	SEQ ID NO:179
TPP-2453	Macaca fascicularis CEACAM6-Domain 1-His	Chain 1	PRT	SEQ-ID NO:180
TPP-5468	TPP-2971HU1-hIgG1Kappa	Heavy Chain	PRT	SEQ-ID NO:181
TPP-5468	TPP-2971HU1-hIgG1Kappa	Light Chain	PRT	SEQ-ID NO:182
APP-1574	Papain-cleaved Fab fragment of TPP-5468	Heavy Chain	PRT	SEQ-ID NO:183
APP-1574	Papain-cleaved Fab fragment of TPP-5468	Light Chain	PRT	SEQ-ID NO:184
TPP-8697	Human CEACAM6-Domain 1-His - I30L	Chain 1	PRT	SEQ-ID NO:185
TPP-8698	Human CEACAM6-Domain 1-His - I30F	Chain 1	PRT	SEQ-ID NO:186

Table 32: Correlation of SEQ ID NO to TPP-ID and associated sequence features (heavy and light chain of antibody, variable regions, complementarity determining regions (CDR)) for proteins (PRT) and nucleic acids (DNA)

CLAIMS:

1. An isolated anti-CEACAM6 antibody or antigen-binding fragment thereof comprising:

i. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:48, an H-CDR2 comprising SEQ ID NO:49, and an H-CDR3 comprising SEQ ID NO:50 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:52, a L-CDR2 comprising SEQ ID NO:53, and a L-CDR3 comprising SEQ ID NO:54, or

ii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:106, an H-CDR2 comprising SEQ ID NO:107, and an H-CDR3 comprising SEQ ID NO:108 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:110, a L-CDR2 comprising SEQ ID NO:111, and a L-CDR3 comprising SEQ ID NO:112, or

iii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:4, an H-CDR2 comprising SEQ ID NO:5, and an H-CDR3 comprising SEQ ID NO:6 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:8, a L-CDR2 comprising SEQ ID NO:9, and a L-CDR3 comprising SEQ ID NO:10, or

iv. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:34, an H-CDR2 comprising SEQ ID NO:35, and an H-CDR3 comprising SEQ ID NO:36 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:38, a L-CDR2 comprising SEQ ID NO:39, and a L-CDR3 comprising SEQ ID NO:40, or

v. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:120, an H-CDR2 comprising SEQ ID NO:121, and an H-CDR3 comprising SEQ ID NO:122 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:124, a L-CDR2 comprising SEQ ID NO:125, and a L-CDR3 comprising SEQ ID NO:126, or

vi. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:24, an H-CDR2 comprising SEQ ID NO:25, and an H-CDR3 comprising SEQ ID NO:26 and a light chain antigen-binding region that

comprises a L-CDR1 comprising SEQ ID NO:28, a L-CDR2 comprising SEQ ID NO:29, and a L-CDR3 comprising SEQ ID NO:30, or

vii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:76, an H-CDR2 comprising SEQ ID NO:77, and an H-CDR3 comprising SEQ ID NO:78 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:80, a L-CDR2 comprising SEQ ID NO:81, and a L-CDR3 comprising SEQ ID NO:82, or

viii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:134, an H-CDR2 comprising SEQ ID NO:135, and an H-CDR3 comprising SEQ ID NO:136 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:138, a L-CDR2 comprising SEQ ID NO:139, and a L-CDR3 comprising SEQ ID NO:140, or

ix. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:148, an H-CDR2 comprising SEQ ID NO:149, and an H-CDR3 comprising SEQ ID NO:150 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:152, a L-CDR2 comprising SEQ ID NO:153, and a L-CDR3 comprising SEQ ID NO:154, or

x. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:14, an H-CDR2 comprising SEQ ID NO:15, and an H-CDR3 comprising SEQ ID NO:16 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:18, a L-CDR2 comprising SEQ ID NO:19, and a L-CDR3 comprising SEQ ID NO:20, or

xi. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:62, an H-CDR2 comprising SEQ ID NO:63, and an H-CDR3 comprising SEQ ID NO:64 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:66, a L-CDR2 comprising SEQ ID NO:67, and a L-CDR3 comprising SEQ ID NO:68, or

xii. a heavy chain antigen-binding region that comprises an H-CDR1 comprising SEQ ID NO:92, an H-CDR2 comprising SEQ ID NO:93, and an H-CDR3 comprising SEQ ID NO:94 and a light chain antigen-binding region that comprises a L-CDR1 comprising SEQ ID NO:96, a L-CDR2 comprising SEQ ID NO:97, and a L-CDR3 comprising SEQ ID NO:98.

2. The antibody or antigen-binding fragment thereof according to claim 1 comprising:

i. a variable heavy chain sequence as presented by SEQ ID NO: 47 and a variable light chain sequence as presented by SEQ ID NO: 51, or

ii. a variable heavy chain sequence as presented by SEQ ID NO: 105 and a variable light chain sequence as presented by SEQ ID NO: 109, or

iii. a variable heavy chain sequence as presented by SEQ ID NO: 3 and a variable light chain sequence as presented by SEQ ID NO: 7, or

iv. a variable heavy chain sequence as presented by SEQ ID NO: 33 and a variable light chain sequence as presented by SEQ ID NO: 37, or

v. a variable heavy chain sequence as presented by SEQ ID NO: 119 and a variable light chain sequence as presented by SEQ ID NO: 123, or

vi. a variable heavy chain sequence as presented by SEQ ID NO: 23 and a variable light chain sequence as presented by SEQ ID NO: 27, or

vii. a variable heavy chain sequence as presented by SEQ ID NO: 75 and a variable light chain sequence as presented by SEQ ID NO: 79, or

viii. a variable heavy chain sequence as presented by SEQ ID NO: 133 and a variable light chain sequence as presented by SEQ ID NO: 137, or

ix. a variable heavy chain sequence as presented by SEQ ID NO: 147 and a variable light chain sequence as presented by SEQ ID NO: 151, or

x. a variable heavy chain sequence as presented by SEQ ID NO: 13 and a variable light chain sequence as presented by SEQ ID NO: 17, or

xi. a variable heavy chain sequence as presented by SEQ ID NO: 61 and a variable light chain sequence as presented by SEQ ID NO: 65, or

xii. a variable heavy chain sequence as presented by SEQ ID NO: 91 and a variable light chain sequence as presented by SEQ ID NO: 95.

3. The antibody according to any one of the preceding claims, which is an IgG antibody.

4. The antibody according to any one of the preceding claims comprising:

i. a heavy chain region corresponding to SEQ ID NO: 57 and a light chain region corresponding to SEQ ID NO: 58, or

ii. a heavy chain region corresponding to SEQ ID NO: 115 and a light chain region corresponding to SEQ ID NO: 116, or

iii. a heavy chain region corresponding to SEQ ID NO: 43 and a light chain region corresponding to SEQ ID NO: 44, or

iv. a heavy chain region corresponding to SEQ ID NO: 129 and a light chain region corresponding to SEQ ID NO: 130, or

v. a heavy chain region corresponding to SEQ ID NO: 85 and a light chain region corresponding to SEQ ID NO: 86, or

vi. a heavy chain region corresponding to SEQ ID NO: 143 and a light chain region corresponding to SEQ ID NO: 144, or

vii. a heavy chain region corresponding to SEQ ID NO: 157 and a light chain region corresponding to SEQ ID NO: 158, or

viii. a heavy chain region corresponding to SEQ ID NO: 71 and a light chain region corresponding to SEQ ID NO: 72, or

ix. a heavy chain region corresponding to SEQ ID NO: 101 and a light chain region corresponding to SEQ ID NO: 102.

5. The antigen-binding fragment according to claims 1 or 2, which is an scFv, Fab, Fab' fragment or a F(ab')2 fragment.

6. The antibody or antigen-binding fragment according to any one of the preceding claims, which is a monoclonal antibody or antigen-binding fragment.

7. An antibody-drug conjugate, comprising an antibody or antigen binding fragment thereof according to any one of the claims 1 to 6.

8. An isolated nucleic acid sequence that encodes the antibody or antigen-binding fragment according to any one of the claims 1 to 6.

9. A vector comprising a nucleic acid sequence according to claim 8.

10. An isolated cell expressing an antibody or antigen-binding fragment according to any one of the claims 1 to 6 and /or comprising a nucleic acid according to claim 8 or a vector according to claim 9.

11. An isolated cell according to claim 10, wherein said cell is a prokaryotic or a eukaryotic cell.

12. A method of producing an antibody or antigen-binding fragment according to any one of the claims 1 to 6 comprising culturing of a cell according to claim 11 and purification of the antibody or antigen-binding fragment.

13. An antibody or antigen-binding fragment according to any one of the claims 1 to 6 or an antibody-drug conjugate according to claim 7 for use as a medicament.

14. An antibody or antigen-binding fragment according to any one of the claims 1 to 6 or an antibody-drug conjugate according to claim 7 for use as a diagnostic agent.

15. An antibody or antigen-binding fragment according to any one of the claims 1 to 6 or an antibody-drug conjugate according to claim 7 for use as a medicament for the treatment of cancer.

16. A pharmaceutical composition comprising an antibody or antigen-binding fragment according to any one of the claims 1 to 6 or an antibody-drug conjugate according to claim 7.

17. A combination of a pharmaceutical composition according to claim 16 and one or more therapeutically active compounds.