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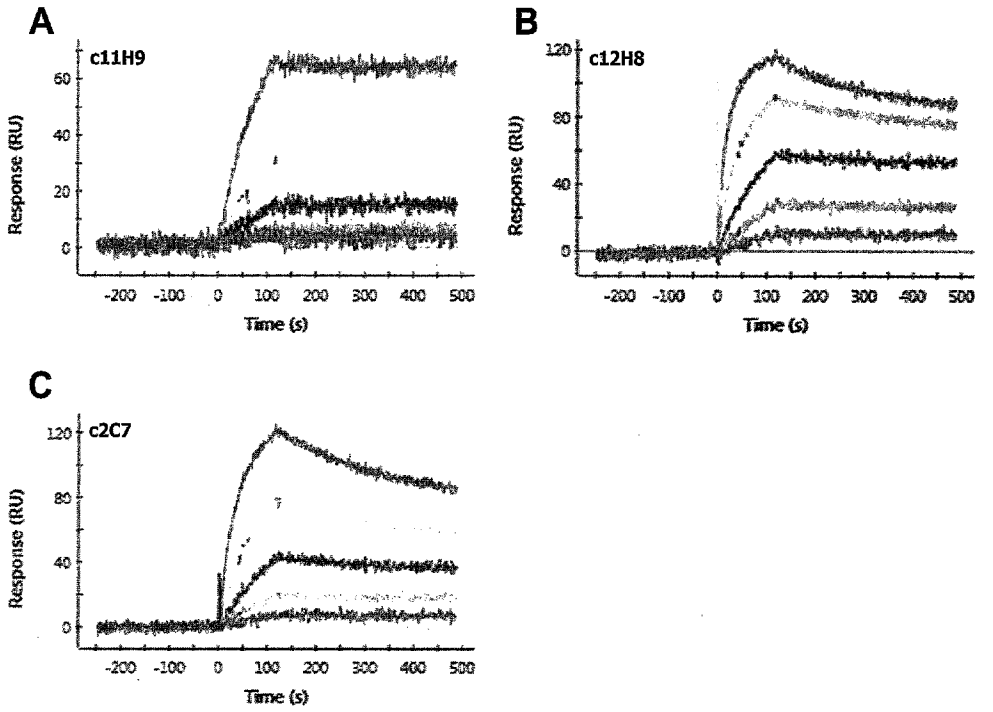
(72) **Inventeurs/Inventors:**
LENFERINK, ANNE E.G., CA;
O'CONNOR, MAUREEN D., CA;
MARCIL, ANNE, CA;
DUROCHER, YVES, CA

(73) **Propriétaire/Owner:**
NATIONAL RESEARCH COUNCIL OF CANADA, CA

(74) **Agent:** NATIONAL RESEARCH COUNCIL OF CANADA

(54) **Titre : ANTICORPS SPECIFIQUES DE L'ANHYDRASE CARBONIQUE IX ET LEURS UTILISATIONS**
(54) **Title: CARBONIC ANHYDRASE IX-SPECIFIC ANTIBODIES AND USES THEREOF**



(57) **Abrégé/Abstract:**
The present invention relates to isolated or purified antibodies or fragments thereof specific for Carbohydrate Anhydrase IX (CA-IX) and their use as therapeutic tools. Specifically, the present invention is directed to high-affinity Carbohydrate Anhydrase IX-specific antibodies and fragments thereof and their use as antibody-drug conjugates. Compositions for use in therapy as well as therapeutic methods are also described.

ABSTRACT

The present invention relates to isolated or purified antibodies or fragments thereof specific for Carbohydrate Anhydrase IX (CA-IX) and their use as therapeutic tools. Specifically, the present invention is directed to high-affinity Carbohydrate Anhydrase IX-specific antibodies and fragments thereof and their use as antibody-drug conjugates. Compositions for use in therapy as well as therapeutic methods are also described.

CARBONIC ANHYDRASE IX-SPECIFIC ANTIBODIES AND USES THEREOF

FIELD OF THE INVENTION

The present invention relates to Carbohydrate Anhydrase IX-specific antibodies, fragments thereof, and uses thereof. More specifically, the present invention relates to high-affinity Carbohydrate Anhydrase IX-specific antibodies and fragments thereof and their use as antibody-drug conjugates.

BACKGROUND OF THE INVENTION

Carbonic anhydrases (CA) are a family of 16 distinct but related metalloenzymes that catalyze the reversible hydration of carbon dioxide (CO_2) to bicarbonate (HCO_3^-) and protons (H^+) (Pastorekova et al., 2004; see Figure 1). Members of the CA, with the exception of CA-IX and CA-XII, can be found in many normal human organs, tissues and subcellular compartments where they play an important role in the regulation of the extracellular and intracellular pH (pHe and pHi, respectively) and the secretion of electrolytes (Zatovicova et al., 2005; Thiry et al., 2006).

In addition to its pH-balancing activities, CA-IX has been shown to be involved in cell adhesion and migration (Svastova et al., 2011) and has been associated with cancer progression, metastasis and poor clinical outcome (Neri et al., 2011). CA-IX (also known as MN, P54/58N or Renal Cell Carcinoma (RCC)-associated protein G250) is a transmembrane protein with an extracellular catalytic site and an NH_2-terminal proteoglycan (PG)-like domain. The C-terminal intracellular portion of CA-IX is involved in the inside-out regulation of the extracellular catalytic domain through the phosphorylation of Thr-443 by protein kinase A (PKA) (Hulikova et al., 2009; Ditte et al., 2011). Expression of CA-IX is tightly controlled by hypoxia-inducible factor 1 alpha (HIF-1α). CA-IX is expressed on the surface of tumor cells located in pre-necrotic areas of tumors (Wykoff et al., 2000) where it is involved in promoting tumor cell survival, the accelerated degradation of the extracellular matrix (ECM) and metastasis.

CA-IX has a very selective expression pattern in normal tissue. The mucosa of the gall bladder and stomach express high levels of CA-IX. Low expression levels of CA-IX levels can be found in the intestinal epithelium, and even lower levels in pancreatic duct epithelium, male reproductive organs, and cells that line the body cavity. All other normal tissues do not express CA-IX. Cancerous tissues however, especially those of the cervix, kidney and lung, express high levels of CA-IX thus making CA-IX a very attractive therapeutic tumor target. While various small molecule inhibitors have been shown to effectively inhibit the catalytic activity of

CA-IX (Supuran et al., 2008; Neri et al., 2011; Pacchiano et al., 2010; Lou et al., 2011), the lack of target specificity has been an ongoing challenge.

In order to address this issue and to confer specificity in targeting CA-IX, various antibodies have been raised against this important target.

One of the earliest monoclonal antibodies (mAb) raised against CA-IX is M75 (Pastorekova et al., 1992), which binds to CA-IX's PG-like domain. M75 has been predominately used as tool for CA-IX detection *in vitro* and *in vivo* (Chrastina et al., 2003a, 2003b; Zatovicova et al., 2010).

A second anti-CA-IX mAb, mAb G250 (Oosterwijk et al., 1986), was shown to interact with CA-IX's catalytic domain without however inhibiting its enzyme activity. A chimeric version of G250 (designated cG250) was developed as a therapeutic antibody (Surfus et al., 1996; Oosterwijk, 2008) with a mechanism of action that was shown to rely predominantly on an Antibody-Dependent Cellular Cytotoxicity (ADCC) response. cG250 does however not improve the disease-free survival rate of patients (> 6-year span) compared to a placebo (Bleumer et al., 2004). Despite the lack of therapeutic potential of the cG250 antibody itself, the mAb continues to be developed for the treatment of cancer in combination with IL2 or IFN-α, as an imaging diagnostic agent and for *in vitro* diagnostics (IVD) immunohistochemistry (IHC) assays.

In addition, cG250 is also used as a vehicle for the delivery of radionuclides. Specifically, Brouwers et al. (2004) successfully used cG250 to shuttle ^{177}Lu and ^{90}Y into tumor cells, causing growth retardation of xenograft tumors. Clinical phase II/III studies with these labeled mAbs are currently underway (Stillebroer et al., 2012). Also in development are antibody-drug conjugates (ADC) based on cG250, however little is known their efficacy. Such antibody-drug conjugates are an attractive option in cancer therapy, as they combine the selective targeting ability of the antibody with the cell-killing capabilities of the cytotoxic drug.

In view of its specific tumor expression, CA-IX as a therapeutic target has become an active area of research. Although several antibodies have been identified showing enzyme inhibition, only one has been evaluated *in vivo* (VII/20 mAb; Zatovicova et al., 2010). Similarly, the use of these mAb for the delivery of cytotoxic agents or radionuclides to tumor cells expressing CA-IX has been an area of much investigative research. For example, Petrul et al. (2012) isolated the 3ee9 Fab, which was subsequently engineered into a mAb and further developed as an ADC by conjugation to monomethyl auristatin E. This ADC showed potent antitumor efficacy and a Phase I clinical trial to determine the maximal tolerated dose (MTD) was terminated early due to safety concerns.

While there is interest and research activity surrounding the use of CA-IX as a target for ADC, there is currently little certainty surrounding ongoing investigations involving these known antibodies. The ability of an antibody to function as an ADC is difficult to predict, and relies on design strategies, target biology and routing behaviour that go beyond its ability to be internalized by its specific target. Therefore, there remains a need in the art to develop further anti-CA-IX antibodies that have potential as ADC candidates. Needless to say such antibodies should display a high target affinity and specific while avoiding off-target effects, toxicity, and therapeutic resistance.

SUMMARY OF THE INVENTION

The present invention relates to Carbohydrate Anhydrase IX-specific antibodies, fragments thereof, and uses thereof. More specifically, the present invention relates to high-affinity Carbohydrate Anhydrase IX-specific antibodies and fragments thereof and their use as antibody-drug conjugates.

The present invention provides an isolated or purified antibody or fragment thereof, comprising

a) a light chain comprising a complementarity determining region (CDR) L1 sequence selected from the group consisting of:

RASGNIHNYLA (SEQ ID NO:1);

RSSQSLVHSNGNTYLH (SEQ ID NO:7); and

KSSQSLLDSDGKTYLN (SEQ ID NO:13),

a CDR L2 sequence selected from the group consisting of:

NTITLAD (SEQ ID NO:2);

KVSNRFS (SEQ ID NO:8); and

LVSKLDS (SEQ ID NO:14), and

a CDR L3 sequence selected from the group consisting of:

QHFWNIPFT (SEQ ID NO:3);

SQNTHVPPT (SEQ ID NO:9); and

CQGTHFPW (SEQ ID NO:15),

and

a) a heavy chain comprising a complementarity determining region (CDR) H1 sequence selected from the group consisting of:

GFTFTSCYIH (SEQ ID NO:4);

GFTFNTYAMY (SEQ ID NO:10); and

GYTFTNYGMN (SEQ ID NO:16),

a CDR H2 sequence selected from the group consisting of:

WIYPGNGNTKYNEIFKG (SEQ ID NO:5);

RIRSKSNNYAIYYADSVKD (SEQ ID NO:11); and

WINTYTGEPTYADDFKG (SEQ ID NO:17), and

a CDR H3 sequence selected from the group consisting of:

GDTTANTMDY (SEQ ID NO:6);

GWDWFAY (SEQ ID NO:12); and

GGIATPTSY (SEQ ID NO:18),

wherein the antibody or fragment thereof specifically binds the extracellular domain of Carbohydrate Anhydrase IX.

In a more specific example, the isolated or purified antibody or fragment thereof may be selected from the group consisting of:

a) a light chain comprising CDR L1 of sequence RASGNIHNYLA (SEQ ID NO:1), CDR L2 of sequence NTITLAD (SEQ ID NO:2), and CDR L3 of sequence QHFWNIPFT (SEQ ID NO:3); and a heavy chain comprising CDR H1 of sequence GFTFTSCYIH (SEQ ID NO:4), CDR H2 of sequence WIYPGNGNTKYNEIFKG (SEQ ID NO:5), and CDR H3 of sequence GDTTANTMDY (SEQ ID NO:6); and wherein the antibody or fragment thereof binds the catalytic domain of CA-IX;

b) a light chain comprising CDR L1 of sequence RSSQSLVHSNGNTYLH (SEQ ID NO:7), CDR L2 of sequence KVSNRFS (SEQ ID NO:8), CDRL3 of sequence SQNTHVPPT (SEQ

ID NO:9); and a heavy chain comprising CDR H1 of sequence GFTFNTYAMY (SEQ ID NO:10), CDR H2 of sequence RIRSKSNNYAIYYADSVKD (SEQ ID NO:11), and CDR H3 of sequence GWDWFAY(SEQ ID NO:12); and wherein the antibody or fragment thereof binds the PG-like domain of CA-IX; and

c) a light chain comprising CDR L1 of sequence KSSQSLLDSDGKTYLN (SEQ ID NO:13), CDR L2 of sequence LVSKLDS (SEQ ID NO:14), CDRL3 of sequence CQGTHFPW (SEQ ID NO:15); and a heavy chain comprising CDR H1 of sequence GYTFTNYGMN (SEQ ID NO:16), CDR H2 of sequence WINTYTGEPTYADDFKG (SEQ ID NO:17), and CDR H3 of sequence GGIATPTSY (SEQ ID NO:18); and wherein the antibody or fragment thereof binds the PG-like domain of CA-IX.

In one embodiment, the isolated or purified antibody or fragment thereof may comprise

a) a variable light (VL) domain of sequence selected from the group consisting of:

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSR FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELK (SEQ ID NO:19),

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPPTFGGGTKLEIK (SEQ ID NO: 21), and

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQGTHFPWTFGGGTKLEIK (SEQ ID NO:23);

b) a variable heavy (V_H) domain of sequence selected from the group consisting of:

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTK YNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVS S (SEQ ID NO:20);

EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAI YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGWDWFAYWGQGTPVTVSA (SEQ ID NO:22); and

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLKWMGWINTYTGEPT YADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARGGIATPTSYWGQGTTLTVSS (SEQ ID NO:24); or

c) a sequence substantially identical to the variable light (VL) domain of a) or the variable heavy (VH) domain of b) as described above.

The antibody or fragment thereof just defined specifically binds to the extracellular domain of CA-IX.

In specific, non-limiting examples, the isolated or purified antibody or fragment thereof of the present invention may comprise

a) a variable light (V_L) domain of sequence

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSR FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELK (SEQ ID NO:19)

and/or variable heavy (V_H) domain of sequence

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTK YNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVS S (SEQ ID NO:20);

b) a variable light (V_L) domain of sequence

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPPTFGGGTKLEIK (SEQ ID NO: 21)

and/or variable heavy (V_H) domain of sequence

EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAI YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGWDWFAYWGQGTPVTVSA (SEQ ID NO:22);

c) a variable light (V_L) domain of sequence

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQGTHFPWTFGGGTKLEIK (SEQ ID NO:23)

and/or variable heavy (V_H) domain of sequence

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLKWMGWINTYTGEPT
YADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARGGIATPTSYWGQGTTLTVSS
(SEQ ID NO:24);

or a sequence substantially identical thereto.

The isolated or purified antibody or fragment thereof as described herein may exhibit a high degree of internalization, thus rendering it suitable as a delivery agent for the intracellular delivery of drugs or toxins.

The isolated or purified antibody or fragment thereof as described herein may a full-length IgG, Fv, scFv, Fab, or $F(ab')_2$; the antibody or fragment thereof may also comprise framework regions from IgA, IgD, IgE, IgG, or IgM. The isolated or purified antibody or fragment thereof of the present invention may be chimeric; for example, and without wishing to be limiting, such a chimeric antibody or fragment thereof may comprise the V_L and V_H domains from mouse and framework regions (constant domains) from human IgG1, more specifically human kappa 1 light chain and human IgG1 heavy chain

In a yet more specific non-limiting example, the isolated or purified antibody or fragment thereof of the present invention may comprise

a) a variable light (V_L) domain comprising the sequence

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSR
FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:25)

and variable heavy (V_H) domain comprising the sequence

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTK
YNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVS
SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:26);

b) a variable light (V_L) domain comprising the sequence

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPPTFGGGTKLEIKRTVAAPSV
FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:27)

and variable heavy (V_H) domain comprising the sequence

EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAI
YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGWDWFAYWGQGTPVTVSA
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:28);

c) a variable light (V_L) domain comprising the sequence

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQGTHFPWTFGGGTKLEIKRTVAAPSVF
IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:29)

and variable heavy (V_H) domain comprising the sequence

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLKWMGWINTYTGEPT
YADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARGGIATPTSYWGQGTTLTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:30);

or a sequence substantially identical thereto.

The present invention also provides a nucleic acid molecule encoding the isolated or purified antibody or fragment thereof as described herein. A vector comprising the nucleic acid molecule as just described is also provided.

The isolated or purified antibody or fragment thereof as described herein may be immobilized onto a surface, or may be linked to a cargo molecule. The cargo molecule may be a detectable agent, a therapeutic agent, a drug, a peptide, an enzyme, a growth factor, a cytokine, a receptor trap, an antibody or fragment thereof (e.g., IgG, scFv, Fab, V_HH, etc) a chemical compound, a carbohydrate moiety, DNA-based molecules (anti-sense oligonucleotide, microRNA, siRNA, plasmid), a cytotoxic agent, viral vector (adeno-, lenti-, retro-), one or more liposomes or nanocarriers loaded with any of the previously recited types of cargo molecules, or one or more nanoparticle, nanowire, nanotube, or quantum dots. In a specific, non-limiting example, the cargo molecule is a cytotoxic agent.

Additionally, the present invention provides a composition comprising one or more than one isolated or purified antibody or fragment thereof as described herein and a pharmaceutically-acceptable carrier, diluent, or excipient.

An *in vitro* method of detecting CA-IX is also provided, the method comprising

a) contacting a tissue sample with one or more than one isolated or purified antibody or fragment thereof as described herein linked to a detectable agent; and

b) detecting the detectable agent linked to the antibody or fragment thereof bound to CA-IX in the tissue sample.

In the method described above, the method may detect CA-IX in circulating cells and the sample may be a serum sample. In the method as described, the step of detecting (step b) may be performed using optical imaging, immunohistochemistry, molecular diagnostic imaging, ELISA, or other suitable method.

The present invention further provides an *in vivo* method of detecting CA-IX expression in a subject, comprising:

a) administering one or more than one isolated or purified antibody or fragment thereof as described herein linked to a detectable agent to the subject; and

b) detecting the detectable agent linked to the antibody or fragment thereof bound to CA-IX.

In the method described just described, the step of detecting (step b)) is performed using PET, SPECT, fluorescence imaging, or any other suitable method.

The present invention additionally provides a method of transporting a molecule of interest into cells expressing CA-IX. The method may comprise administering one or more than one isolated or purified antibody or fragment thereof as described herein linked to the molecule of interest to a subject. Once administered, the one or more than one isolated or purified antibody or fragment thereof delivers the molecule of interest to cells expressing CA-IX in the subject. The molecule of interest may be any suitable molecule, for example a molecule selected from the group consisting of a detectable agent, a therapeutic agent, a drug, a peptide, an enzyme, a growth factor, a cytokine, a receptor trap, an antibody or fragment thereof (e.g., IgG, scFv, Fab, V_HH, etc) a chemical compound, a carbohydrate moiety, DNA-based molecules (anti-sense oligonucleotide, microRNA, siRNA, plasmid), a cytotoxic agent, viral vector (adeno-, lenti-, retro-), one or more liposomes loaded with any of the previously recited types of cargo molecules, or one or more nanoparticle, nanowire, nanotube, or quantum dots. In a non-limiting example, the molecule of interest is a cytotoxic agent.

Presently, three novel antibodies (11H9, 12H8 and 2C7) have been identified that specifically bind human CA-IX. Two of the monoclonal antibodies (11H9 and 2C7) were shown to have a slight preference for the recombinant human CA-IX dimer over the monomer, while mAb 12H8 binds the rhCA-IX ECD dimer. The antibodies were also engineered as chimeric antibodies using the human IgG1 heavy chain. The resulting recombinantly-expressed chimeric antibodies (c11H9, c12H8 and c2C7) behaved similarly to the hybridoma-expressed mAb. SPR experiments showed that all three chimeric mAb have a relative slow off-rate, showing binding characteristics similar to the original mAb. The anti-CA-IX mAb also showed no inhibition of the enzyme activity of rhCA-IX ECD. The minimal epitopes of the antibodies were determined by epitope mapping using Yeast Surface Display. The minimal epitope for c12H8 was determined to be LPRMQEDSP (SEQ ID NO:52; corresponding to aa 40-48 of CA-IX); and that of c11H9 was determined to be EDLPGEED (SEQ ID NO:53; corresponding to aa 81-88 and aa 87-94 of CA-IX. It was also shown that mAb 12H8, 11H9 and 2C7 were either equal to or better than the M75 mAb (a known antibody) in reducing cell viability. Chimeric (c)11H9, c12H8 and c2C7 antibodies were similarly tested and shown to retain the ADC potential of their respective monoclonal versions. Additionally, ADC assays using non-conjugated chimeric antibodies and chimeric antibodies conjugated to DM1 (c11H9-DM1, c12H8-DM1 and c2C7-DM1) were performed. Results showed the specificity of c11H9-DM1, c12H8-DM1 and c2C7-DM1 in terms of killing the cells, whereas the unconjugated antibodies had no effect.

Additional aspects and advantages of the present invention will be apparent in view of the following description. The detailed descriptions and examples, while indicating preferred embodiments of the invention, are given by way of illustration only, as various changes and

modifications within the scope of the invention will become apparent to those skilled in the art in light of the teachings of this invention.

BRIEF DESCRIPTION OF THE DRAWINGS

These and other features of the invention will now be described by way of example, with reference to the appended drawings, wherein:

FIGURE 1 is a schematic diagram showing the domains, subcellular localization and catalytic activity of the human (h) carbonic anhydrase (CA) family. The cytoplasmic and mitochondrial hCA-I, -II, -III, -VII, -VIII, -X, -XI and –XIII are composed of only a catalytic domain; the secreted hCA-VI has a short C-terminal domain; and the membrane-associated hCA-IV, -VI, -IX, -XII, and -XIV have a transmembrane anchor and, except hCA-IV, also a cytoplasmic tail. hCA-IX is the only member of the CA family with a N-terminal proteoglycan (PG) sequence, which is involved in the cell-cell adhesion process. This figure was adapted from Pastorekova et al., 2004.

FIGURE 2 is a schematic diagram of the construct containing the synthetic hCA-IX ECD with an N-terminal His-tag.

FIGURE 3 shows a Coomassie Brilliant Blue stained SDS-PAGE of the NRC-produced rhCA-IX extracellular domain (ECD) under reducing (lane 2) and non-reducing (lane 1) conditions. The disulphide-bonded dimer rhCA-IX dimer has a molecular weight of ~110 kDa, whereas the monomer and the reduced dimer are ~48 kDa.

FIGURE 4A is the SEC profiles of the hCA-IX ECD produced in CHO cells, showing the presence of monomers and dimers. Monomer and dimer containing fractions were re-evaluated by SEC after storage for 2 weeks at 4°C (FIGURES 4B and 4C, respectively). FIGURE 4D shows an overlay of FIGURE 4B and FIGURE 4C.

FIGURE 5 shows Western blots of non-purified hybridoma derived CA-IX mAbs (undiluted CM), evaluated for binding to the purified CA-IX ECD antigen. mAb 11H9, 12H8 and 2C7 failed to bind to rhCA-IX ECD under both non-reducing (FIGURE 5A) and reducing conditions (FIGURE 5B). Anti-hCA-IX mAb 10F2 is shown as a positive control.

FIGURE 6 shows the sequence alignment for CDR 1-3 of mAb 11H9, 12H8, 2C7 V_H (FIGURE 6A, SEQ ID NOs: 10-12, 16-18, and 4-6, respectively) and V_L (FIGURE 6B; SEQ ID NOs: 7-9, 13-15, and 1-3, respectively) regions and the corresponding phylogenetic tree (FIGURE 6C and 6D, respectively). Consensus symbols: * (asterisk)= single, fully conserved residue; :

(colon)= conservation between groups of strongly similar properties; scoring >0.5 (Gonnet PAM 250 matrix); . (period)= conservation between groups of weakly similar properties; scoring =< 0.5 (Gonnet PAM 250 matrix) (Dereeper et al., 2008 and 2010; Edgar, 2004)

FIGURE 7 shows a SDS-PAGE of the recombinantly expressed c11H9, c12H8 and c2C7 mAbs (human IgG1 framwork) expressed in CHO cells using a 1:1 V_L:V_H ratio in the small-scale (50 mL) expression experiment. Conditioned medium was harvested on day 7, ProtA purified, and quantitated. Both the conditioned medium (CM) and ProtA purified chimeric mAb (P) were evaluated.

FIGURE 8 shows SPR sensorgrams for the recombinantly expressed and purified chimeric mAb c11H9 (FIGURE 8A), c12H8 (FIGURE 8B) and c2C7 (FIGURE 8C). An anti-human Fc antibody was directly immobilized onto the chip surface via amine coupling chemistry. This immobilized antibody was used to capture mAbs on the. Purified rhCA-IX ECD dimer was flowed at various concentrations over the captured mAbs and kinetic rate constants for association and dissociation measured to determine the binding constant K_D.

FIGURE 9 shows the real-time SPR binding of the recombinantly expressed c11H9 (FIGURE 9A), c12H8 (FIGURE 9B) and c2C7 (FIGURE 9C) to rhCA-IV, rhCA-XII, rhCA-XIV, and rmCA-IX. Data indicate that c11H9, c12H8 and c2C7 are specific for the hCA-IX, as no binding was detected against other relevant human and murine CA forms tested.

FIGURE 10 shows the results of thermostability experiments using the DSC for recombinantly expressed c11H9 (FIGURE 10A), c12H8 (FIGURE 10A), and c2C7 (FIGURE 10A), shown in dashed lines in comparison the anti-HER2 therapeutic antibody Cetuximab, in solid line. The thermostability of the c12H8 and c2C7 is similar to that of Cetuximab, whereas c11H9 is slightly less thermostable.

FIGURE 11 shows results of Epitope mapping of the hybridoma-derived mAb 11H9 (FIGURE 11A), 12H8 (FIGURE 11B) and 2C7 (FIGURE 11C) using the PepScan technology (pepscan.com). The data indicates that mAb 11H9 binds to peptides presented either as a linear or single loop peptide, whereas mAb 12H8 and 2C7 preferably bind to single loop peptides. Further analysis indicates that mAb 11H9 and 12H8 bind to distinct epitopes in the PG domain, whereas the data for mAb 2C7 implies that it binds to the catalytic domain (inconclusive). FIGURE 11D is a schematic summary of the location of the binding epitopes of 11H8, 12H8 and 2C7 based on the results of Figures 11 A, B, and C respectively.

FIGURE 12 A, B and C are schematic representations of the principle of the epitope binning assay for hybridoma-derived 11H9, 12H8 and 2C7 mAb by Surface Plasmon Resonance

(SPR). FIGURE 12 D and E are a color-coded 'checker board' representation of the results, showing that mAb 11H9, 12H8, and 2C7 do not compete for binding (see legend) when either using the rhCA-IX ECD monomer or dimer.

FIGURE 13A shows the nine (9) peptides covering the entire hCA-IX expressed on the yeast cell surface membrane to map the binding epitope of the recombinantly-expressed c11H9, c12H8, and c2C7 mAb. Fine mapping using fourteen (14) peptides covering the hCA-IX PG domain (FIGURE 13B) was only further used to identify specific peptide binding epitopes of these mAb.

FIGURE 14 are graphs used in the evaluation of the enzyme-inhibiting attributes of hybridoma-derived mAb 11H9, 12H8 and 2C7. FIGURE 14A is a graph showing that the rhCA-IX ECD (mixture) is catalytically active and can be fully inhibited by 10 µM Acetozolamide. FIGURE 14B is a bar graph showing that none of 11H9, 12H8, and 2C7 mAb can inhibit the rhCA-IX ECD enzyme activity; the dotted line indicates 100% CA-IX catalytic activity. Displayed are the average values + SEM of a duplicate experiment.

FIGURE 15 shows SDS-PAGE evaluation (whole cell lysate) of the non-transfected human renal carcinoma cell lines SK-RC-52 and SK-RC-59 for the expression of hCA-IX under non-reducing (FIGURE 15A) and reducing (FIGURE 15B) conditions.

FIGURE 16 shows the graphical results of measuring whether the hybridoma-derived mAb 11H9, 12H8 and 2C7 bind to their cognate target expressed by the human renal carcinoma SK-RC-52 (FIGURE 16A; high hCA-IX) and SK-RC-59 (FIGURE 16B; low hCA-IX) cell lines. The % of live cells in each of the experiments is on the left Y-axis while the mean fluorescent intensity due to mAb binding is on the right Y-axis. The M75 mAb (Zavada et al., 1993) and the commercial hCA-IX mAb (mAb2188) were used as positive controls; the secondary mAb alone (2nd) was used to evaluate non-specific signals.

FIGURE 17 shows bar charts for evaluating the ADC potential of hybridoma-derived mAb 11H9, 12H8 and 2C7 in a surrogate ADC assay using the sk-rc-52 cells. FIGURE 17A shows experiments done at 10 nM while FIGURE 17B shows experiments done at 1 and 10 nM. The tested anti-CA-IX mAb cause reduced cell viability similar to the M75 mAb control; the upper dotted line indicates 100% viability in the non-treated cells, whereas the lower dotted line indicates the cell viability in the M75 mAb treated cells. Non-treated (CTL) and secondary Ab-treated (mAb-Zap) cells were used as negative controls. Displayed are the average values +/- SEM of a triplicate experiment.

FIGURE 18 shows a dose response (0-100 nM) of the potential ADC candidates c11H9, c12H8 and c2C7 in ADC assays using the SK-RC-52 cells. FIGURE 18A shows experiments done using the surrogate ADC assay in which the antibodies are decorated with a secondary antibody that is conjugated to Saporin. Non-treated (CTL) and secondary Ab-treated (mAb-Zap) cells were used as negative controls. FIGURE 18B shows the results of experiments done using the recombinantly expressed 'naked' antibodies c2C7, c11H9 and c12H8, which all serve as negative controls, and the mertansine (DM1) conjugated recombinantly expressed c2C7, c11H9 and c12H8 antibodies. The surrogate ADC assay (A) and the ADC assay (B) give very similar IC_{50} results DM1 conjugation renders the c11H9, c12H8 and c2C7 mAb into functional ADC. In both assays the average values +/- SEM of a triplicate experiment are displayed.

FIGURE 19 is a bar graph showing results of the cardiotoxicity evaluation using the surrogate iCell-cardiomyocyte *in vitro* model. No significant difference in cell viability was observed with the 'naked' CA-IX antibodies or corresponding ADC tested compared to non-specific negative human IgG1 or vehicle controls.

FIGURE 20 shows results of the evaluation of cross-reactivity of CA-IX antibodies to CA-XII extracellular domain (ECD). SPR measurements using 100 nM of human CA-XII extracellular domain (ECD) showed no binding to c2C7 (FIGURE 20 A), c11H9 (FIGURE 20 B), or c12H8 (FIGURE 20 C) antibodies.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to Carbohydrate Anhydrase IX-specific antibodies, fragments thereof, and uses thereof. More specifically, the present invention relates to high-affinity Carbohydrate Anhydrase IX-specific antibodies and fragments thereof and their use as antibody-drug conjugates.

The present invention provides an isolated or purified antibody or fragment thereof, comprising

a) a light chain comprising a complementarity determining region (CDR) L1 sequence selected from the group consisting of:

RASGNIHNYLA (SEQ ID NO:1);

RSSQSLVHSNGNTYLH (SEQ ID NO:7); and

KSSQSLLDSDGKTYLN (SEQ ID NO:13),

LVSKLDS (SEQ ID NO:14), and

a CDR L3 sequence selected from the group consisting of:

QHFWNIPFT (SEQ ID NO:3);

SQNTHVPPT (SEQ ID NO:9); and

CQGTHFPW (SEQ ID NO:15),

and

b) a heavy chain comprising a complementarity determining region (CDR) H1 sequence selected from the group consisting of:

GFTFTSCYIH (SEQ ID NO:4);

GFTFNTYAMY (SEQ ID NO:10); and

GYTFTNYGMN (SEQ ID NO:16),

a CDR H2 sequence selected from the group consisting of:

WIYPGNGNTKYNEIFKG (SEQ ID NO:5);

RIRSKSNNYAIYYADSVKD (SEQ ID NO:11); and

WINTYTGEPTYADDFKG (SEQ ID NO:17), and

a CDR H3 sequence selected from the group consisting of:

GDTTANTMDY (SEQ ID NO:6);

GWDWFAY (SEQ ID NO:12); and

GGIATPTSY (SEQ ID NO:18),

wherein the antibody or fragment thereof specifically binds the extracellular domain of Carbohydrate Anhydrase IX.

The term “antibody”, also referred to in the art as “immunoglobulin” (Ig), as used herein refers to a protein constructed from paired heavy and light polypeptide chains; various Ig isotypes exist, including IgA, IgD, IgE, IgG, and IgM. When an antibody is correctly folded, each chain

folds into a number of distinct globular domains joined by more linear polypeptide sequences. For example, the immunoglobulin light chain folds into a variable (V_L) and a constant (C_L) domain, while the heavy chain folds into a variable (V_H) and three constant (C_H, C_{H2}, C_{H3}) domains. Interaction of the heavy and light chain variable domains (V_H and V_L) results in the formation of an antigen binding region (Fv). Each domain has a well-established structure familiar to those of skill in the art.

The light and heavy chain variable regions are responsible for binding the target antigen and can therefore show significant sequence diversity between antibodies. The constant regions show less sequence diversity, and are responsible for binding a number of natural proteins to elicit important biochemical events. The variable region of an antibody contains the antigen-binding determinants of the molecule, and thus determines the specificity of an antibody for its target antigen. The majority of sequence variability occurs in six hypervariable regions, three each per variable heavy (V_H) and light (V_L) chain; the hypervariable regions combine to form the antigen-binding site, and contribute to binding and recognition of an antigenic determinant. The specificity and affinity of an antibody for its antigen is determined by the structure of the hypervariable regions, as well as their size, shape, and chemistry of the surface they present to the antigen. Various schemes exist for identification of the regions of hypervariability, the two most common being those of Kabat and of Chothia and Lesk. Kabat et al (1991) define the “complementarity-determining regions” (CDR) based on sequence variability at the antigen-binding regions of the V_H and V_L domains. Chothia and Lesk (1987) define the “hypervariable loops” (H or L) based on the location of the structural loop regions in the V_H and V_L domains. As these individual schemes define CDR and hypervariable loop regions that are adjacent or overlapping, those of skill in the antibody art often utilize the terms “CDR” and “hypervariable loop” interchangeably, and they may be so used herein. A more recent scheme is the IMGT numbering system (Lefranc et al., 2003), which was developed to facilitate comparison of variable domains. In this system, conserved amino acids (such as Cys23, Trp41, Cys104, Phe/Trp118, and a hydrophobic residue at position 89) always have the same position. Additionally, a standardized delimitation of the framework regions (FR1: positions 1 to 26; FR2: 39 to 55; FR3: 66 to 104; and FR4: 118 to 129) and of the CDR (CDR1: 27 to 38, CDR2: 56 to 65; and CDR3: 105 to 117) is provided.

The CDR/loops are referred to herein according to the Kabat scheme for all CDR. The CDR of the antibodies of the present invention are referred to herein as CDR L1, L2, L3 for CDR in the light chain, and CDR H1, H2, H3 for CDR in the heavy chain.

An “antibody fragment” as referred to herein may include any suitable antigen-binding antibody fragment known in the art. The antibody fragment may be a naturally-occurring antibody

fragment, or may be obtained by manipulation of a naturally-occurring antibody or by using recombinant methods. For example, an antibody fragment may include, but is not limited to a Fv, single-chain Fv (scFv; a molecule consisting of V_L and V_H connected with a peptide linker), Fab, $F(ab')_2$, and multivalent presentations of any of these. Antibody fragments such as those just described may require linker sequences, disulfide bonds, or other type of covalent bond to link different portions of the fragments; those of skill in the art will be familiar with various approaches.

The antibody or fragment thereof of the present invention specifically binds to the extracellular domain of human (h)Carbonic Anhydrase (CA) IX (Genbank Accession no. NC_000009.12). CA-IX is a metalloenzyme that catalyzes the reversible hydration of carbon dioxide to bicarbonate and protons (Figure 1). CA-IX is a transmembrane protein with an extracellular catalytic site and an NH_2-terminal proteoglycan (PG)-like domain. An antibody and a fragment thereof "specifically binds" CA-IX if it binds CA-IX with an equilibrium dissociation constant (K_D, i.e., a ratio of K_d/K_a, K_d and K_a are the dissociation rate and the association rate, respectively) less than 10^{-5} M (e.g., less than 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, 10^{-10} M, 10^{-11} M, 10^{-12} M, or 10^{-13} M), while not significantly binding other components present in a test sample (e.g., with a K_D that is at least 10 times, such as 50 times or 100 times, more than K_D for binding CA-IX). Affinities of an antibody and a fragment thereof disclosed herein and CA-IX can be readily determined using the method described in Example 5 of the present disclosure.

The antibody or fragment thereof as described herein should exhibit a high degree of internalization. Without wishing to be bound by theory, the antibodies or fragments thereof presently described bind to the extracellular domain of CA-IX. The antibodies or fragments thereof are then internalized by the cell and delivered into subcellular organelles, including endosomes and lysosomes. The antibody or fragment thereof as described herein may also reduce cell viability. Antibody internalization may be measured by any appropriate methods known in the art, including antibody internalization assays offered by Life Technologies, Zap Antibody Internalization Kit by Advanced targeting Systems, and/or quantitative assessment described in Liao-Chan et al., 2015.

The terms "antibody" and "antibody fragment" ("fragment thereof") are as defined above. As previously stated, the antibody or fragment thereof may be from any source, human, mouse, or other; may be any isotype, including IgA, IgD, IgE, IgG, and IgM; and may be any type of fragment, including but not limited to Fv, scFv, Fab, and $F(ab')_2$.

In a more specific embodiment, the present invention provides an isolated or purified antibody or fragment thereof selected from the group consisting of:

a) a light chain comprising CDR L1 of sequence RASGNIHNYLA (SEQ ID NO:1), CDR L2 of sequence NTITLAD (SEQ ID NO:2), and CDR L3 of sequence QHFWNIPFT (SEQ ID NO:3); and a heavy chain comprising CDR H1 of sequence GFTFTSCYIH (SEQ ID NO:4), CDR H2 of sequence WIYPGNGNTKYNEIFKG (SEQ ID NO:5), and CDR H3 of sequence GDTTANTMDY (SEQ ID NO:6); and wherein the antibody or fragment thereof binds the catalytic domain of CA-IX;

b) a light chain comprising CDR L1 of sequence RSSQSLVHSNGNTYLH (SEQ ID NO:7), CDR L2 of sequence KVSNRFS (SEQ ID NO:8), CDRL3 of sequence SQNTHVPPT (SEQ ID NO:9); and a heavy chain comprising CDR H1 of sequence GFTFNTYAMY (SEQ ID NO:10), CDR H2 of sequence RIRSKSNNYAIYYADSVKD (SEQ ID NO:11), and CDR H3 of sequence GWDWFAY(SEQ ID NO:12); and wherein the antibody or fragment thereof binds the PG-like domain of CA-IX (the epitope may be EEDLPGEE); and

c) a light chain comprising CDR L1 of sequence KSSQSLLDSDGKTYLN (SEQ ID NO:13), CDR L2 of sequence LVSKLDS (SEQ ID NO:14), CDRL3 of sequence CQGTHFPW (SEQ ID NO:15); and a heavy chain comprising CDR H1 of sequence GYTFTNYGMN (SEQ ID NO:16), CDR H2 of sequence WINTYTGEPTYADDFKG (SEQ ID NO:17), and CDR H3 of sequence GGIATPTSY (SEQ ID NO:18); and wherein the antibody or fragment thereof binds the PG-like domain of CA-IX (the epitope may be LPRMQEDSPLGGG).

In one embodiment, the isolated or purified antibody or fragment thereof may comprise

a) a variable light (VL) domain of sequence selected from the group consisting of:

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSR FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELK (SEQ ID NO:19),

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPPTFGGGTKLEIK (SEQ ID NO: 21), and

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQGTHFPWTFGGGTKLEIK (SEQ ID NO:23);

b) a variable heavy (V_H) domain of sequence selected from the group consisting of:

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTK YNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVS S (SEQ ID NO:20);

EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAI YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGWDWFAYWGQGTPVTVSA (SEQ ID NO:22); and

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLKWMGWINTYTGEPT YADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARGGIATPTSYWGQGTTLTVSS (SEQ ID NO:24); or

c) a sequence substantially identical to the variable light (VL) domain of a) or the variable heavy (VH) domain of b) as described above.

The antibody or fragment thereof just defined specifically binds to the extracellular domain of CA-IX.

In specific, non-limiting examples, the isolated or purified antibody or fragment thereof of the present invention may comprise

a) a variable light (V_L) domain of sequence

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSR FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELK (SEQ ID NO:19)

and/or variable heavy (V_H) domain of sequence

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTK YNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVS S (SEQ ID NO:20);

b) a variable light (V_L) domain of sequence

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPPTFGGGTKLEIK (SEQ ID NO: 21)

and/or variable heavy (V_H) domain of sequence

EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAI YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGWDWFAYWGQGTPVTVSA (SEQ ID NO:22);

c) a variable light (V_L) domain of sequence

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQGTHFPWTFGGGTKLEIK (SEQ ID NO:23)

and/or variable heavy (V_H) domain of sequence

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLKWMGWINTYTGEPT YADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARGGIATPTSYWGQGTTLTVSS (SEQ ID NO:24);

or a sequence substantially identical thereto.

In a yet more specific example, the isolated or purified antibody specific for CA-IX may comprise:

a) a variable light (V_L) domain comprising the sequence

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSR FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:25)

and variable heavy (V_H) domain comprising the sequence

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTK YNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:26);

b) a variable light (V_L) domain comprising the sequence

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPPTFGGGTKLEIKRTVAAPSV
FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:27)

and variable heavy (V_H) domain comprising the sequence

EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAI
YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGWDWFAYWGQGTPVTVSA
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:28);

c) a variable light (V_L) domain comprising the sequence

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQGTHFPWTFGGGTKLEIKRTVAAPSVF
IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:29)

and variable heavy (V_H) domain comprising the sequence

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLKWMGWINTYTGEPT
YADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARGGIATPTSYWGQGTTLTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:30);

or a sequence substantially identical thereto.

A substantially identical sequence may comprise one or more conservative amino acid mutations. It is known in the art that one or more conservative amino acid mutations to a reference sequence may yield a mutant peptide with no substantial change in physiological,

chemical, physico-chemical or functional properties compared to the reference sequence; in such a case, the reference and mutant sequences would be considered “substantially identical” polypeptides. A conservative amino acid substitution is defined herein as the substitution of an amino acid residue for another amino acid residue with similar chemical properties (e.g. size, charge, or polarity). These conservative amino acid mutations may be made to the framework regions of the antibody or fragment thereof while maintaining the CDR sequences listed above and the overall structure of the antibody or fragment; thus the specificity and binding of the antibody are maintained.

In a non-limiting example, a conservative mutation may be an amino acid substitution. Such a conservative amino acid substitution may substitute a basic, neutral, hydrophobic, or acidic amino acid for another of the same group. By the term “basic amino acid" it is meant hydrophilic amino acids having a side chain pK value of greater than 7, which are typically positively charged at physiological pH. Basic amino acids include histidine (His or H), arginine (Arg or R), and lysine (Lys or K). By the term “neutral amino acid” (also “polar amino acid”), it is meant hydrophilic amino acids having a side chain that is uncharged at physiological pH, but which has at least one bond in which the pair of electrons shared in common by two atoms is held more closely by one of the atoms. Polar amino acids include serine (Ser or S), threonine (Thr or T), cysteine (Cys or C), tyrosine (Tyr or Y), asparagine (Asn or N), and glutamine (Gln or Q). The term “hydrophobic amino acid” (also “non-polar amino acid”) is meant to include amino acids exhibiting a hydrophobicity of greater than zero according to the normalized consensus hydrophobicity scale of Eisenberg (1984). Hydrophobic amino acids include proline (Pro or P), isoleucine (Ile or I), phenylalanine (Phe or F), valine (Val or V), leucine (Leu or L), tryptophan (Trp or W), methionine (Met or M), alanine (Ala or A), and glycine (Gly or G). "Acidic amino acid" refers to hydrophilic amino acids having a side chain pK value of less than 7, which are typically negatively charged at physiological pH. Acidic amino acids include glutamate (Glu or E), and aspartate (Asp or D).

Sequence identity is used to evaluate the similarity of two sequences; it is determined by calculating the percent of residues that are the same when the two sequences are aligned for maximum correspondence between residue positions. Any known method may be used to calculate sequence identity; for example, computer software is available to calculate sequence identity. Without wishing to be limiting, sequence identity can be calculated by software such as NCBI BLAST2 service maintained by the Swiss Institute of Bioinformatics (and as found at ca.expasy.org/tools/blast/), or any other appropriate software that is known in the art.

The substantially identical sequences of the present invention may be at least 90% identical; in another example, the substantially identical sequences may be at least 90, 91, 92, 93, 94, 95,

96, 97, 98, 99, or 100% identical, or any percentage there between, at the amino acid level to sequences described herein. Importantly, the substantially identical sequences retain the activity and specificity of the reference sequence. In a non-limiting embodiment, the difference in sequence identity may be due to conservative amino acid mutation(s). In a non-limiting example, the present invention may be directed to an antibody or fragment thereof comprising a sequence at least 95%, 98% or 99% identical to that of the antibodies described herein.

The present invention further encompasses an antibody or fragment thereof that is chimeric (or chimerized), veneered, or humanized. The antibody or fragment thereof may be chimeric, in that the antibody or fragment thereof is a combination of protein sequences originating from more than one species. As is known to those of skill in the art, a chimeric antibody is produced by combining genetic material from a nonhuman source (for example but not limited to a mouse) with genetic material from a human. For example and without wishing to be limiting, human constant domains can be fused to mouse V_H and V_L sequences (see Gonzales et al 2005). Veneering, also referred to in the art as “variable region resurfacing”, of antibodies involves replacing solvent-exposed residues in the framework region of the native antibody or fragment thereof with the amino acid residues in their human counterpart (Padlan, 1991; Gonzales et al 2005); thus, buried non-humanized residues, which may be important for CDR conformation, are preserved while the potential for immunological reaction against solvent-exposed regions is minimized. Humanization of an antibody or antibody fragment comprises replacing an amino acid in the sequence with its human counterpart, as found in the human consensus sequence, without loss of antigen-binding ability or specificity; this approach reduces immunogenicity of the antibody or fragment thereof when introduced into human subjects. In this process, one or more than one of the CDR defined herein may be fused or grafted to a human variable region (V_H, or V_L), to other human antibody (IgA, IgD, IgE, IgG, and IgM), to human antibody fragment framework regions (Fv, scFv, Fab), or to human proteins of similar size and nature onto which CDR can be grafted (Nicaise et al, 2004). In such a case, the conformation of said one or more than one hypervariable loop is likely preserved, and the affinity and specificity of the sdAb for its target (i.e., Axl) is likely minimally affected. As is known by those of skill in the art, it may be necessary to incorporate certain native amino acid residues into the human framework in order to retain binding and specificity. Humanization by CDR grafting is known in the art (for example, see Tsurushita et al, 2005; Jones et al, 1986; Tempest et al, 1991; Riechmann et al, 1988; Queen et al, 1989; reviewed in Gonzales et al, 2005 – see also references cited therein), and thus persons of skill would be amply familiar with methods of preparing such humanized antibody or fragments thereof.

The present invention thus provides an isolated or purified antibody or fragment thereof specific for CA-IX may be a chimeric antibody comprising the variable domain as defined above linked to human IgG1 constant domains. For example, and without wishing to be limiting in any manner, the human IgG1 constant domains may comprise a human kappa 1 light chain constant domain and human IgG1 heavy chain constant domains.

The antibody or fragment thereof of the present invention may also comprise additional sequences to aid in expression, detection or purification of a recombinant antibody or fragment thereof. Any such sequences or tags known to those of skill in the art may be used. For example, and without wishing to be limiting, the antibody or fragment thereof may comprise a targeting or signal sequence (for example, but not limited to ompA), a detection/purification tag (for example, but not limited to c-Myc, His_5, His_6, or His_8G), or a combination thereof. In another example, the signal peptide may be MVLQTQVFISLLLWISGAYG (SEQ ID NO:31) or MDWTWRILFLVAAATGTHA (SEQ ID NO:32). In a further example, the additional sequence may be a biotin recognition site such as that described by Cronan et al in WO 95/04069 or Voges et al in WO/2004/076670. As is also known to those of skill in the art, linker sequences may be used in conjunction with the additional sequences or tags, or may serve as a detection/purification tag.

The antibody or fragment thereof of the present invention may also be in a multivalent display format, also referred to herein as multivalent presentation. Multimerization may be achieved by any suitable method known in the art. For example, and without wishing to be limiting in any manner, multimerization may be achieved using self-assembly molecules such as those described in Zhang et al (2004a; 2004b) and WO2003/046560. The described method produces pentabodies by expressing a fusion protein comprising the antibody or fragment thereof of the present invention and the pentamerization domain of the B-subunit of an AB_5 toxin family (Merritt & Hol, 1995); the pentamerization domain assembles into a pentamer. A multimer may also be formed using the multimerization domains described by Zhu et al. (2010); this form, referred to herein as a “combody” form, is a fusion of the antibody or fragment of the present invention with a coiled-coil peptide resulting in a multimeric molecule (Zhu et al., 2010). Other forms of multivalent display are also encompassed by the present invention. For example, and without wishing to be limiting, the antibody or fragment thereof may be presented as a dimer, a trimer, or any other suitable oligomer. This may be achieved by methods known in the art, for example direct linking connection (Nielson et al, 2000), c-jun/Fos interaction (de Kruif & Logtenberg, 1996), “Knob into holes” interaction (Ridgway et al, 1996).

Each subunit of the multimers described above may comprise the same or different antibodies or fragments thereof of the present invention, which may have the same or different specificity. Additionally, the multimerization domains may be linked to the antibody or antibody fragment using a linker, as required; such a linker should be of sufficient length and appropriate composition to provide flexible attachment of the two molecules, but should not hamper the antigen-binding properties of the antibody. For example, and without wishing to be limiting in any manner, the antibody or fragments thereof may be presented in a bi-specific antibody.

The invention also encompasses the antibody or fragment thereof as described above linked to a cargo molecule. The cargo molecule may be any suitable molecule. For example, and without wishing to be limiting in any manner, the cargo molecule may be a detectable agent, a therapeutic agent, a drug, a peptide, an enzyme, a growth factor, a cytokine, a receptor trap, an antibody or fragment thereof (e.g., IgG, scFv, Fab, V_HH, V_H, V_L, etc) a chemical compound, a carbohydrate moiety, DNA-based molecules (anti-sense oligonucleotide, microRNA, siRNA, plasmid), a cytotoxic agent, viral vector (adeno-, lenti-, retro-), one or more liposomes or nanocarriers loaded with any of the previously recited types of cargo molecules, or one or more nanoparticle, nanowire, nanotube, or quantum dots. The antibody or fragment thereof may be linked to the cargo molecule using any method known in the art (recombinant technology, chemical conjugation, etc.).

In one non-limiting example, the cargo molecule may be a detectable label, a radioisotope, a paramagnetic label such as gadolinium or iron oxide, a fluorophore, a fluorescent agent, Near Infra-Red (NIR) fluorochrome or dye such as Cy5.5, an echogenic microbubble, an affinity label (for example biotin, avidin, etc), a detectable protein-based molecule, nucleotide, quantum dot, nanoparticle, nanowire, or nanotube or any other suitable agent that may be detected by imaging methods. In a specific, non-limiting example, the anti-CA-IX or fragment thereof may be linked to a near infrared fluorescence (NIRF) imaging dye, for example and not wishing to be limiting Cy5.5, Alexa680, Dylight680, or Dylight800.

In another specific, non-limiting embodiment, the antibody or fragment thereof as described herein is linked to a drug, thus providing an antibody-drug conjugate (ADC). The drug may be any type of drug, for example but not limited to a cytotoxic agent. The cytotoxic agent may include, but is not limited to anti-microtubule agents (such as taxanes, maytansines and auristatins), DNA damaging agents (such as calicheamicin and duocarmydin), RNA polymerase inhibitors (such as alpha-amantin), and other potent cytotoxic drugs (such as anthracyclines). As is known to those of skill in the art, the antibody-drug conjugate allows for targeted delivery of a drug, thus limiting systemic exposure. In this construct, the antibody or fragment thereof as described herein binds to the extracellular domain of CA-IX; the drug

linked to the antibody or fragment thereof is thus internalized. Upon internalization the cytotoxic agent is released within the target cells upon degradation of the human CA-IX antibody-DM1 complex in lysosomes. Depending on the intracellular concentration of the cytotoxic agent accumulated in cancer cells, rapid apoptosis occurs.

The cargo molecule as described herein may be linked, also referred to herein as "conjugated", to the antibody or fragment thereof by any suitable method known in the art. For example, and without wishing to be limiting, the cargo molecule may be linked to the peptide by a covalent bond or ionic interaction. The linkage may be achieved through a chemical cross-linking reaction, or through fusion using recombinant DNA methodology combined with any peptide expression system, such as bacteria, yeast or mammalian cell-based systems. When conjugating the cargo molecule to the antibody or fragment thereof, a suitable linker may be used. Methods for linking an antibody or fragment thereof to a cargo molecule such as a therapeutic or detectable agent would be well-known to a person of skill in the art.

The present invention also encompasses nucleic acid sequences encoding the molecules as described herein. Given the degeneracy of the genetic code, a number of nucleotide sequences would have the effect of encoding the desired polypeptide, as would be readily understood by a skilled artisan. The nucleic acid sequence may be codon-optimized for expression in various micro-organisms. The present invention also encompasses vectors comprising the nucleic acids as just described. Furthermore, the invention encompasses cells comprising the nucleic acid and/or vector as described.

The present invention further encompasses the isolated or purified antibody or fragments thereof immobilized onto a surface using various methodologies; for example, and without wishing to be limiting, the antibody or fragment may be linked or coupled to the surface via His-tag coupling, biotin binding, covalent binding, adsorption, and the like. Immobilization of the antibody or fragment thereof of the present invention may be useful in various applications for capturing, purifying or isolating proteins. The solid surface may be any suitable surface, for example, but not limited to the well surface of a microtiter plate, channels of surface plasmon resonance (SPR) sensorchips, membranes, beads (such as magnetic-based or sepharose-based beads or other chromatography resin), glass, plastic, stainless steel, a film, or any other useful surface such as nanoparticles, nanowires and cantilever surfaces. A purified antibody or fragment thereof immobilized onto a surface may be used in a variety of methods, including diagnostic methods.

Thus, the present invention further provides an *in vitro* method of detecting CA-IX, comprising contacting a tissue sample with one or more than one isolated or purified antibody or fragment thereof of the present invention linked to a detectable agent. The CA-IX-antibody complex can then be detected using detection and/or imaging technologies known in the art. The tissue sample in the method as just described may be any suitable tissue sample, for example but not limited to a serum sample, a vascular tissue sample, or a tumour tissue sample; the tissue sample may be from a human or animal subject. The step of contacting is done under suitable conditions, known to those skilled in the art, for formation of a complex between the antibody or fragment thereof and CA-IX. The step of detecting may be accomplished by any suitable method known in the art, for example, but not limited to optical imaging, immunohistochemistry, molecular diagnostic imaging, ELISA, or other suitable method. For example, and without wishing to be limiting in any manner, the isolated or purified antibody or fragment thereof linked to a detectable agent may be used in immunoassays (IA) including, but not limited to enzyme IA (EIA), ELISA, “rapid antigen capture”, “rapid chromatographic IA”, and “rapid EIA”. (For example, see Planche et al, 2008; Sloan et al, 2008; Rüssmann et al, 2007; Musher et al, 2007; Turgeon et al, 2003; Fenner et al, 2008). In a specific, non-limiting embodiment, the *in vitro* method is for detection of CA-IX in circulating cells and the tissue sample is a serum sample.

The present invention also provides an *in vivo* method of detecting CA-IX expression in a subject. The method comprises administering one or more than one isolated or purified antibody or fragment thereof as described herein linked to a detectable agent to the subject, then detecting the labelled antibody or fragment thereof bound to CA-IX. The step of detecting may comprise any suitable method known in the art, for example, but not limited to PET, SPECT, or fluorescence imaging, or any other suitable method. The method as just described may be useful in detecting the expression of CA-IX in tissues, for example but not limited to tumor tissues.

The *in vivo* detection step in the methods described above may be whole body imaging for diagnostic purposes or local imaging at specific sites, such as but not limited to sites of solid tumor growth, in a quantitative manner to assess the progression of disease or host response to a treatment regimen. The detection step in the methods as described above may be immunohistochemistry, or a non-invasive (molecular) diagnostic imaging technology including, but not limited to:

- Optical imaging;

- Positron emission tomography (PET), wherein the detectable agent is an isotope such as ^{11}C, ^{13}N, ^{15}O, ^{18}F, ^{64}Cu, ^{62}Cu, $1^{24}I$, ^{76}Br, ^{82}Rb and $^{6}8Ga$, with ^{18}F being the most clinically utilized;

- Single photon emission computed tomography (SPECT), wherein the detectable agent is a radiotracer such as ^{99m}Tc, ^{111}In, ^{123}I, ^{201}Tl, ^{133}Xe, depending on the specific application;

- Magnetic resonance imaging (MRI), wherein the detectable agent may be, for example and not limited to gadolinium, iron oxide nanoparticles and carbon-coated iron-cobalt nanoparticles thereby increasing the sensitivity of MRI for the detection of plaques.

- Contrast-Enhanced Ultrasonography (CEUS) or ultrasound, wherein the detectable agent is at least one acoustically active and gas-filled microbubble. Ultrasound is a widespread technology for the screening and early detection of human diseases. It is less expensive than MRI or scintigraphy and safer than molecular imaging modalities such as radionuclide imaging because it does not involve radiation.

The present invention further provides a method of transporting a molecule of interest into cells expressing CA-IX. The method comprises administering the molecule linked to an antibody or fragment thereof as described herein to a subject. The molecule may be any desired molecule, including the cargo molecules, as previously described; the molecule may be “linked” to the antibody or fragment thereof using any suitable method, including, but not limited to conjugation or expression as a fusion protein. The administration may be by any suitable method, for example parenteral administration, including but not limited to intravenous (iv), subcutaneous (sc), and intramuscular (im) administration. In this method, the antibody or fragment thereof of the present invention delivers the desired molecule to cells in a targeted fashion.

The present invention also encompasses a composition comprising one or more than one isolated or purified antibody or fragment thereof as described herein. The composition may comprise a single antibody or fragment as described above, or may be a mixture of antibodies or fragments. Furthermore, in a composition comprising a mixture of antibodies or fragments of the present invention, the antibodies may have the same specificity, or may differ in their specificities; for example, and without wishing to be limiting in any manner, the composition may comprise antibodies or fragments thereof specific to CA-IX (same or different epitope). The composition may also comprise one or more than one antibody or fragments of the present invention linked to one or more than one cargo molecule. For example, and without

wishing to be limiting in any manner, the composition may comprise one or more than one ADC in accordance with the present invention.

The composition may also comprise a pharmaceutically acceptable diluent, excipient, or carrier. The diluent, excipient, or carrier may be any suitable diluent, excipient, or carrier known in the art, and must be compatible with other ingredients in the composition, with the method of delivery of the composition, and is not deleterious to the recipient of the composition. The composition may be in any suitable form; for example, the composition may be provided in suspension form, powder form (for example, but limited to lyophilised or encapsulated), capsule or tablet form. For example, and without wishing to be limiting, when the composition is provided in suspension form, the carrier may comprise water, saline, a suitable buffer, or additives to improve solubility and/or stability; reconstitution to produce the suspension is effected in a buffer at a suitable pH to ensure the viability of the antibody or fragment thereof. Dry powders may also include additives to improve stability and/or carriers to increase bulk/volume; for example, and without wishing to be limiting, the dry powder composition may comprise sucrose or trehalose. In a specific, non-limiting example, the composition may be so formulated as to deliver the antibody or fragment thereof to the gastrointestinal tract of the subject. Thus, the composition may comprise encapsulation, time-release, or other suitable technologies for delivery of the antibody or fragment thereof. It would be within the competency of a person of skill in the art to prepare suitable compositions comprising the present compounds.

The present invention will be further illustrated in the following examples. However, it is to be understood that these examples are for illustrative purposes only and should not be used to limit the scope of the present invention in any manner.

Example 1: Production and purification of rhCA-IX ECD

A 416 amino acid long recombinant fragment of the extracellular domain of human (h)CA-IX with a C-terminal His-tag was prepared. The sequence of the recombinant fragment is shown in SEQ ID NO:33.

Construct. A PTT5 construct containing a synthetic recombinant fragment of the extracellular domain (ECD) of hCA-IX linked to a C-terminal His-tag was synthesized by GeneART. A schematic of the plasmid construct is shown in Figure 2.

Transient transfection. 2 and 50 mL transfections of the plasmid DNA into CHO cells were

prepared. The day before the transfection, CHO-3E7 cells were diluted to $0.7x10^6$ cells/ml in complete growth medium (FreeStyle™ F17 media (Invitrogen) supplemented with L-glutamine (Hyclone) 4 mM final and Kolliphor® P188 0.1% final) and grown in shaker flasks (agitation rate of 100 rpm) at 37°C, 5% CO_2 in a humidified incubator. At the time of transfection, the cell density was between $1.7x10^6$ and $2.2x10^6$ cells/mL and viability was greater than 97%. The requisite number of cells was transferred to a sterile flask and antibiotics/antimycotics 100 x solution (Hyclone #SV30079) were added. For each transfection, a 2.0 ml cell suspension was transferred to a 6-well plate. The DNA-PEI mixture was prepared by a multi-step process that is outlined briefly: a master mix of AKTdd pTT22 (constitutively active mutant of AKT) and ssDNA (0.33 µg AKTdd pTT22 + 0.77 µg ssDNA/ 2 ml transfection) in complete cell culture media was prepared and added to labelled 1.5 ml tubes. Appropriate quantities of plasmid DNA (pTT5_CAIX coopt_H10G) were added to each tube such that the final volume, including the master mix, is 100 µl. Finally, 20 µl of PEI pro™ (polyethtleneimine from Polyplus-transfection #115-375), diluted to 0.055 mg/ml was added to the tubes containing DNA. The DNA mixture was vortexed and allowed to incubate for 3-10 minutes, after which the DNA-PEI mixture was added to the cells in the six-well plates. The contents of the plates were mixed with gentle swirling and incubated at 37°C, 5% CO_2 humidified incubator. 55 µl of 40% Tryptone N1(Organotechnie) 1% final and 5.5 µl of VPA (Valproic acid sodium salt from Sigma) 0.5 mM final was added 4 - 24 h post-transfection and the cells were incubated for another 6 days at 32°C.The same protocol was followed for 50 ml transfections, except that all quantities were increased proportionately and transfections were carried out in a 250 ml shake flasks.

Harvest. For 2 ml transfections, the transfected cell population was transferred to a 1.5 ml tube. The cells were removed by centrifugation at 1500g for 10 minutes and the supernatant was transferred to a new tube. For 50 ml transfections, the transfected cell population was transferred to a 50 ml tube and the cells were removed by centrifugation at 250 g for 10 minutes. The supernatant was filtered using a Millipore steriflip unit (Millipore).

Purification. The filtered culture supernatant was passed through a 1 ml protein A MabSelect SuRe resin (GE Healthcare) column. Five (5) bed volumes PBS D-PBS pH 7.4 w/o Ca, w/o Mg (Hyclone) were added to remove unbound material. The protein was eluted with 1 ml of 100 mM Na Citrate pH 3.0 and the eluate was neutralized with 1 M Tris, pH 9. Buffer exchange into PBS was carried out using dilution and filtration using Ultracel 10K centrifuge filters.

The rhCA-IX ECD was expressed in CHO cells, purified by Ni-agarose and verified by Sodium Dodecyl Sulfate PolyAcrylamide Gel Electrophoresis (SDS-PAGE) under non-reducing and

reducing conditions (Figure 3). The protein was shown to be a 50/50 mixture of rhCA-IX ECD monomer (~48 kDa) and dimer (~110 kDa).

The rhCA-IX ECD monomer/dimer was further purified by size exclusion chromatography (SEC) of the protein mixture (Figure 4A). Fractions with the highest protein concentration were selected and kept at 4°C for several weeks. Prior to further biophysical characterization measurements, samples were reanalyzed by SEC (Figures 4B-D). The results of this evaluation showed that both the monomer and dimer are stable upon storage.

Example 2: Generation of anti-CA-IX antibodies

To produce antibodies that target the extracellular domain of hCA-IX, mice were immunized with the rhCA-IX ECD obtained in Example 1. Hybridomas were generated and conditioned medium was evaluated for mAb binding to the rhCA-IX ECD protein.

Immunizations. 6-week old A/J mice were bled (pre-immune serum) and immunized i.p. and s.c. with 33 µg of rhCA-IX monomer/dimer mixture in incomplete Freund adjuvant, as part of a 3-protein multiplexed immunization mixture. Three weeks later, a second injection of 33 µg of rhCA-IX protein in PBS was done and mice were bled 7-10 days later. The serum titer was measured by ELISA. Three to eight months later, a final i.p. booster injection using 33 µg of rhCA-IX protein in PBS was done 4 days prior to fusion experiment.

Fusion of the harvested spleen cells. All manipulations were done under sterile conditions. Spleen cells were harvested from immunized mice in IMDM (Hy-Clone) and fused to NS0 myeloma cell line using PEG fusion protocol. To this end, spleen cells and myeloma cells were washed in IMDM, counted in RBC lysing buffer (Sigma) and mixed together at a 5:1 ratio. Pelleted cells were fused together by adding 1 ml of a 50% solution of PEG 4000 (EMD-Millipore) in PBS preheated at 37°C drop-wise over one minute, and incubated at 37°C for an additional 90 sec. The reaction was stopped by addition of 30 ml of IMDM at 22°C over 2 min. After a 10 min incubation, freshly fused cells were spun at 233 x g for 10 min. Cells were washed once in IMDM supplemented with 10% heat inactivated FBS (Sigma), and suspended at a concentration of $2x10^5$ input myeloma cells per ml in HAT selection medium (IMDM containing 20% heat inactivated FBS, penicillin-streptomycin (Sigma), 1 ng/ml mouse IL-6 (Biosource), HAT media supplement (Sigma) and L-glutamine) and incubated at 37°C, 5% CO_2. The next day, hybridoma cells were washed and suspended at a concentration of $2x10^5$ input myeloma cells per ml in semi-solid medium D (StemCell) supplemented with 5% heat inactivated FBS, 1 ng/ml mouse IL-6 and 10 µg/ml FITC- Fab'2 Goat anti-mouse IgG (H+L) (Jackson). The cell mixture was plated in Petri dish (Genetix) and further incubated for 6-7 days at 37°C, 5% CO_2. Secretor clones were then transferred using a mammalian cell clone

picker (ClonepixFL, Molecular Devices) into sterile 96-well plates (Costar) containing 200 µl of IMDM supplemented with 20% heat inactivated FBS, penicillin-streptomycin (Sigma), 1 ng/ml mouse IL-6 (Biosource), HT media supplement (Sigma) and L-glutamine and incubated for 2-3 days at 37°C, 5% CO_2.

Hybridoma selection. Hybridoma supernatant were screened by ELISA to detect specific binders. To this end, 96-well half-area plates (Costar) were coated with 25 µl of CA-IX at 5 µg/ml in PBS and incubated overnight at 4°C. Microplates were washed 3 times with PBS, blocked with PBS-BSA 1%, and 25 µl of hybridoma supernatant were added and incubated at 37°C, 5% CO_2 for 2 hours. Plates were washed 4 times with PBS-Tween 20 0,05% and incubated for 1h at 37°C, 5% CO_2 with 25 µl of secondary antibody alkaline phosphatase conjugated F(ab)'$_2$ goat anti-mouse IgG (H+L) (Jackson Immunoresearch) diluted 1/3000 in blocking buffer. After 4 washes with PBS-Tween 20 0,05%, 25 µl of a 1 mg/ml pNPP substrate solution was added and further incubated for one hour at 37°C. OD_{405nm} measurements were taken using a microplate reader (Spectramax 340 PC, Molecular Devices).

From 2 fusions of mouse spleen cells, 51 CA-IX mAb producing hybridomas were identified from which conditioned medium (CM) was collected and evaluated for binding to the rhCA-IX ECD protein by ELISA. Results for the selected clones are shown in Table 1.

Table 1. Evaluation of the CM collected from mAb-producing hybridomas by ELISA (rhCA-IX ECD).

Fusion	Clone	Species	Isotype	ELISA on protein
F101	11H9	mouse	IgG2A,κ	+++
F101	12H8	mouse	IgG1,κ	+++
F117	2C7	mouse	IgG1,κ	+++

All mAb were then purified via Protein A spin column, dialyzed twice against PBS and concentrated using an Amicon filter (cut-off MW 30,000). The final concentration of the antibody solutions was determined by absorbance (280 nm). Results for clones 11H9, 12H8 and 2C7 are shown in Table 2.

Table 2: Hybridoma mAb concentration by nanodrop after Protein A purification.

Fusion	Clone	volume (uL)	Concentration (µg/uL)	Produced (µg/15 mL)
F101	11H9	350	0.14	49

F101	12H8	170	0.2	34
F117	2C7	200	1.99	398

Example 3: Characterization of anti-CA-IX mAb

The anti-CA-IX monoclonal antibodies obtained in Example 2 were characterized using Western blot and Reverse Phase Protein Array (RPPA).

Western blot 1.6 μg of purified rhCA-IX ECD (as was used for the immunization) was resolved by SDS-PAGE (10%) under reducing conditions. Nitrocellulose membranes were prepared and probed with the individual CA-IX Abs either non-purified CM (200 μL) or purified at a concentration of 5 μg/mL. Immunoreactive bands were visualized by chemiluminescence (Perkin-Elmer). The analysis of the non-purified mAb 11H9, 12H8 or 2C7 indicated that these mAb did not detect rhCA-IX ECD under either one of these conditions (Figure 5), however after purification the 12H8 mAb was able to detect the rhCA-IX under both reducing and non-reducing conditions.

Reverse Phase Protein Array (RPPA). Proteins were spotted in duplicate using a Genetix QArray2 contact printer with SMP3 split pins (ArrayIt) on 16 pads nitrocellulose slides (Whatman FAST) using a two pins configuration to print two identical proteins simultaneously. Each of the 16 pads was printed with an identical array of 182 spots (13 x 14) of both native and denatured in the same array, but using distinct printing parameters on the robot. Printing was done at 20°C and 60% constant humidity. The source plate containing native proteins was kept at about 12°C on the robot's chilling device and the plate with denatured proteins was kept at 22°C during printing to avoid any SDS precipitation. Once printed, the slides were stored for one hour at room temperature in a desiccator at 5 to 10% humidity, to dry the spotted proteins.

Each array was simultaneously probed with a hybridoma supernatant (secreted mAb, Example 2) and an anti-GFP antibody to normalize for the spotted protein volume. Slides were assembled in the 16-well incubation chambers (Whatman) and in the multi-slide frame (Whatman) that is a reusable holder for up to four slides. In this assembly, a liquid-tight well was created on top of each individual array pad. To block nonspecific binding, 100 µl of blocking solution (1x PBS / 3% BSA / 0.1% Tween20) was added to each well. Each chamber was sealed with aluminum tape to prevent evaporation and incubated (1h, RT) with gentle agitation. The nitrocellulose pads were never allowed to dry from this step on. mAb were prepared by mixing 30 µl of each crude hybridoma supernatant with 30 µl of incubation solution (1x PBS / 2% BSA / 0.05% Tween20 / Rabbit anti-GFP-AlexaFluor555 (0.9 μg/ml)). Blocking solution was aspired and replaced by the diluted mAb solution, incubation chambers

were sealed with aluminum tape, and incubated while protected from light (2h RT, 130 rpm shaking). mAb solutions were removed, wells were washed three times with 100 µl washing solution (1x PBS / 0.1% Tween20), and the chambers were dismantled. At this point, slides were washed three times 5 minutes in 1x PBS / 0.1% Tween20 followed by one 5 minutes wash in 1x PBS. After the last wash, excess liquid was removed without letting the nitrocellulose dry. To detect the mAb bound to their antigen, 270 µl of the secondary antibody Cy5-conjugated AffiniPure $F(ab')_2$ fragment donkey anti-mouse IgG (H+L) (1 µg/ml in 1x PBS / 2% BSA / 0.05% Tween20, was added. The slide was then covered with a plastic cover-slip and incubated protected from light in a high humidity chamber (RT) for 45 minutes, with shaking (100 rpm). The slides were then washed (as described above) and dried by centrifugation in a vertical position.

Slides were scanned with a ScanArray Gx microarray scanner for Cy5 fluorescence (Ex=649 nm, Em=670 nm) and AF555 (Ex=555 nm, Em=565 nm). Scanned images were quantified using the QuantArray software. mAb affinities for antigens were calculated using NRC proprietary software using a four-step normalization process:

- The quantified signal of both fluorophores Cy5 and AF555 was subtracted with local background signal of each spot.
- Bad spots (with AF555 intensity lower than 33% of average) were excluded.
- To normalize for the total amount of protein in each spot, the Cy5 (anti-mouse IgG) signal was divided by the AF555 (anti-GFP spiked-in normalizer) signal.
- Duplicate spots were averaged. To normalize for 'slide-to-slide' signal intensity variations, the binding intensity of each mAb was divided by the median of the entire slide mAb binding intensities to native proteins.

The result is the mAb binding affinity in fluorescence unit (FU) above median. Antibody-antigen binding was considered specific when the binding affinity value was at least 2 times above the binding affinities standard deviation of all spotted proteins.

The RPPA results (Table 3) showed 1) the specificity of these mAb for rhCA-IX (i.e. no other proteins were detected in the protein mixture), and 2) that all three mAb bind to both native and denatured rhCA-IX ECD. mAb 11H9 and 12H8 bind slightly better to the native protein, whereas mAb 2C7 seems to have a slight increased preference for the denatured protein.

Table 3: RPPA results showing the rhCA-IX ECD binding specificity of mAbs 11H9, 12H8 and 2C7

Purified Antigen				
Clone	**Native (A)**	**Denatured (B)**	**Ratio (A)/(B) (Possibly epitope related)**	
11H9	119.58	85.82	1.39	
12H8	158.01	142.32	1.11	
2C7	178.94	208.4	0.86	
Antigen in protein mixture				
Clone	**Native (C)**	**Denatured (D)**	**mAb binding specificity**	**mAb concentration in hybridoma CM (µg/ml)**
11H9	57.83	8.33	rhCA-IX ECD	4.64
12H8	50.26	4.15	rhCA-IX ECD	2.52
2C7	44.18	3.68	rhCA-IX ECD	20.6

Example 4: Generation of chimeric anti-CA-IX antibodies

To facilitate large scale production of mAb and to ensure consistency in production, mAb were recombinantly expressed in CHO cells.

Antibody sequencing: The V_H and V_L mAb 11H9, 12H8 and 2C7 were sequenced and found to be as follows:

2C7 V_L – SEQ ID NO:19

2C7 V_H – SEQ ID NO:20

11H9 V_L – SEQ ID NO:21

11H9 V_H – SEQ ID NO:22

12H8 V_L – SEQ ID NO:23

12H8 V_H – SEQ ID NO:24

The V_L and V_H sequences were cloned into a human kappa1 light chain and human IgG1 heavy chain frameworks (constant domains), respectively, in the pTT5 vector by Genscript (Piscataway NJ, USA), thereby generating chimeric (c) mAb. The sequences for the chimeric antibodies were as follows:

c2C7 Light chain – SEQ ID NO:25

c2C7 Heavy chain – SEQ ID NO:26

c11H9 Light chain – SEQ ID NO:27

c11H9 Heavy chain – SEQ ID NO:28

c12H8 Light chain – SEQ ID NO:29

c12H8 Heavy chain – SEQ ID NO:30

In addition, all light chain sequences comprised a signal sequence MVLQTQVFISLLLWISGAYG (SEQ ID NO:31) at the N-terminus, while heavy chain sequences comprised the signal sequence MDWTWRILFLVAAATGTHA (SEQ ID NO:32) at the N-terminus.

CDR regions (Table 4) were also analyzed for a consensus binding sequence by reconstructing a phylogenetic tree (Figure 6) of the CDR 1-3 regions of the V_H and V_L chains using web-based software (Dereeper A et al., 2008; phylogeny.lirmm.fr/phylo_cgi/index.cgi). The results of this analysis indicated that the CDR regions of both the V_L and V_H regions of mAb 11H9 and 12H8 are more similar to each other than to that of mAb 2C7.

Table 4. CDR region sequences for mAb 11H9, 12H8 and 2C7.

mAb	Light Chain CDR		Heavy Chain CDR	
2C7	L1	RASGNIHNYLA (SEQ ID NO:1)	H1	GFTFTSCYIH (SEQ ID NO:4)
	L2	NTITLAD (SEQ ID NO:2)	H2	WIYPGNGNTKYNEIFKG (SEQ ID NO:5)
	L3	QHFWNIPFT (SEQ ID NO:3)	H3	GDTTANTMDY (SEQ ID NO:6)
11H9	L1	RSSQSLVHSNGNTYLH (SEQ ID NO:7)	H1	GFTFNTYAMY (SEQ ID NO:10)
	L2	KVSNRFS (SEQ ID NO:8)	H2	RIRSKSNNYAIYYADSVKD (SEQ ID NO:11)
	L3	SQNTHVPPT (SEQ ID NO:9)	H3	GWDWFAY (SEQ ID NO:12)
12HD8	L1	KSSQSLLDSDGKTYLN	H1	GYTFTNYGMN

		(SEQ ID NO:13)		(SEQ ID NO:16)
	L2	LVSKLDS (SEQ ID NO:14)	H2	WINTYTGEPTYADDFKG (SEQ ID NO:17)
	L3	CQGTHFPW (SEQ ID NO:15)	H3	GGIATPTSY (SEQ ID NO:18)

Recombinant antibody production and purification: Chimeric mAb expression was validated through a 2 mL expression scout, where CHO cells were transiently transfected with V_L- and V_H-containing constructs (1:1 ratio); conditioned medium (CM) was harvested on day 7, and mAb expression levels were evaluated by SDS-PAGE (data not shown). The chimeric (c)11H9, c12H8 and c2C7 mAb expressed well and a small-scale production (50 mL) was initiated by transiently transfecting CHO cells with the same construct ratio. Conditioned medium (CM) was harvested on day 7, chimeric mAb were purified (ProtA), quantitated, and evaluated by SDS-PAGE. Results are shown in Table 5 and Figure 7. The data show that all three chimeric mAbs are well expressed by the transiently transfected CHO cells. To distinguish these recombinant antibodies expressed in the human IgG1 framwork from the hybridoma derived antibodies, a 'c' for 'chimeric' is added to the ID of these mAbs.

Table 5: Recombinant c11H9, c12H8 and c2C7 concentration from 50 mL CHO scout culture by nanodrop after Protein A purification.

Clone	Frame work	Isotype	volume (uL)	Conc (µg/uL)	Produced (µg/50 mL)
c11H9	human	IgG1	~500	1.461	730
c12H8	human	IgG1	~500	5.285	2642.5
c2C7	human	IgG1	~500	2.184	1092

Example 5: Biophysical characterization of anti-CA-IX antibodies

The anti-CA-IX antibodies obtained in Examples 2 and 4 were characterized using Surface Plasmon Resonance (SPR). The chimeric antibodies of Example 4 were also analyzed for CA cross-reactivity and by Differential Scanning Calorimetry (DSC).

Surface Plasmon Resonance (SPR): SPR experiments were carried out by capturing the CA-IX mAb (Example 2) from the CM with an anti-mouse Fc antibody immobilized on the chip surface via amine coupling, after which 60 nM rhCA-IX EDC mixture, rhCA-IX EDC monomer, or dimer (Example 1) were flowed over the mAb surface to measure association (binding) followed by flowing running buffer to measure dissociation of any complex formed. All SPR

assays were carried out using a BioRad ProteOn XPR36 instrument (Bio-Rad Laboratories (Canada) Ltd. (Mississauga, ON)) with PBST running buffer at a temperature of 25°C. The polyclonal goat anti-mouse Fc (Jackson Immuno Research Laboratories Inc.) capture surface was generated using a GLC sensorchip activated by a 1:10 dilution of the standard BioRad sNHS/EDC solutions injected for 140 s at 100 µL/min in the analyte (horizontal) direction. Immediately after the activation, a 10 µg/mL solution of anti-human Fc antibody in 10 mM NaOAc pH 4.5 was injected in the analyte (horizontal) direction at a flow rate of 25 µL/min until approximately 4000 resonance units (RUs) were immobilized. Remaining active groups were quenched by a 140 s injection of 1M ethanolamine at 100 µL/min in the horizontal direction; this also ensures mock-activated interspots are created for blank referencing.

The screening of the chimeric antibody variants (Example 4) for binding to the rhCA-IX antigen targets occurred in two steps: an indirect capture of the antibody variants onto the anti-human Fc antibody surface in the ligand direction followed by the simultaneous injection of 5 concentrations of purified rhCA-IX antigen (Example 1) and one buffer blank for double referencing in the analyte direction. The change in response due to binding was measured during this antigen injection phase followed by injection of running buffer to measure dissociation of the complex formed. Firstly, one buffer injection for 30 s at 100 µL/min in the ligand direction was used to stabilize the baseline. For each antibody variant capture, non-purified variants in cell-culture media were diluted to 4% in PBST. One to five variants or controls were simultaneously injected in individual ligand channels for 240 s at flow 25 µL/min. This resulted in a capture of approximately 400 to 600 RUs onto the anti-human Fc surface. The first ligand channel was left empty to use as a blank control if required. This capture step was immediately followed by two buffer injections in the analyte direction to stabilize the baseline. Then 60nM, 20nM, 6.7nM, 2.2nM and 0.74nM rhCA-IX antigen along with a buffer blank was simultaneously injected at 50 µL/min for 120 s with a 300 s dissociation phase.

For both mAb and chimaeric antibodies, the captured antibody surfaces were regenerated by an 18 s pulse of 0.85% phosphoric acid for 18 s at 100 µL/min to prepare for the next injection cycle. Sensorgrams were aligned and double-referenced using the buffer blank injection and interspots, and the resulting sensorgrams were analyzed using ProteOn Manager software v3.1. The double-referenced sensorgrams were fit to the 1:1 binding model to determine the rate constants for association and dissociation (k_a and k_d) and the corresponding affinity (K_D).

Results are shown in Table 6. mAb 11H9 and 2C7 have a slight preference for the rhCA-IX dimer over the monomer. No data could be obtained for mAb 12H8 when using the monomer, however this mAb binds to the rhCA-IX ECD dimer in a similar manner as mAb 11H9 and 2C7.

To verify that the recombinantly-expressed chimeric antibodies behave similarly to the hybridoma-expressed mAb, SPR antigen-binding experiments were carried out by capturing the c11H9, c12H8 and c2C7 mAb with a goat anti-human Fc antibody surface immobilized on the chip surface. Results are shown in Figure 8 and Table 6. All three chimeric mAb (c11H8, c12H9 and c2C7) have a relative slow off-rate, confirming similar binding characteristics compared to the original mAb.

Table 6: Overview SPR results of purified hybridoma-derived mAb 11H9, 12H8, and 2C7 and the CHO expressed recombinant chimeric Ab c11H9, c12H8 and c2C7 using hCA-IX ECD monomer and/or dimer preps.

	mAb capture levels	k_a	k_d	K_D
Hybridoma-derived mAb				
Clone	**rhCA-IX ECD Mixture (Monomer+Dimer)**			
11H9	300	2.63×10^{5}	4.84×10^{-4}	1.84×10^{-9}
12H8	125	1.13×10^{6}	9.70×10^{-12}	8.60×10^{-18}
2C7	675	6.74×10^{5}	1.17×10^{-3}	1.73×10^{-9}
Clone	**rhCA-IX ECD Monomer**			
11H9	300	2.88×10^{5}	1.65×10^{-3}	5.72×10^{-9}
12H8	125	-	Biphasic	-
2C7	675	1.29×10^{6}	2.59×10^{-3}	3.20×10^{-9}
Clone	**rhCA-IX ECD Dimer**			
11H9	300	3.42×10^{5}	5.84×10^{-5}	1.71×10^{-10}
12H8	125	2.27×10^{6}	3.22×10^{-4}	1.43×10^{-10}
2C7	675	9.67×10^{5}	1.36×10^{-3}	1.41×10^{-9}
Recombinantly expressed Abs				
Clone	**rhCA-IX ECD Dimer**			
c11H9	400	1.46×10^{5}	3.12×10^{-5}	2.14×10^{-10}
c12H8	350	5.88×10^{5}	5.76×10^{-4}	9.79×10^{-10}
c2C7	380	2.96×10^{5}	8.90×10^{-4}	3.01×10^{-9}

Cross-reactivity determination by SPR: To evaluate the cross-reactivity of c11H9, c12H8, and c2C7 to other hCA, binding of the chimeric antibodies to rhCA-IV, rhCA-XII and rhCA-XIV as well as to recombinant murine (rm)CA-IX was measured by SPR by indirect capture (as described previously). CA proteins for the analyte injection were purchased from Sino Biologics Inc.; the proteins were reconstituted as recommended by the manufacturer and diluted to 100nM in SPR running buffer for binding analysis. The results, shown in Figure 9,

indicate that c11H9, c12H8 and c2C7 are specific for the hCA-IX, as no binding was detected against rhCA-IV, rhCA-XII and rhCA-XIV, or rmCA-IX at the concentration of 100 nM tested.

Differential Scanning Calorimetry (DSC): To determine the thermostability of c11H9, c12H8 and c2C7, a DSC was performed using a MicroCal auto-VP DSC. Briefly, the stability of 0.125 mg/mL solutions of c11H9, c12H8, and c2C7 in PBS were monitored at a scan rate of 90°C/hour between 25°C and 100°C. Melting temperatures (T_m) were determined from the integrated thermograms using Origin 7 software. The anti-HER1 antibody Cetuximab was used as a positive control. Results are shown in Figure 10. c12H8 and c2C7 display a thermostability similar to Cetuximab, whereas c11H9 seems slightly less stable than c12H8 and c2C7.

Example 6: Epitope mapping

The monoclonal antibodies of Example 2 and/or the chimeric antibodies of Example 4 were used to perform various methods of epitope mapping.

Pepscan: Epitope mapping services were provided by Pepscan (Lelystad, The Netherlands; pepscan.com). CLIPS™ technology (Chemical LInkage of Peptides onto Scaffolds) was used to gain insight into the binding epitope. The method is based on the chemical linkage of homocysteines that flank synthetic peptides (15 aa long) covering the entire hCA-IX protein, in addition to a synthetic scaffold containing a benzyl-bromide group (Timmerman et al., 2009). The purified mAb of Example 2 were screened against peptides in a 'linear' and single 'cycle' format.

The peptide binding results for 11H9, 12H8 and 2C7 are shown in Figure 11A, B, C. 12H8 and 2C9 preferred binding to the 'cycle' peptide whereas 11H9 did not display such preference. Results also showed that 11H9 and 12H8 bind to non-overlapping epitopes EEDLPGEE (SEQ ID NO:34) and LPRMQEDSPLGGG (SEQ ID NO:35), respectively, in the unstructured PG domain. For 2C7, signals were detected for epitopes in the catalytic domain, though they were too weak to determine a specific binding epitope. However, when combined with the yeast-surface display data (see below) showing sensitivity to reduction, a putative epitope for mAb 2C7 can be identified in the structured catalytic domain: PSDFSRYFQYEGSL (SEQ ID NO:36). See Figure 11D.

Epitope binning by SPR: To evaluate whether mAb belong to the same class, SPR epitope binning experiments were carried out with purified hybridoma-derived mouse monoclonal 11H9, 12H8 and 2C7 (Example 2), as well as recombinantly CHO expressed c11H9, c12H8 and c2C7 (Example 3). Antibodies were directly immobilized on the chips surface ('mAb1'),

after which either the rhCA-IX ECD monomer or dimer was flowed, followed by flowing the same antibody ('mAb2'); these methods are described in Abdiche et al. (2011). All experiments were performed on a ProteOn XPR36 biosensor at 25°C using PBST as running buffer (PBS with 0.05% v/v Tween20). GLM sensor chips and coupling reagents (10mM sodium acetate, pH 4.5, sulfo-N-hydroxysuccinimide (SNHS), 1-ethyl-3-(3-dimethylaminporpyl)-carbodiamide hydrochloride (EDC), and ethanolamide) were purchased from BioRad, Inc (Hercules, CA).

Creating antibodies array - Antibodies (Mab1) were immobilized on the GLM chip surface at 30 µl/min. The activation reagents (at stock concentration of 0.4M EDC and 0.1M SNHS in water) were diluted 20-fold each in water. The top (A1) horizontal channel (the Analyte channel in the Proteon control software) was activated for 3 min with the diluted activation reagents. Next, c11H9, c12H8, and c2C7 were each diluted to 20 µg/ml in 10 mM acetate pH4.5 and injected for 3 min in separate vertical (L1 to L6) channels (the Ligand channel in the Proteon control software), followed with a 3 min injection of ethanolamine to block the reactive spots. The multi-channel module (MCM) was then rotated and another 3 min injection of ethanolamine was done on the activated horizontal channel (A1). This four-step 'activation-binding-and-2x deactivation' procedure was then repeated on each of the horizontal channels (A2 to A6).

Sandwich epitope binning - The two-step sandwich epitope binning was done at 30 µl/min in the analyte orientation. 100nM CA-IX antigen was injected for 3 min, immediately followed by a 3 min injection of Mab2 at 100nM. Immobilized mAb (mAb1) surfaces were regenerated by a 18s injection of 0.85% phosphoric acid at 100 µl/min. This two-step injection (CA-IX-mAb2) was repeated for each individual Mab2 with monomer and dimer CA-IX. Each mAb were also tested simultaneously and used as Mab1 (immobilized on the chip) and mAb2 (in solution). To monitor the CA-IX dissociation from the immobilized Mab1 PBST was injected instead of mAb2.

Results are shown in Figures 12B. The data shows that none of the antibodies compete for binding to either the rhCA-IX ECD monomer or dimer, indicating that these three mAb bind to distinct, non-overlapping CA-IX epitopes.

Epitope mapping by yeast surface display (YSD): The hCA-IX ectodomain (ECD) and fragments thereof were expressed and covalently displayed on the surface of yeast cells (Feldhaus et al., 2003). The hCA-IX fragments covering the entire hCA-IX ECD (Figure 13A) or the PG domain alone (Figure 13B) were expressed as fusion proteins (Aga2-HA-(CA-IX)-MYC (pPNL6 vector) or (CA-IX)-Aga2-MYC (pPNL200 vector)) on the yeast cell surface. The YSD vectors (pPNL6 and pPNL200) were from The Pacific Northwest National Laboratory, USA. The displayed CA-IX fragments were used to map the amino acid sequences to which

11H9, 12H8, and 2C7 bind. The binding of the mAb to yeast cells was performed using a whole yeast cell ELISA. The amount of properly displayed fusion protein was measured by probing with an anti-MYC antibody, followed by an HRP-conjugated secondary antibody. The anti-MYC signal was then used to normalize the binding signal for c11H9, c12H8, and c2C7. For determination of linear versus conformational epitopes, yeast cells with displayed CA-IX fragments were heated at 80°C for 30 min, then chilled on ice for 20 min prior to labeling with antibodies. The binding of mAb to denatured yeast cells was normalized to the anti-MYC signal. The ratio of normalized anti-CA-IX signals of each mAb on native versus denatured hCA-IX peptide was thus indicative of the conformational nature of the epitope. In the native hCA-IX experiments, the commercial M75 mAb was used as a positive control; the epitope of this mAb is known (Zavada et al., 2000) and is located in the hCA-IX PG domain.

Tables 7 (native hCA-IX ECD) and 8 (denatured hCA-IX ECD) show that the binding epitopes for c11H9 and c12H8 are located in hCA-IX's PG domain (as is that for M75), whereas c2C7 binds to an epitope in the catalytic domain, thereby confirming the PepScan observations. This data set also indicates that the c11H9 and c12H8 epitopes are likely to be unstructured, whereas that of the c2C7 mAb is probably structured, given the observation that binding is lost to the denatured hCA-IX protein fragments.

Table 7: Results of the epitope mapping experiments by YSD of c11H9, c12H8 and c2C7 on native peptides covering the hCA-IX ECD. Anti-CA-IX antibody binding intensity is normalized on CA-IX_MYC expression on cells. -, no binding; +, binding.

						Anti-hCA-IX antibody binding intensity			
Clone	YSD vector	Fused protein	CA-IX Fragment	CA-IX amino acids	CA-IX Domain	c11H9	c12H8	c2C7	M75 control
1A	PNL6	Aga2-HA-CA9-MYC	**1**	53-111	**PG**	**+**	**-**	**-**	**++**
2B	PNL6	Aga2-HA-CA9-MYC	**2**	38-136	**+PG+**	**++**	**++**	**-**	**++**
3A	PNL6	Aga2-HA-CA9-MYC	**3**	1-136	**SP+PG+**	**+++**	**+**	**-**	**++++**
4A	PNL6	Aga2-HA-CA9-MYC	**4**	135-391	**CA**	**-**	**-**	**++**	**-**
5A	PNL6	Aga2-HA-CA9-MYC	**5**	112-391	**+CA**	**-**	**-**	**+++**	**-**
6B	PNL6	Aga2-HA-CA9-MYC	**6**	135-414	**CA+**	**-**	**-**	**+++**	**-**
7B	PNL6	Aga2-HA-CA9-MYC	**7**	112-414	**+CA+**	**-**	**-**	**+++**	**-**
8B	PNL6	Aga2-HA-CA9-MYC	**8**	38-414	**+PG+CA+**	**+++**	**+++**	**+**	**+++**

9A	PNL6	Aga2-HA-CA9-MYC	**9**	1-414	**SP+PG+CA+**	**++++**	**++**	Low level display of CA-IX	**++++**
11B	PNL6	Aga2-HA-X-MYC	Plasmid Ctrl	Neg Ctrl	**------**	**-**	**-**	**-**	**-**
EBY 100	No-plasmid	None	Strain Ctrl	Neg Ctrl	**------**	**-**	**-**	**-**	**-**
12B	PNL200	CA9-Aga2-MYC	**1**	53-111	**PG**	**++**	**-**	**-**	ND
13A	PNL200	CA9-Aga2-MYC	**2**	38-136	**+PG+**	**++**	**+++**	**-**	ND
14A	PNL200	CA9-Aga2-MYC	**3**	1-136	**SP+PG+**	**++++**	**+**	**-**	ND
15B	PNL200	CA9-Aga2-MYC	**4**	135-391	**CA**	**-**	**-**	**+**	ND
16B	PNL200	CA9-Aga2-MYC	**5**	112-391	**+CA**	**-**	**-**	**+**	ND
17B	PNL200	CA9-Aga2-MYC	**6**	135-414	**CA+**	**-**	**-**	**+++++**	ND
18A	PNL200	CA9-Aga2-MYC	**7**	112-414	**+CA+**	**-**	**-**	**+++++**	ND
19B	PNL200	CA9-Aga2-MYC	**8**	38-414	**+PG+CA+**	**++++**	**++++**	**+++++**	ND
20A	PNL200	CA9-Aga2-MYC	**9**	1-414	**SP+PG+CA+**	Low level display of CA-IX	Low level display of CA-IX	Low level display of CA-IX	ND
22A	PNL200	X-Aga2-MYC	Plasmid Ctrl	Neg Ctrl	**------**	**-**	**-**	**-**	ND
EBY 100	No plasmid	None	Strain Ctrl	Neg Ctrl	**------**	**-**	**-**	**-**	ND

Table 8: Results of the epitope mapping experiments by YSD of c11H9, c12H8 and c2C7 on denatured peptides covering the hCA-IX ECD. Anti-CA-IX antibody binding intensity is normalized on CA-IX_MYC expression on cells. -, no binding; +, binding.

						Anti-hCA-IX antibody binding intensity			
Clone	**YSD vector**	**Fused protein**	**hCA-IX Fragment**	**hCA-IX amino acids**	**hCA-IX Domain**	**c11H9**	**c12H8**	**c2C7**	**M75 control**
1A	PNL6	Aga2-HA-CA9-MYC	**1**	53-111	**PG**	**++++**	**+**	**-**	ND
2B	PNL6	Aga2-HA-CA9-MYC	**2**	38-136	**+PG+**	**++++**	**++++**	**-**	ND
3A	PNL6	Aga2-HA-CA9-MYC	**3**	1-136	**SP+PG+**	**++++++**	**+**	**-**	ND
4A	PNL6	Aga2-HA-CA9-MYC	**4**	135-391	**CA**	**-**	**-**	**-**	ND
5A	PNL6	Aga2-HA-CA9-MYC	**5**	112-391	**+CA**	**-**	**-**	**-**	ND
6B	PNL6	Aga2-HA-CA9-MYC	**6**	135-414	**CA+**	**-**	**-**	**-**	ND
7B	PNL6	Aga2-HA-CA9-MYC	**7**	112-414	**+CA+**	**-**	**-**	**-**	ND

8B	PNL6	Aga2-HA-CA9-MYC	**8**	38-414	**+PG+CA+**	**+++++**	**++++**	-	ND
9A	PNL6	Aga2-HA-CA9-MYC	**9**	1-414	**SP+PG+CA+**	Low level display of CA-IX	Low level display of CA-IX	-	ND
11B	PNL6	Aga2-HA-X-MYC	Plasmid Ctrl	Neg Ctrl	**------**	-	-	-	ND
EBY 100	No-plasmid	None	Strain Ctrl	Neg Ctrl	**------**	-	-	-	ND
12B	PNL200	CA9-Aga2-MYC	**1**	53-111	**PG**	**++++++**	-	-	ND
13A	PNL200	CA9-Aga2-MYC	**2**	38-136	**+PG+**	**+++**	**++**	-	ND
14A	PNL200	CA9-Aga2-MYC	**3**	1-136	**SP+PG+**	**++++++**	-	-	ND
15B	PNL200	CA9-Aga2-MYC	**4**	135-391	**CA**	-	-	-	ND
16B	PNL200	CA9-Aga2-MYC	**5**	112-391	**+CA**	-	-	-	ND
17B	PNL200	CA9-Aga2-MYC	**6**	135-414	**CA+**	-	-	-	ND
18A	PNL200	CA9-Aga2-MYC	**7**	112-414	**+CA+**	-	-	-	ND
19B	PNL200	CA9-Aga2-MYC	**8**	38-414	**+PG+CA+**	**++++++**	**++++**	-	ND
20A	PNL200	CA9-Aga2-MYC	**9**	1-414	**SP+PG+CA+**	Low level display of CA-IX	Low level display of CA-IX	-	ND
22A	PNL200	X-Aga2-MYC	Plasmid Ctrl	Neg Ctrl	**------**	-	-	-	ND
EBY 100	No-plasmid	None	Strain Ctrl	Neg Ctrl	**------**	-	-	-	ND

For higher resolution mapping of the epitopes in the hCA-IX PG domain, tiling peptides of 15 amino acid (aa) residues (with a 5 aa overlap) encompassing aa 37-140 of the native hCA-IX PG domain (Tables 9 and 10) were prepared. Corresponding DNA sequences were PCR-amplified, cloned into pPNL6 using GAP repair (Gietz et al., 1992), and displayed on the yeast surface.

Table 9: Amino acid sequence of 15 amino acid tiling peptides encompassing amino acids 37-140 of the entire hCA-IX (see Figure 13B).

Fragment #	**hCA-IX amino acids**	**Amino acid sequence**	**SEQ ID NO:**

1	37-51	PQRLPRMQEDSPLGG	38
2	47-61	SPLGGGSSGEDDPLG	39
3	57-71	DDPLGEEDLPSEEDS	40
4	67-81	SEEDSPREEDPPGEE	41
5	77-91	PPGEEDLPGEEDLPG	42
6	87-101	EDLPGEEDLPEVKPK	43
7	97-111	EVKPKSEEEGSLKLE	44
8	107-121	SLKLEDLPTVEAPGD	45
9	117-131	EAPGDPQEPQNNAHR	46
10	126-140	QNNAHRDKEGDDQSH	47
11	37-71	PQRLPRMQEDSPLGGGSSGEDDPLGEEDLPSEEDS	48
12	67-111	SEEDSPREEDPPGEEDLPGEEDLPGEEDLPEVKPKSEEEGSLKLE	49
13	107-140	SLKLEDLPTVEAPGDPQEPQNNAHRDKEGDDQSH	50
14	37-140	PQRLPRMQEDSPLGGGSSGEDDPLGEEDLPSEEDSPREEDPPGEEDLPGEEDLPGEEDLPEVKPKSEEEGSLKLEDLPTVEAPGDPQEPQNNAHRDKEGDDQSH	51

Table 10: Results of the epitope mapping experiments by YSD of c11H9, c12H8 and c2C7 on native peptides covering the hCA-IX ECD PG domain. Anti-CA-IX antibody binding intensity is normalized on CA-IX_MYC expression on cells. -, no binding; +, binding.

						Anti-hCA-IX antibody binding intensity			
Clone	**YSD vector**	**Fused protein**	**hCA-IX PG domain Fragment**	**Peptide length (amino acids)**	**hCA-IX amino acids**	**c11H9**	**c12H8**	**c2C7**	**M75**
1 A+B	PNL6	Aga2-HA-CA9-MYC	1	15	37-51	-	+++	-	-
2 A+B	PNL6	Aga2-HA-CA9-MYC	2	15	47-61	-	-	-	-
3 A+B	PNL6	Aga2-HA-CA9-MYC	3	15	57-71	-	-	-	++
4 A+B	PNL6	Aga2-HA-CA9-MYC	4	15	67-81	-	-	-	-
5 A+B	PNL6	Aga2-HA-CA9-MYC	5	15	77-91	+	-	-	+
6 A+B	PNL6	Aga2-HA-CA9-MYC	6	15	87-101	+	-	-	-
7 A+B	PNL6	Aga2-HA-CA9-MYC	7	15	97-111	-	-	-	-
8 A+B	PNL6	Aga2-HA-CA9-MYC	8	15	107-121	-	-	-	-
9 A+B	PNL6	Aga2-HA-CA9-MYC	9	15	117-131	-	-	-	-
10 A+B	PNL6	Aga2-HA-CA9-MYC	10	15	126-140	-	-	-	-
11 A+B	PNL6	Aga2-HA-CA9-MYC	11	35	37-71	-	+++	-	+++
12 A+B	PNL6	Aga2-HA-CA9-MYC	12	45	67-111	++	-	-	++
13 A+B	PNL6	Aga2-HA-CA9-MYC	13	34	107-140	-	-	-	-

14 A+B	PNL6	Aga2-HA-CA9-MYC	14	104	37-140	+++	+++	-	+++
15 A+B	PNL6	Aga2-HA-X-MYC	Plasmid Ctrl	none	------	-	-	-	-

Yeast cell ELISA with these YSD tiling peptides showed that c11H9 and M75 share similar, although not identical binding epitopes; the c11H9 epitope contained the repeat GEEDLP (SEQ ID NO:37) sequence, which appeared four times in the PG domain. c12H8 bound to an epitope that was distinguishable in the PG domain from that of c11H9 and M75; specifically, c12H8 bound to an epitope containing the unique sequence PQRLPRMQEDSPLGG (SEQ ID NO:38) located at the N-terminus. These data were in agreement with PepScan and SPR binning experimental results. Taking all experimental results together, the putative epitopes for the antibodies were proposed to be: EEDLPGEE (SEQ ID NO:34) for 11H9, PQRLPRMQEDSPLGG (SEQ ID NO:38) for 12H8, and PSDFSRYFQYEGSL (SEQ ID NO: 36) for 2C7.

Using similar methods, additional fine mapping of the epitope for c12H8 by YSD was carried out by N-and C-terminal deletion of fragment #1 in Table 9 (data not shown). In this manner, the minimal epitope for c12H8 was defined as LPRMQEDSP (SEQ ID NO:52), corresponding to aa 40-48 of CA-IX. Similarly, N-and C-terminal deletion of fragment #5 and #6 in Table 9, the minimal epitope for c11H9 was determined to be EDLPGEED (SEQ ID NO:53), which corresponds to aa 81-88 and aa 87-94 of CA-IX. Epitope mapping of the M75 epitope (data not shown) is in agreement with previous reports (see for example Zavada et al, 2000) that the minimal epitope for this antibody is GEEDLP (SEQ ID NO:37).

Example 7: Functional characterization of anti-CA-IX mAb

The ability of the anti-CA-IX mAb obtained in Example 2 to inhibit *in vitro* enzyme activity was evaluated, the cell line was verified and an ADC assay was performed.

In vitro rhcCA-IX enzyme activity inhibition: To determine whether the CA-IX mAb can inhibit the enzyme activity of the rhCA-IX ECD protein, an activity assay, detecting the esterase activity of the enzyme using 4-Methylumbelliferyl acetate (Sigma Aldrich) as substrate was performed. The kinetic measurements were carried out in 96-well solid black microplates (Corning) at pH 7.5 in a reaction mixture containing 25 mM MOPS, 15 mM Na_2SO_4, 0.5 mM EDTA and 2% (v/v) DMSO (final concentration). A final enzyme concentration of 0.5 µM for the dimer or 1 µM for the monomer was used. The enzyme was pre-incubated for 30 minutes at room temperature with increasing concentration of mAb (0.0625 to 4 µM) diluted in DPBS (Hyclone). Reactions were initiated by the addition of 100 µM 4-Methylumbelliferylacetate. The

rate of substrate hydrolysis was determined by monitoring 4-Methylumbelliferone-released fluorescence (excitation λ, 380 nm; emission λ, 440nm) as a function of time using the EnVision 2104 plate reader (Perkin Elmer). The substrate autohydrolysis control values were substracted from the observed total reaction velocities. Acetazolamide (Sigma Aldrich) at a concentration of 10 µM fully inhibited the activity of the rhCA-IX enzyme. Rates were determined in the initial and 'end portion' of each of the curves. Several concentrations of the rhCA-IX ECD mixture of Example 1 were tested and bench-marked against rhCA-IX purchased from R&D (data not shown). Using 1 µM rhCA-IX ECD, enzyme activity of the mAb was measured using a 4:1 (2C7) or 1:1 (11H9, 12H8) molar mAb:rhCA-IX ECD ratio. Results are shown in Figure 14 and Table 11. None of the tested mAb showed any enzyme inhibition activity.

Table 11: Enzyme inhibition data for hybridoma-derived 11H9, 12H8 and 2C7 using the rhCA-IX ECD mixture. For 2C7, a ratio of (mAb:rhCA-IX ECD mixture) of 4:1 was used. For 11H9 and 12H8, a ratio of (mAb:rhCA-IX ECD mixture) of 1:1 was used.

Clone	Data1	Data2	% rhCA-IX ECD Activity	STDEV	% rhCA-IX ECD Inhibition	Comments
2C7	125.73	128.77	127.25	2.15	-	No inhibition
11H9	107.08	104.47	105.77	1.84	-	No inhibition
12H8	102.8	-	102.8	-	-	No inhibition

Cell line verification: Non-transfected human renal tumor sk-rc-59 and sk-rc-52 cell lines (Dr G Ritter, MSKCC, NY, USA) were obtained to evaluate binding of the anti-CA-IX mAb to cell surface CA-IX. Western blot analysis of these cell lines under non-reducing and reducing conditions (Figure 15) confirmed the hCA-IX expression levels of the sk-rc-52 cell line (arrow), whereas no CA-IX could be detected in the sk-rc-59 cell line. Equal protein quantities were loaded (BCA protein assay) and confirmed by actin blot.

Flow cytometry: mAb were evaluated in a flow cytometry experiment using the sk-rc-59 (low CA-IX expression) and sk-rc-52 (high CA-IX expression) cell lines. Cells were grown to 80% confluency in T75 flasks using MEM/10% FBS medium supplemented with non-essential amino acids (NEAA), washed with dPBS (37°C) and harvested using non-enzymatic cell dissociation buffer (37°C). Cells were then transferred to 50 mL tubes, spun down (1100 rpm, RT, 5 min) and re-suspended in cell growth medium. Cells were counted and divided in 10^6 cell containing aliquots, spun down (1100 rpm, RT, 2 min), re-suspended in ice-cold dPBS/10%

FBS containing anti-CA-IX mAb (10 µg/mL final concentration) and incubated (50 min, 4°C). Cells were then washed with ice-cold dPBS/10% FBS, spun down (1100 rpm, 4°C, 3 min), and re-suspended in 500 µL ice-cold dPBS/10% FBS containing Alexa-488 Goat anti-mouse IgG (10 µg/mL final concentration). After incubation in the dark (25 min, 4°C), cells were washed with ice-cold dPBS/10% FBS, spun down (1100 rpm, 4°C, 3 min), re-suspended in ice-cold dPBS/10% FBS containing Propidium Iodine (PI; 10 µg/mL final concentration) and finally filtered over a gauze mesh prior to FACS analysis using a BD Biosciences LSR IITM flow cytometer. As controls, a commercially available mAb (R&D, Clone#303123) and the M75 mAb (provided by Dr E Oosterwijk, Radboud University Nijmegen, The Netherlands) were used. Experiments were plotted per cell line and results are shown in Figure 16. These results showed that mAb 11H9 binds slightly better to hCA-IX expressed by the sk-rc-52 cell line compared to 12H8 and 2C7, whereas virtually no binding was detected on the low hCA-IX expressing sk-rc-59 cells.

Surrogate ADC Assay: mAb were evaluated in a surrogate ADC assay using the high hCA-IX-expressing sk-rc-52 cells. The ADC assay was carried out using a commercially available ADC kit (atsbio.com) according to the manufacturer's instructions with some modifications. Briefly, sk-rc-52 (expressing high levels of hCA-IX) and sk-rc-59 (expressing low levels of hCA-IX) cells were seeded in RPMI/5% FBS in 96-well plates at a density of 5000 and 3000 cells/well, respectively. The next day, 10 nM of mAb was mixed with 20 nM of the Mab-Zap secondary antibody from the ADC kit, incubated (30 min, RT) prior to diluting the mixture 11x in RPMI/5% cell growth medium, and 10 µL of these mixtures were added to the cells (experiment carried out in triplicate). After 72h of incubation (37°C, 5% CO_2, humidified incubator), cell viability (bio mass) was determined using Sulforhodamine. For this procedure, 25 µl of 50% TCA was added to each well and plates were incubated (1h, 4°C). Plates were then washed 4x with tap water and air-dried at room temp. 100 µl of 0.4% (wt/vol in 1% acetic acid) SRB solution was added to each well and incubated (30 min, RT). Plates were then quickly rinsed 4x with 1% (vol/vol) acetic acid, air-dried at room temp, after which 100 µl of 10 mM Tris base solution (pH 10.5) was added followed by shaking (5 min, RT), and the OD (510nm/540nm) was measured. The CA-IX mouse mAb M75 was used as a positive control. Viability of the cells is expressed as the ratio of the mAb-ZAP secondary conjugate alone. Results (Figure 17) show that mAb 12H8, 11H9 and 2C7 are either equal to or better than the M75 mAb in reducing cell viability. Next serial dilutions (0-100 nM) of recombinantly expressed c11H9, c12H8 and c2C7 were tested in the surrogate ADC assay using sk-rc-52 cells (as described above). The results (Figure 18A; Table 12) show that the recombinantly expressed chimeric antibodies have retained their ADC potential.

ADC Assay: Recombinantly expressed chimeric c11H9, c12H8 and c2C7 were conjugated to DM1 (mertansine). Briefly, a 10 mM stock solution of SMCC-DM1 was prepared in dimethylacetamide (DMA) and stored at -20°C. Just prior to use, stock solutions were quickly brought to room temperature and two working stocks prepared (2000 μM and 2660 μM) by diluting concentrated stock into DMA. For small-scale optimization experiments, two aliquots (100 μL) of antibody (2 mg/mL) was mixed 10 μL each of 10-fold conjugation buffer (1000 mM sodium phosphate, 200 mM NaCl, 30 mM EDTA, pH 7.2). To start the reaction, 5 μL of the appropriate working stocks were added to the appropriate tubes and mixed quickly. The reaction was allowed to proceed overnight, protected from light at 25°C (no agitation). Reactions were stopped by passing the mixture through two desalting columns pre-equilibrated with PBS at pH 6.0, 0.02% w/v Polysorbate-20. Drug antibody ratio (DAR) was determined by UPLC-SEC using ratios of integrated absorbance at 252 nm and 280 nm vs the ratio of the extinction coefficients for the free drug and antibody at these two wavelengths. A linear relationship between DAR and the drug-linker:Ab ratio used in the reaction was determined and used to optimize the reaction ratio to achieve the target DAR of 3.5. The above protocol was repeated using the optimized drug-linker:Ab at large scale. Both the 'naked' non-conjugated c11H9, c12H8 and c2C7 and the c11H9-DM1, c12H8-DM1 and c2C7-DM1 antibodies were tested in an ADC assay (dose response 0-100 nM) using the sk-rc-52 cell line. The results (Figure 18B, Table 12) show the specificity of these ADCs in terms of killing the cells whereas the 'naked' antibodies had no effect. These results (and the calculated IC_{50}) are very similar to those obtained in the surrogate ADC assay.

Table 12. IC_{50} values for non-conjugated and DM1 conjugated chimeric anti-CA-IX antibodies.

Construct	IC_{50} (nM)
c11H9	6.32
c11H9-DM1	5.84
c12H8	23.55
c12H8-DM1	17.88
c2C7	2.20
c2C7-DM1	10.11

Example 8: Evaluation of Cardiotoxicity in Cardiomyocytes

Both on-target and off-target toxicity relating to the drug payload carried by an ADC is critical information that needs to be evaluated early in an ADC candidate selection. Prior clinical data reported for an anti-CA-IX ADC candidate in Phase I described unresolved issues concerning

cardiotoxicity. Human stem-cell derived cardiomyocytes (Cellular Dynamics; Cohen et al, 2011) from Cellular Dynamics were used to evaluate cardiotoxicity of the anti-CA-IX mAb obtained in Example 4, and their derived ADC in an *in vitro* setting.

Human-induced pluripotent (iPS) cardiomyocytes were obtained from Cellular Dynamics Inc. iPS cardiomyocytes (iCells) were thawed and cultured according to the manufacturers instructions. Briefly, cells were thawed, resuspended in iCell plating media, seeded in 0.1% gelatin-coated 96-well plates (15,000 cells/well) and maintained in a humidified incubator with 5% CO_2 at 37°C for 4 hours. Cells were then washed to remove debris and the plating media was replaced with iCell Maintenance Media which was then changed every other day during the course of the experiment. Cells were treated 4 days post-thaw with either the unconjugated antibodies c2C7 and c12H8 or the corresponding DM1-conjugated ADCs at a concentration of 10 nM, and incubated for an additional 5 days. A non-specific negative control human IgG1 and the corresponding DM1-conjugated ADC were also used for treated the cells using the same protocol. Cell viability was measured 3 and 5 days post-treatment using the CellTiter-Glo Luminescent cell viability Assay (Promega, Madison, WI). Briefly, the plates and reagents were equilibrated to room temperature for 30 minutes. A volume of CellTiter-Glo reagent was added to the volume of cell culture medium present in each well and mixed on an orbital shaker for 45 minutes. The luminescence was then recorded using an EnVision plate reader (PerkinElmer Inc.)

Results are shown in Figure 19. When compared to a non-specific human IgG1 negative control antibody and corresponding ADC, neither c2C7, c12H8 or their corresponding DM1 conjugate ADCs had any significant impact on cell viability at the concentration tested.

Example 9: CA-IX Species and CA-XII binding by Surface Plasmon Resonance

For ADC therapeutic development, a clinically relevant non-human primate model is required to evaluate safety. Here SPR using a ProteON XPR36 instrument (BioRad) was used to measure binding of two antibodies (Example 4) to the ECD of mouse, dog and cynomolgus monkey CA-IX.

A ProteON GLC chip was activated with sEDS and sNHS prior to immobilzing approximately 4000 RUs of Goat anti-human Fc (Jackson InnumoResearch) via amine (lysine) coupling in 10 mM acetate buffer pH 4.5. This surface was then used to capture c2C7 and c12H8 on different flow cells. Recombinantly-expressed (CHO cells) SEC purified dimeric CA-IX extracellular domain (ECD) from human, mouse, dog and cynomolgus monkey and human CA-XII, were prepared in PBS with 0.02% Polysorbate-20. These dilutions were then flowed over the captured antibodies at 5 different concentrations from 100 nM to 1.23 nM using a flow

rate 50 μL/min. Surfaces were regenerated after each concentration cycle using 0.85% phosphoric acid prior to the next injection. Kinetic association and dissociation rate constants were determined from non-linear fitting of the observed responses to a 1:1 binding mocel. These rate constants were used to calculate the binding constant K_D. Specific binding for the purposes of evaluating the suitability of these animal models was determined as having a binding constant K_D < 20 nM.

Table 13. Selection of non-human primate models for pre-clinical toxicology. Specific binding of CA-IX antibodies to different species of CA-IX extracellular domains was measured by SPR. Specific binding was based on the criteria of having a measured K_D < 20 nM.

Antibody	Human	Cynomolgus	Dog	Mouse
Control	Yes	Yes	No	No
c2C7	Yes	Yes	No	No
c12H8	Yes	Yes	No	No

Results are shown in Table 13 and Figure 20. Of the three species tested, cynomolgus monkey was the only one which met the affinity criteria (Table 13). Therefore, cynomolgus monkey will be the clinically-relevant non-human primate model for testing toxicology for c2C7, c12H8 and the corresponding DM1-conjugated ADC. Since CA-XII is often co-expressed with CA-IX in the same tumors, there should be no cross-reactivity between the CA-IX antibodies and CA-XII. Using SPR, there was no observable binding of any of the anti-CA-IX antibodies to CA-XII (Figure 20).

The embodiments and examples described herein are illustrative and are not meant to limit the scope of the invention as claimed. Variations of the foregoing embodiments, including alternatives, modifications and equivalents, are intended by the inventors to be encompassed by the claims. Furthermore, the discussed combination of features might not be necessary for the inventive solution.

LISTING OF SEQUENCES

SEQ ID NO:	Sequence	Description
1	RASGNIHNYLA	2C7 CDR L1
2	NTITLAD	2C7 CDR L2
3	QHFWNIPFT	2C7 CDR L3
4	GFTFTSCYIH	2C7 CDR H1
5	WIYPGNGNTKYNEIFKG	2C7 CDR H2
6	GDTTANTMDY	2C7 CDR H3
7	RSSQSLVHSNGNTYLH	11H9 CDR L1
8	KVSNRFS	11H9 CDR L2
9	SQNTHVPPT	11H9 CDR L3
10	GFTFNTYAMY	11H9 CDR H1
11	RIRSKSNNYAIYYADSVKD	11H9 CDR H2
12	GWDWFAY	11H9 CDR H3
13	KSSQSLLDSDGKTYLN	12H8 CDR L1
14	LVSKLDS	12H8 CDR L2
15	CQGTHFPW	12H8 CDR L3
16	GYTFTNYGMN	12H8 CDR H1
17	WINTYTGEPTYADDFKG	12H8 CDR H2
18	GGIATPTSY	12H8 CDR H3
19	DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLL VYNTITLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNI PFTFGAGTKLELK	mAb 2C7 VL
20	QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLE WIGWIYPGNGNTKYNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAV YFCARGDTTANTMDYWGQGTSVTVSS	mAb 2C7 VH
21	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPG QSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS QNTHVPPTFGGGTKLEIK	mAb 11H9 VL
22	EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLE WVARIRSKSNNYAIYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDT AMYYCVRGWDWFAYWGQGTPVTVSA	mAb 11H9 VH
23	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQ SPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQ GTHFPWTFGGGTKLEIK	mAb 12H8 VL
24	QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLK WMGWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDMAT YFCARGGIATPTSYWGQGTTLTVSS	mAb 12H8 VH
25	DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLL VYNTITLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWNI PFTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC	Chimeric 2C7 Light chain
26	QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLE WIGWIYPGNGNTKYNEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAV YFCARGDTTANTMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS	Chimeric 2C7 Heavy Chain

	NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG	
27	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPG QSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS QNTHVPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	Chimeric 11H9 Light Chain
28	EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLE WVARIRSKSNNYAIYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDT AMYYCVRGWDWFAYWGQGTPVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG	Chimeric 11H9 Heavy chain
29	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQ SPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCCQ GTHFPWTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	Chimeric 12H8 Light Chain
30	QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVQQAPGKGLK WMGWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDMAT YFCARGGIATPTSYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG	Chimeric 12H8 Heavy chain
31	MVLQTQVFISLLLWISGAYG	Light chain signal sequence
32	MDWTWRILFLVAAATGTHA	Heavy chain signal sequence
33	MAPLCPSPWLPLLIPAPAPGLTVQLLLSLLLLVPVHPQRLPRMQEDSP LGGGSSGEDDPLGEEDLPSEEDSPREEDPPGEEDLPGEEDLPGEED LPEVKPKSEEEGSLKLEDLPTVEAPGDPQEPQNNAHRDKEGDDQSH WRYGGDPPWPRVSPACAGRFQSPVDIRPQLAAFCPALRPLELLGFQ LPPLPELRLRNNGHSVQLTLPPGLEMALGPGREYRALQLHLHWGAA GRPGSEHTVEGHRFPAEIHVVHLSTAFARVDEALGRPGGLAVLAAFL EEGPEENSAYEQLLSRLEEIAEEGSETQVPGLDISALLPSDFSRYFQY EGSLTTPPCAQGVIWTVFNQTVMLSAKQLHTLSDTLWGPGDSRLQL NFRATQPLNGRVIEASFPAGVDSSPRAAEPVQLNSCLAAGDGSHHH HHHHHHHG	Recombinant hCA-IX ECD
34	EEDLPGEE	11H9 epitope
35	LPRMQEDSPLGGG	12H8 epitope
36	PSDFSRYFQYEGSL	Putative 2C7 epitope
37	GEEDLP	CA-IX repeat sequence
38	PQRLPRMQEDSPLGG	hCA-IX amino acid

		37-51
39	SPLGGGSSGEDDPLG	hCA-IX amino acid 47-61
40	DDPLGEEDLPSEEDS	hCA-IX amino acid 57-71
41	SEEDSPREEDPPGEE	hCA-IX amino acid 67-81
42	PPGEEDLPGEEDLPG	hCA-IX amino acid 77-91
43	EDLPGEEDLPEVKPK	hCA-IX amino acid 87-101
44	EVKPKSEEEGSLKLE	hCA-IX amino acid 97-111
45	SLKLEDLPTVEAPGD	hCA-IX amino acid 107-121
46	EAPGDPQEPQNNAHR	hCA-IX amino acid 117-131
47	QNNAHRDKEGDDQSH	hCA-IX amino acid 126-140
48	PQRLPRMQEDSPLGGGSSGEDDPLGEEDLPSEEDS	hCA-IX amino acid 37-71
49	SEEDSPREEDPPGEEDLPGEEDLPGEEDLPEVKPKSEEEGSLKLE	hCA-IX amino acid 67-111
50	SLKLEDLPTVEAPGDPQEPQNNAHRDKEGDDQSH	hCA-IX amino acid 107-140
51	PQRLPRMQEDSPLGGGSSGEDDPLGEEDLPSEEDSPREEDPPGEEDLPGEEDLPGEEDLPEVKPKSEEEGSLKLEDLPTVEAPGDPQEPQNNAHRDKEGDDQSH	hCA-IX amino acid 37-140
52	LPRMQEDSP	12H8 minimal epitope
53	EDLPGEED	11H9 minimal epitope

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Claims:

1. An isolated or purified antibody or fragment thereof, comprising:

a light chain comprising a complementarity determining region (CDR) L1 sequence of RASGNIHNYLA (SEQ ID NO:1), a CDR L2 sequence of NTITLAD (SEQ ID NO:2), and a CDR L3 sequence of QHFWNIPFT (SEQ ID NO:3); and

a heavy chain comprising a complementarity determining region (CDR) H1 sequence of GFTFTSCYIH (SEQ ID NO:4), a CDR H2 sequence of WIYPGNGNTKYNEIFKG (SEQ ID NO:5), and a CDR H3 sequence of GDTTANTMDY (SEQ ID NO:6),

wherein the antibody or fragment thereof specifically binds the extracellular domain of Carbohydrate Anhydrase IX (CA-IX).

2. The isolated or purified antibody or fragment thereof of claim 1, wherein the isolated or purified antibody or fragment thereof comprises:

a variable light (V_L) domain of sequence

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSRF SGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELK (SEQ ID NO:19); and/or

a variable heavy (V_H) domain of sequence

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTKY NEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVSS (SEQ ID NO:20).

3. The isolated or purified antibody or fragment thereof of claim 1 or 2, wherein the antibody or fragment thereof is capable of cellular internalization.

4. The isolated or purified antibody or fragment thereof any one of claims 1 to 3, wherein the antibody or fragment thereof is a full-length IgG, an Fv, an scFv, a Fab, or a $F(ab')_2$.

5. The isolated or purified antibody or fragment thereof of any one of claims 1 to 4, wherein the antibody or fragment thereof comprises framework regions from IgA, IgD, IgE, IgG, or IgM.

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6. The isolated or purified antibody or fragment thereof of any one of claims 1 to 5, wherein the antibody or fragment thereof is chimeric.

7. The isolated or purified antibody or fragment thereof of claim 6, wherein the chimeric antibody or fragment thereof comprises constant regions from human IgG1.

8. The isolated or purified antibody or fragment thereof of claim 6, wherein the chimeric antibody or fragment thereof comprises constant regions from human kappa 1 light chain and human IgG1 heavy chain.

9. The isolated or purified antibody or fragment thereof of claim 8, wherein the isolated or purified antibody or fragment thereof comprises:

a variable light (V_L) domain comprising the sequence

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNTITLADGVPSRF
SGSGSGTQYSLKINSLQPEDFGSYYCQHFWNIPFTFGAGTKLELKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:25); and

a variable heavy (V_H) domain comprising the sequence

QVQLQQSGPELVKPGASVRISCKASGFTFTSCYIHWMKQRPGQGLEWIGWIYPGNGNTKY
NEIFKGRATLTTDKSSSTAYMQLSSLTSEDSAVYFCARGDTTANTMDYWGQGTSVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:26).

10. The isolated or purified antibody or fragment thereof of any one of claims 1 to 9, wherein the antibody or fragment thereof is immobilized onto a surface.

11. The isolated or purified antibody or fragment thereof of any one of claims 1 to 9, wherein the antibody or fragment thereof is linked to a cargo molecule.

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12. The isolated or purified antibody or fragment thereof of claim 11, wherein the cargo molecule is a detectable agent, a therapeutic agent, a drug, a peptide, an enzyme, a growth factor, a cytokine, a receptor trap, an antibody or fragment thereof, a chemical compound, a carbohydrate moiety, a DNA-based molecule, a cytotoxic agent, a viral vector, a liposome or nanocarrier loaded with any of the previously recited types of cargo molecules, a nanoparticle, a nanowire, a nanotube, or a quantum dot.

13. The isolated or purified antibody or fragment thereof of claim 11, wherein the cargo molecule is a cytotoxic agent.

14. A composition comprising one or more than one isolated or purified antibody or fragment thereof of any one of claims 1 to 13 and a pharmaceutically-acceptable carrier, diluent, or excipient.

15. A nucleic acid molecule encoding the isolated or purified antibody or fragment thereof of any one of claims 1 to 9.

16. A vector comprising the nucleic acid molecule of claim 15.

17. An *in vitro* method of detecting CA-IX, comprising

a) contacting a tissue sample with one or more than one isolated or purified antibody or fragment thereof of any one of claims 1 to 9 linked to a detectable agent; and

b) detecting the detectable agent linked to the antibody or fragment thereof bound to CA-IX in the tissue sample.

18. The method of claim 17, wherein method detects CA-IX in circulating cells and the sample is a serum sample.

19. The method of claim 17 or 18, wherein the step of detecting (step b) is performed using optical imaging, immunohistochemistry, molecular diagnostic imaging, or ELISA.

20. The isolated or purified antibody or fragment thereof of claim 11, wherein the cargo molecule is a detectable agent.

21. The isolated or purified antibody or fragment thereof of claim 20, wherein the detectable agent is detectable by PET, SPECT, or fluorescence imaging.

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22. The isolated or purified antibody or fragment thereof of claim 20 or 21, for use to detect CA-IX expression in a subject.

23. Use of the isolated or purified antibody or fragment thereof of claim 20 or 21 to detect CA-IX expression in a subject.

24. The isolated or purified antibody or fragment thereof of any one of claims 11 to 13, for use to transport the cargo molecule into cells of a subject expressing CA-IX.

25. Use of the isolated or purified antibody or fragment thereof of any one of claims 11 to 13 to transport the cargo molecule into cells of a subject expressing CA-IX.

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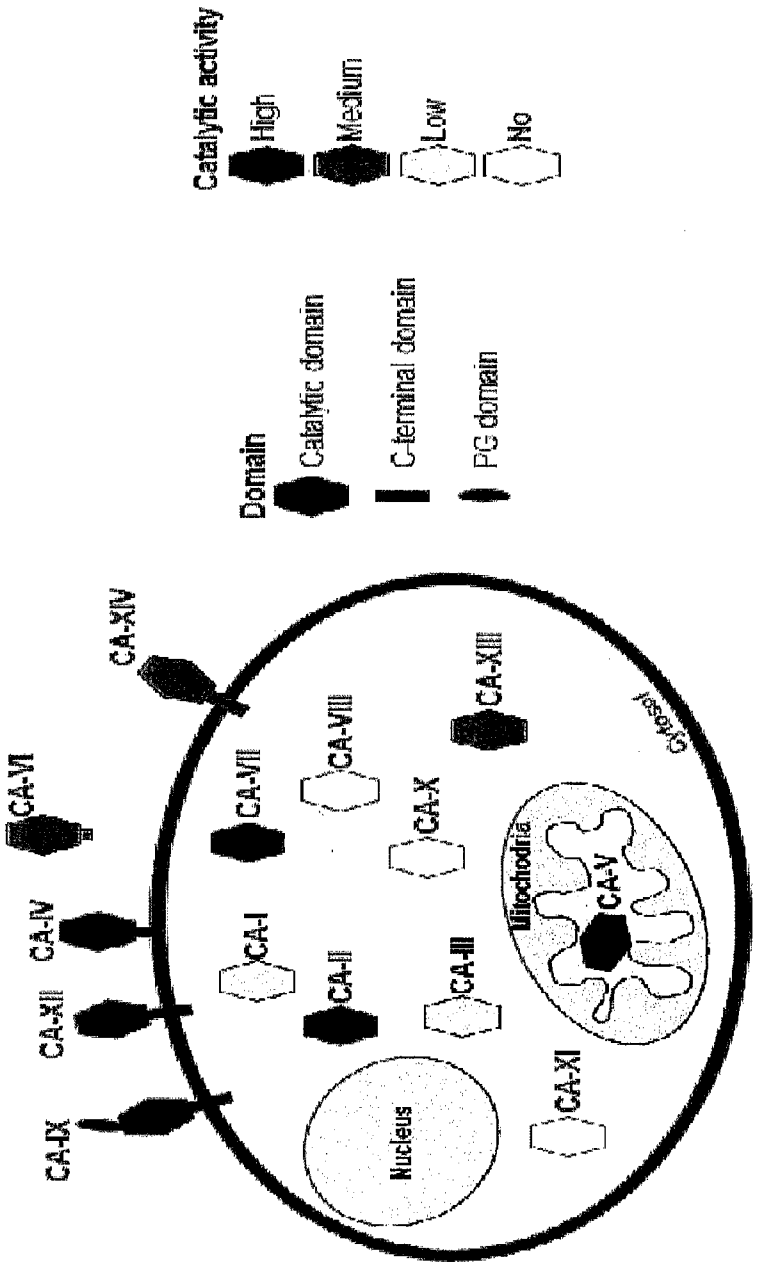
Catalytic activity
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Medium
Low
No
Domain
Catalytic domain
C-terminal domain
PG domain
CA-XIV
CA-VI
CA-VII
CA-VIII
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CA-IV
CA-XII
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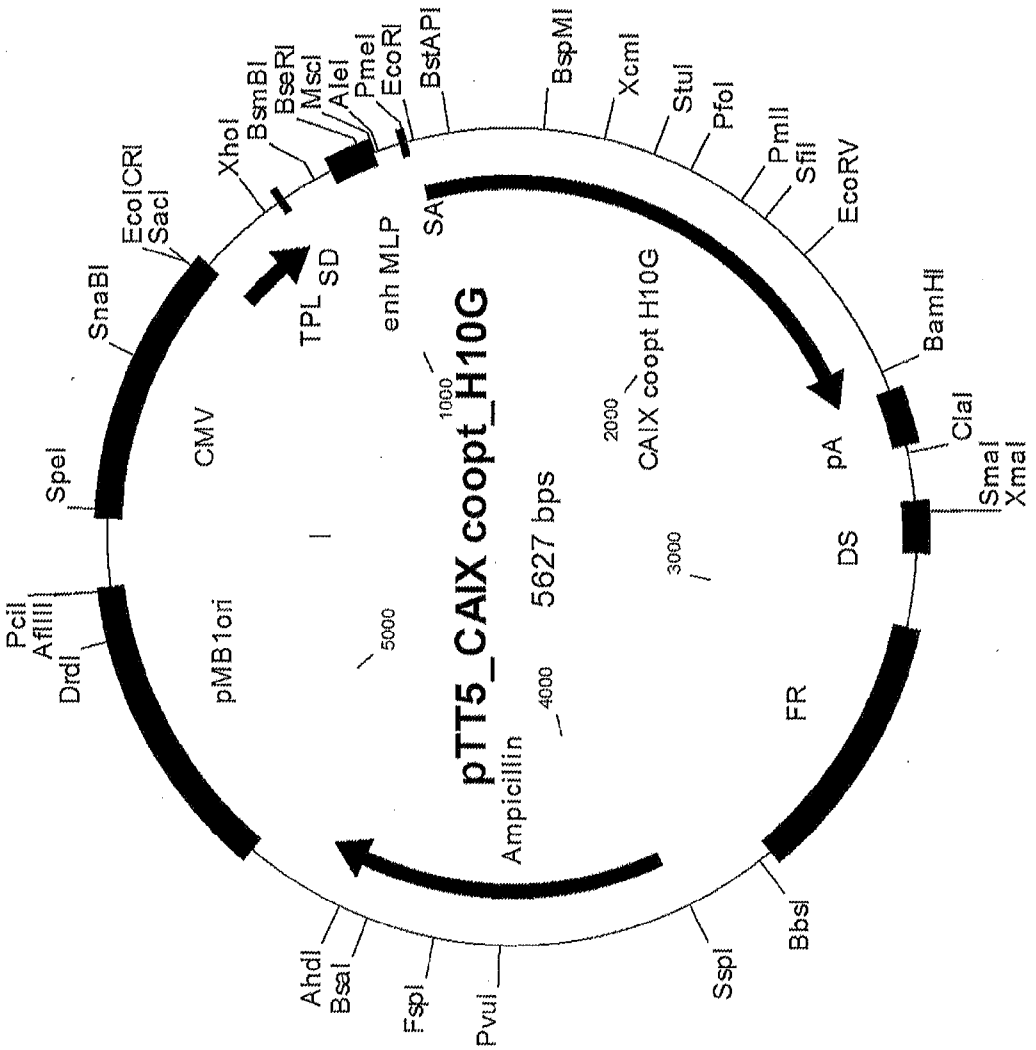
CA-III
Mitochondria
CA-V
Cytosol
Nucleus
CA-XI

FIG. 1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DS
FR
1000
2000
3000
4000
5000
EcoRI
PmeI
AleI
MscI
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SpeI
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AflIII
DrdI
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BsaI
FspI
PvuI
SspI
BbsI
BamHI
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BstAPI

Fig.2

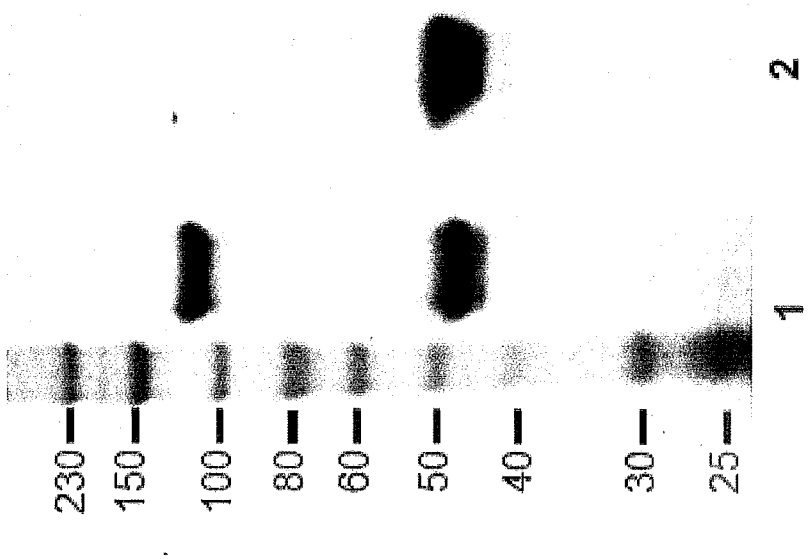


FIG. 3

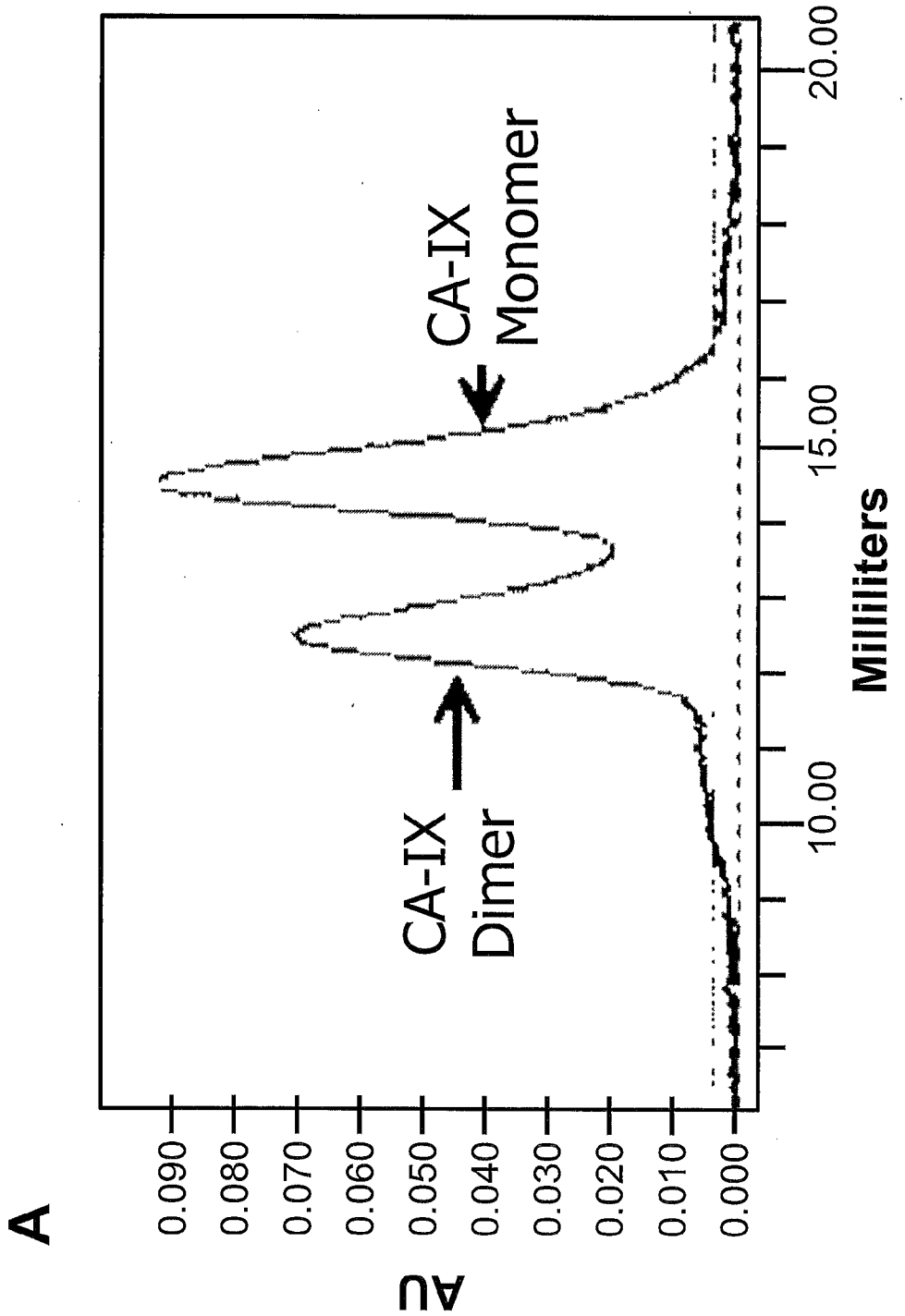
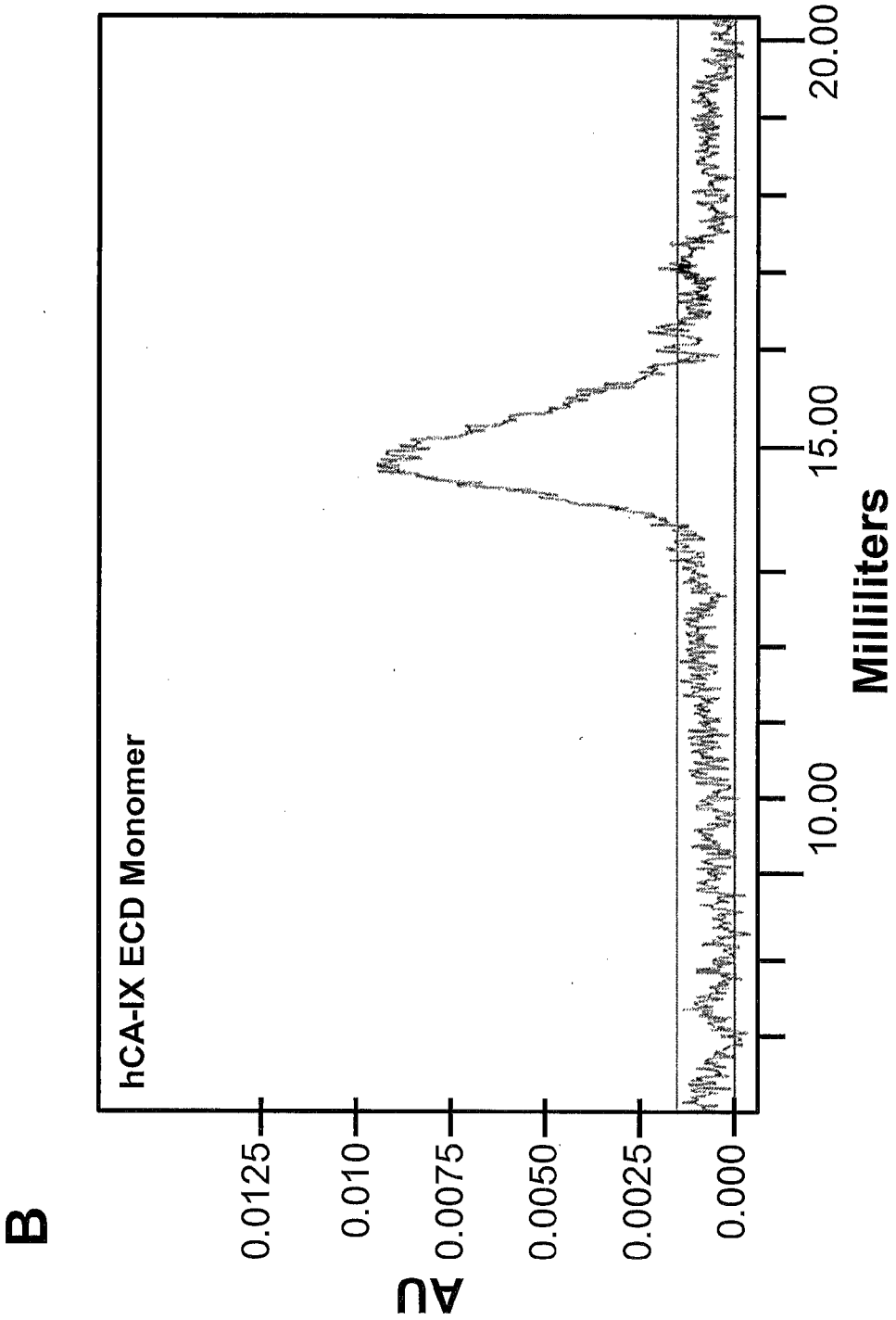

A
AU
0.090
0.080
0.070
0.060
0.050
0.040
0.030
0.020
0.010
0.000
CA-IX
Dimer
CA-IX
Monomer
10.00
15.00
20.00
Milliliters

Fig.4A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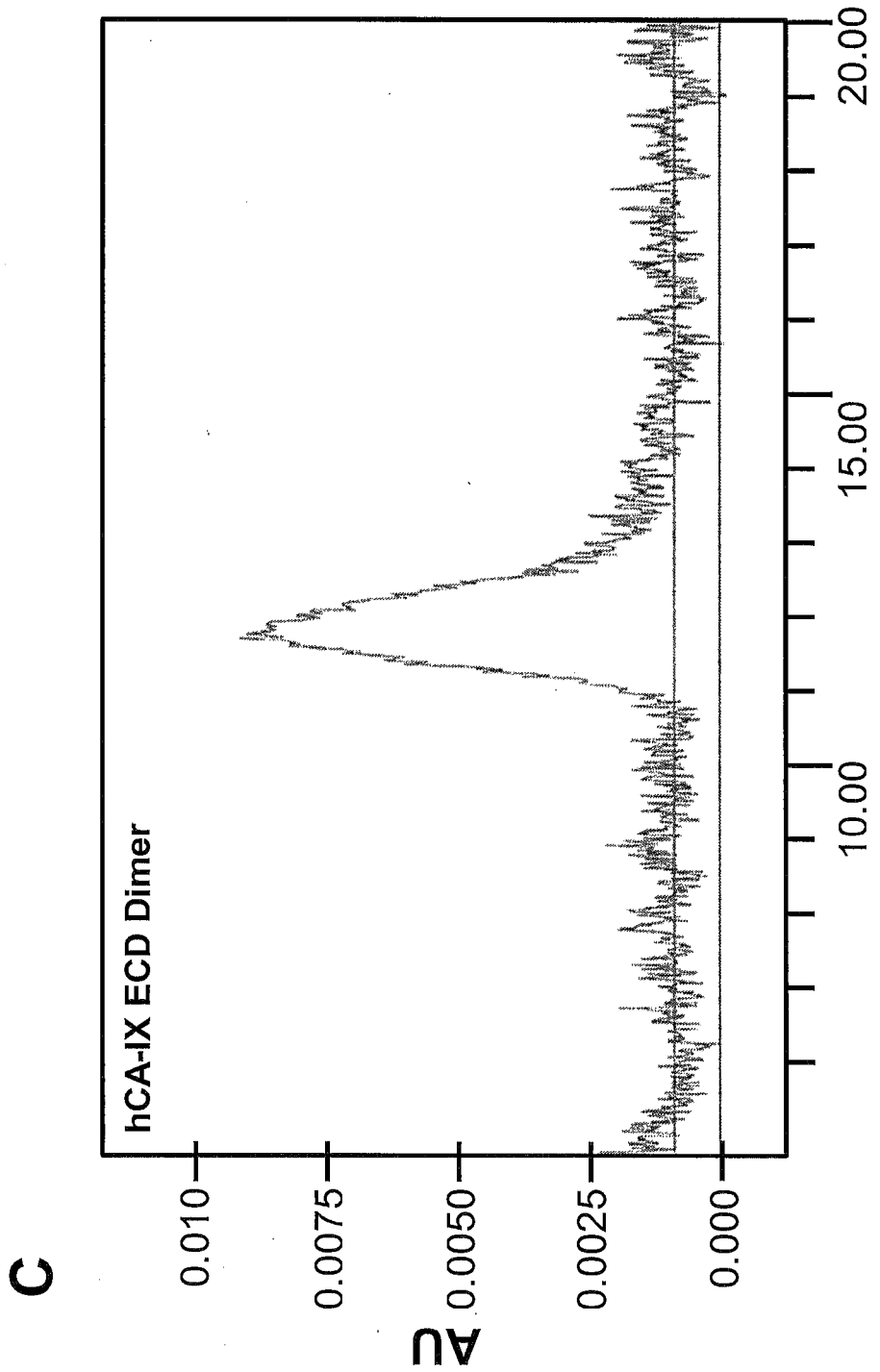
10.00
15.00
20.00
Milliliters

Fig.4B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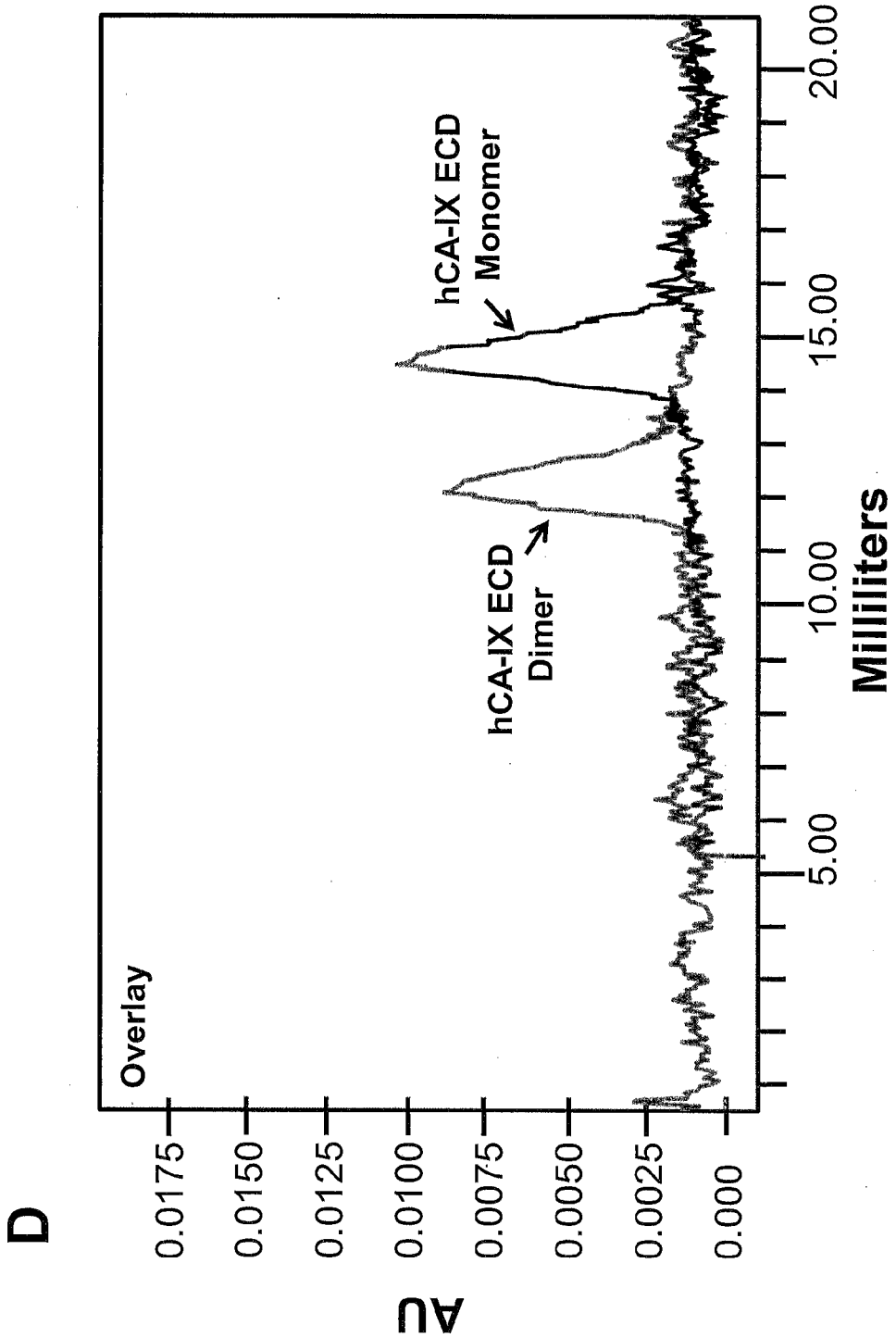
10.00
15.00
20.00
Milliliters

Fig.4C


D
Overlay
hCA-IX ECD
Monomer
hCA-IX ECD
Dimer
AU
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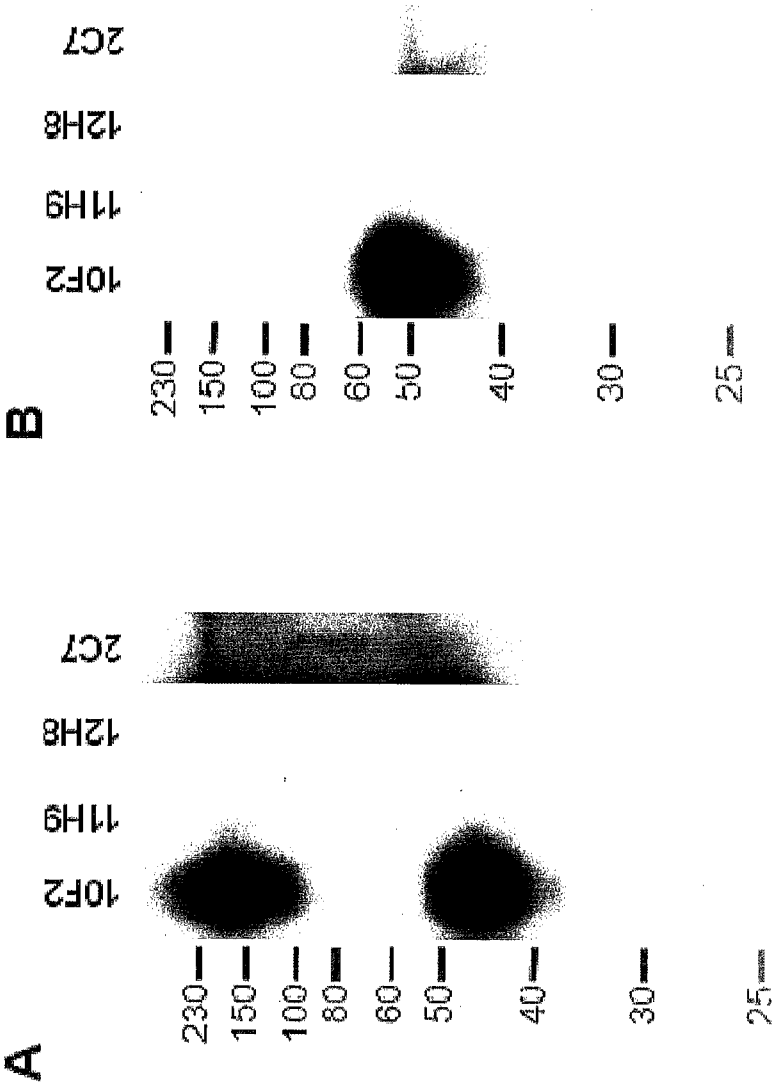
0.0025
0.000
5.00
10.00
15.00
20.00
Milliliters

Fig.4D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10F2
11H9
12H8
2C7
230
150
100
80
60
50
40
30
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100
80
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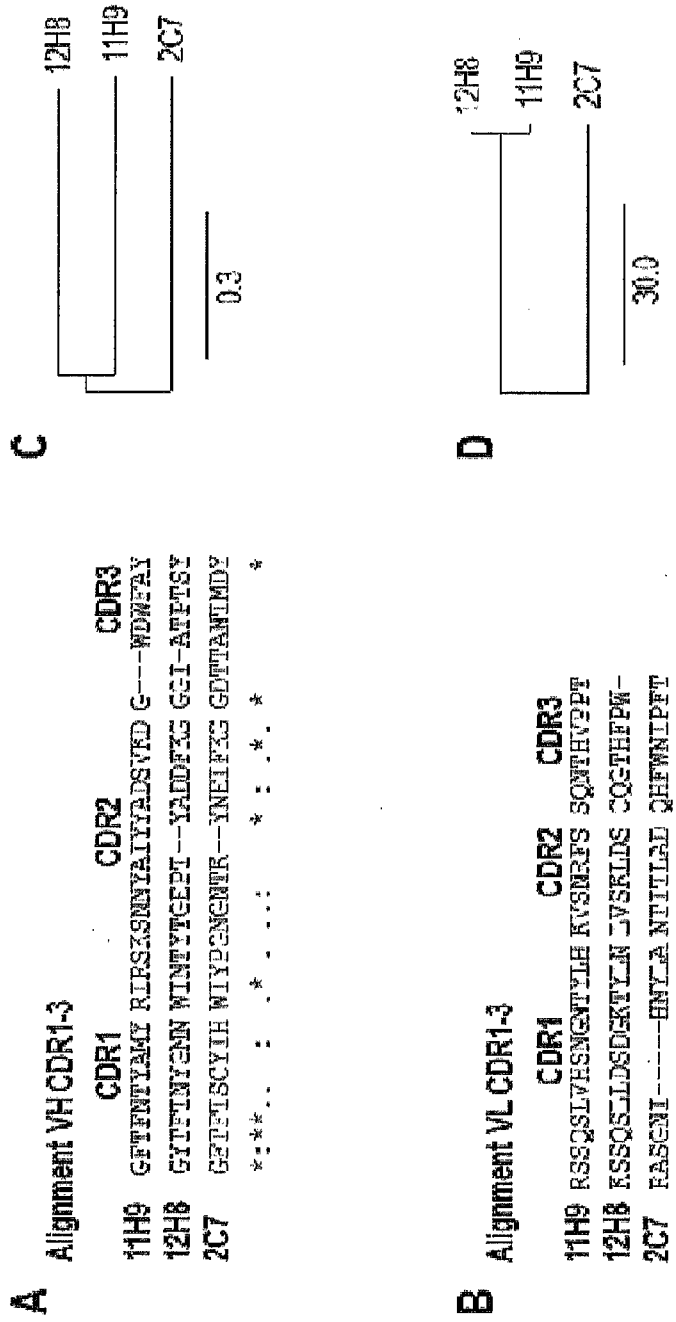
40
30
25

FIG. 5


A
Alignment VH CDR1-3
CDR1 CDR2 CDR3
11H9 GFTFNTYAMY RIRSKSNNYATYYADSVKD G---WDWFAY
12H8 GYTFTNYGMN WINTYTGEPT--YADDFKG GGI-ATFTSY
2C7 GFTFSSYYIH WIYPGNGNTK--YNEIFKG GDTTAWTMDY
B
Alignment VL CDR1-3
CDR1 CDR2 CDR3
11H9 RSSQSLVHSNGNTYLH KVSNRFS SQNTHVPPT
12H8 KSSQSLLDSDGKTYLN LVSKLDS WQGTHFPW-
2C7 RASENI----YYLA NTILAD QHFWNIPFT
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2C7
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11H9
2C7
30.0

FIG. 6

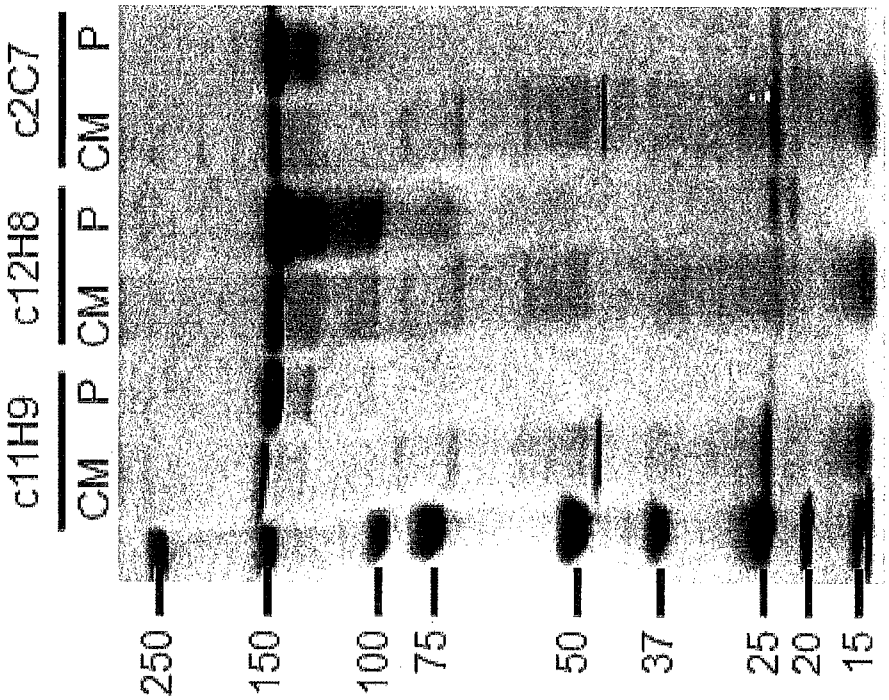
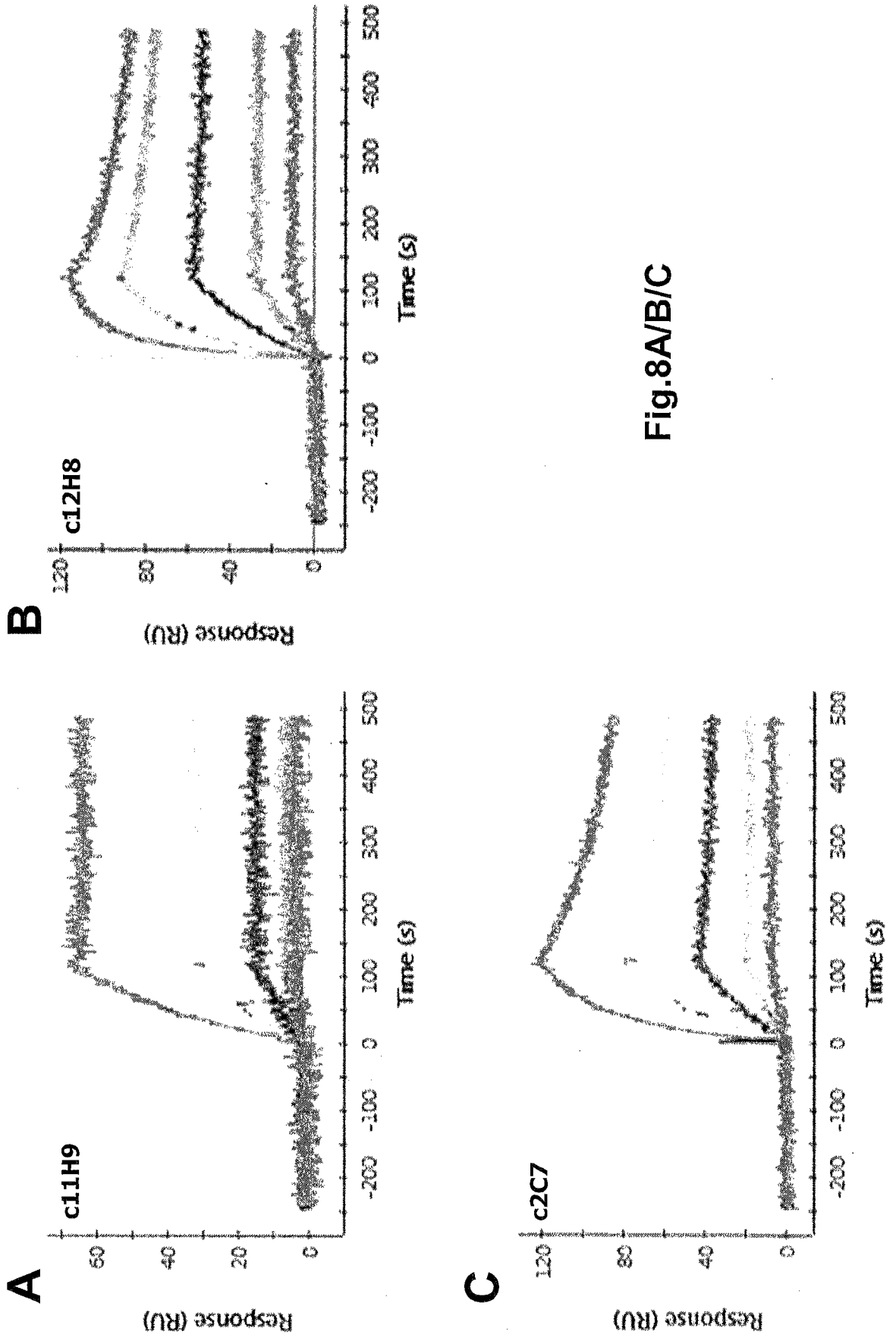


FIG. 7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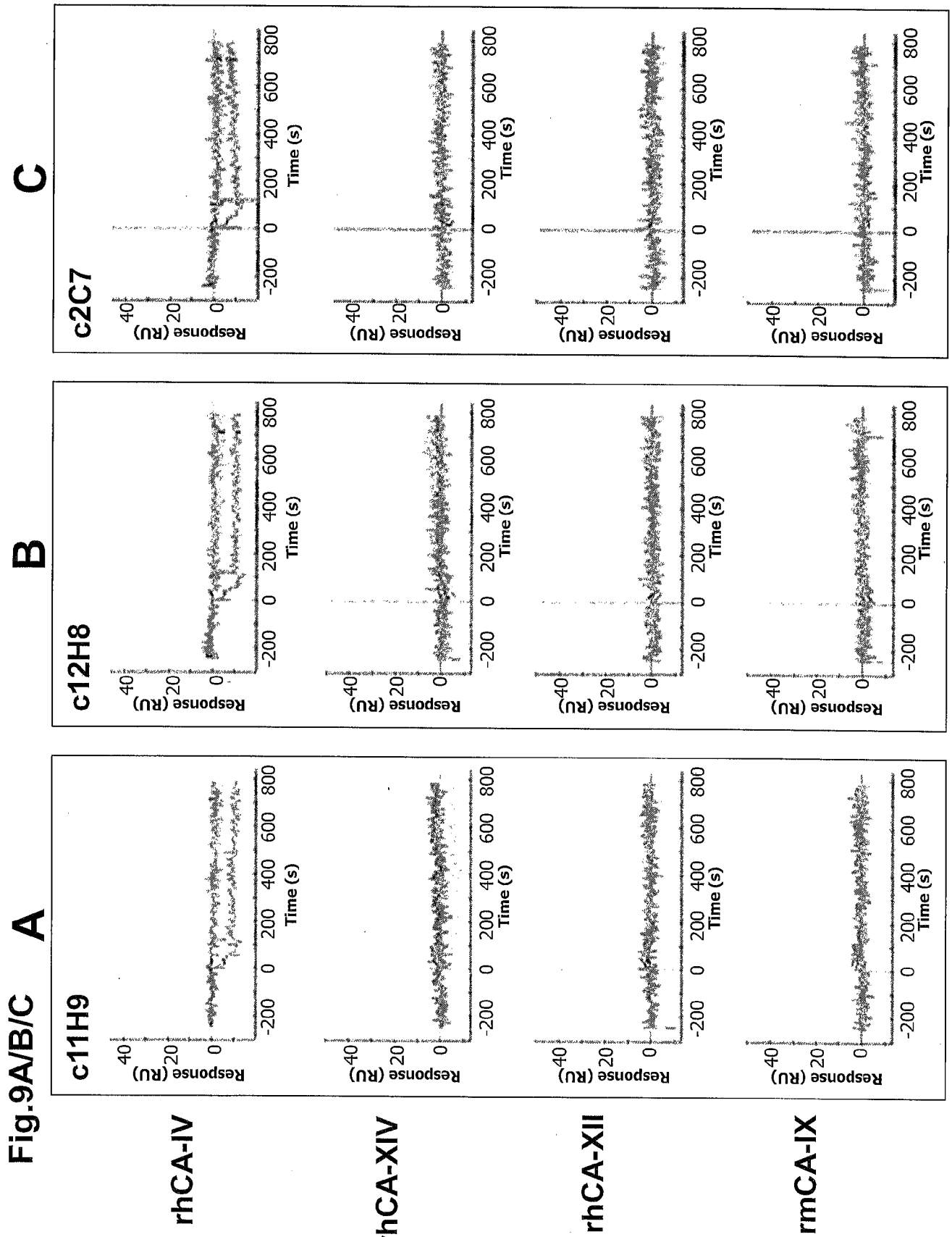
c11H9
Response (RU)
Time (s)
B
c12H8
Response (RU)
Time (s)
C
c2C7
Response (RU)
Time (s)

Fig.8A/B/C

Fig.9A/B/C


A
B
C
c11H9
c12H8
c2C7
rhCA-IV
rhCA-XIV
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rmCA-IX
Response (RU)
Time (s)
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0
200
400
600
800
0
20
40

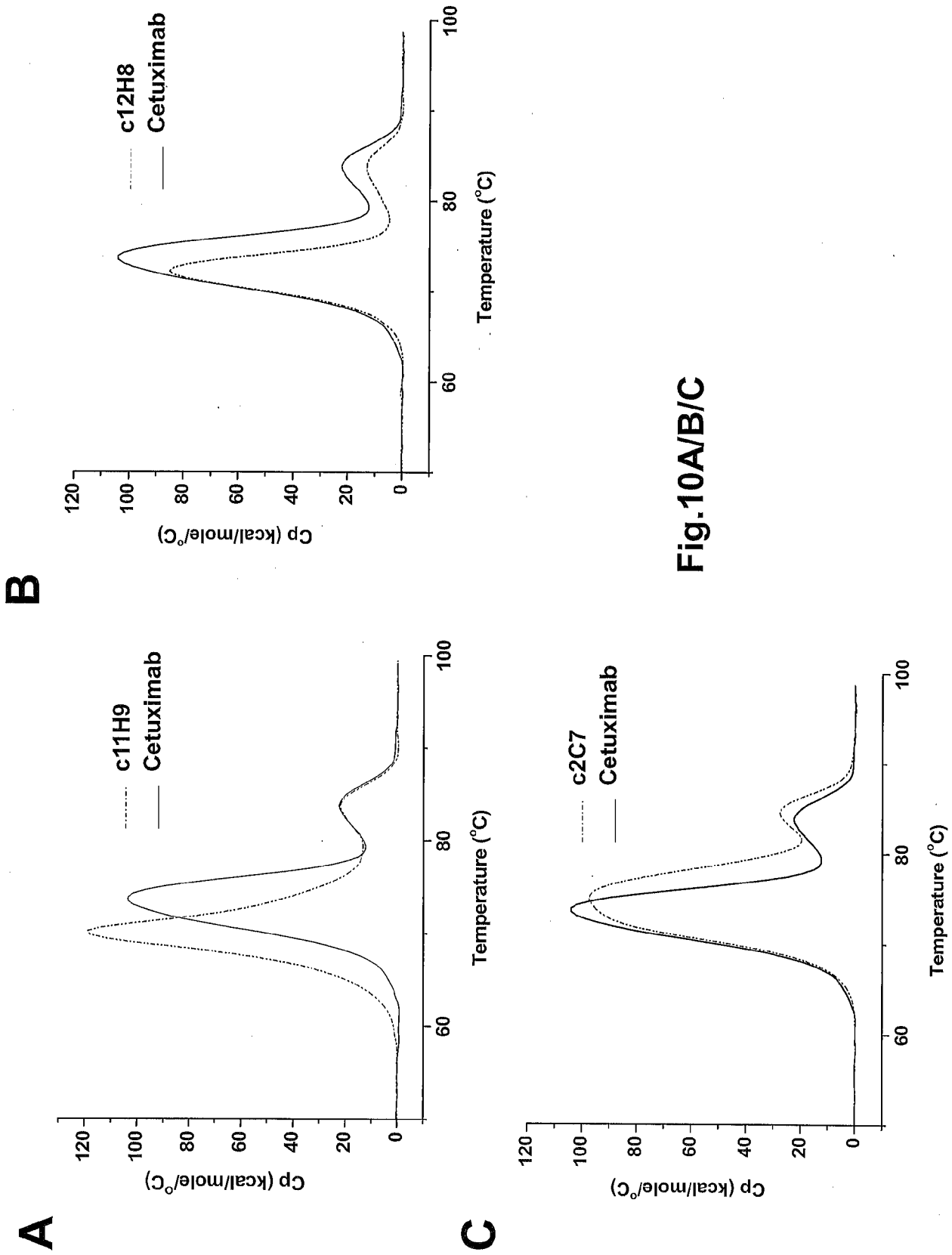
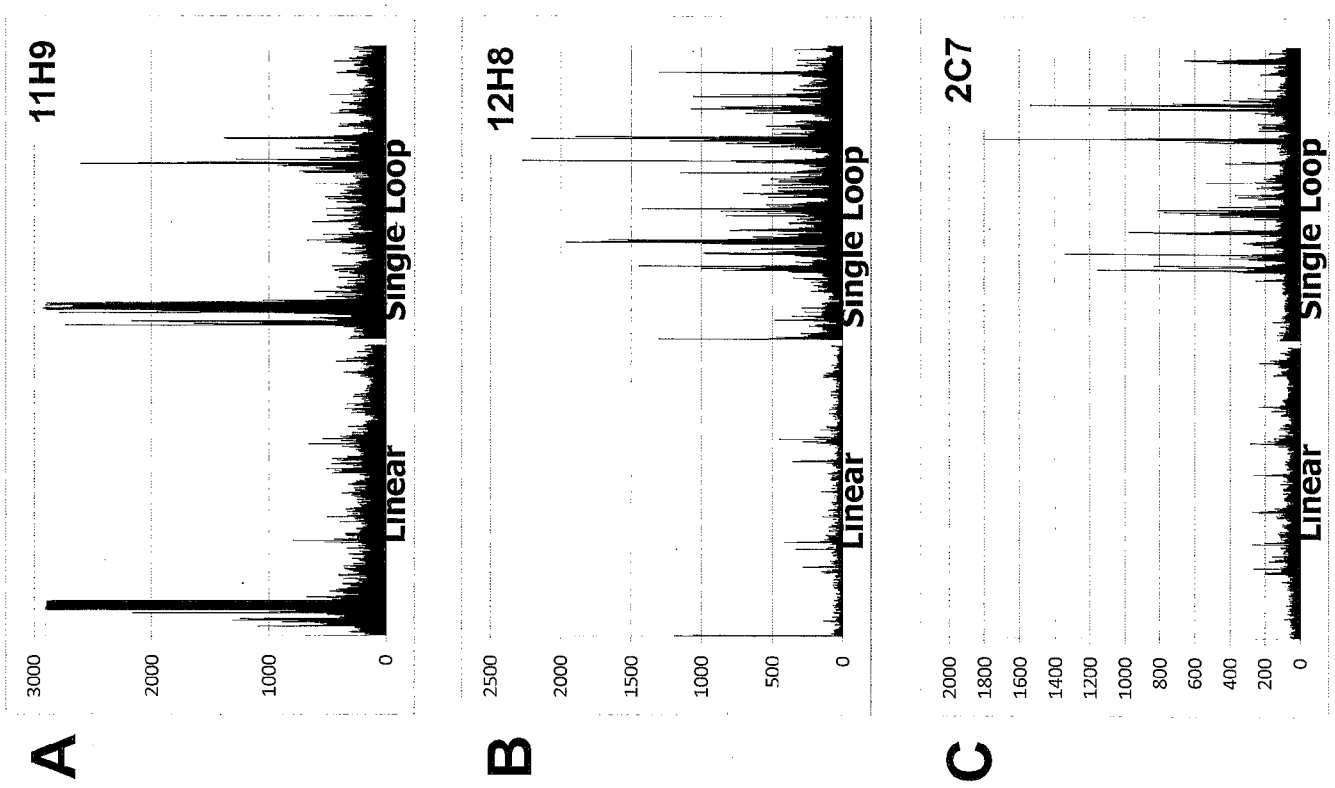

A
c11H9
Cetuximab
Cp (kcal/mole/°C)
Temperature (°C)
B
c12H8
Cetuximab
Cp (kcal/mole/°C)
Temperature (°C)
C
c2C7
Cetuximab
Cp (kcal/mole/°C)
Temperature (°C)

Fig.10A/B/C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2000
1000
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Linear
Single Loop
B
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2500
2000
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1000
500
0
Linear
Single Loop
C
2C7
2000
1800
1600
1400
1200
1000
800
600
400
200
0
Linear
Single Loop

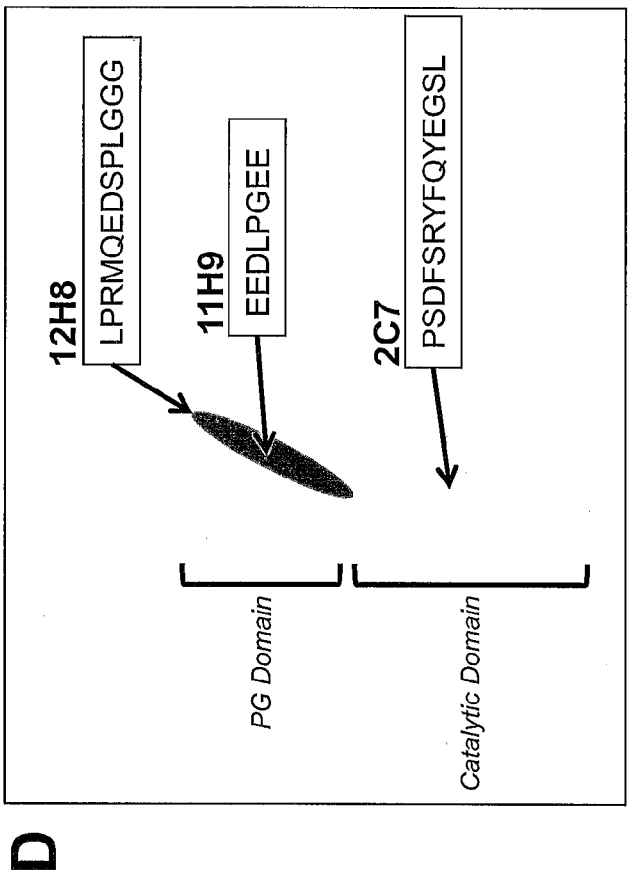

D
12H8
LPRMQEDSPLGGG
11H9
EEDLPGEE
2C7
PSDFSRYFQYEGSL
PG Domain
Catalytic Domain

Fig.11A/B/C/D

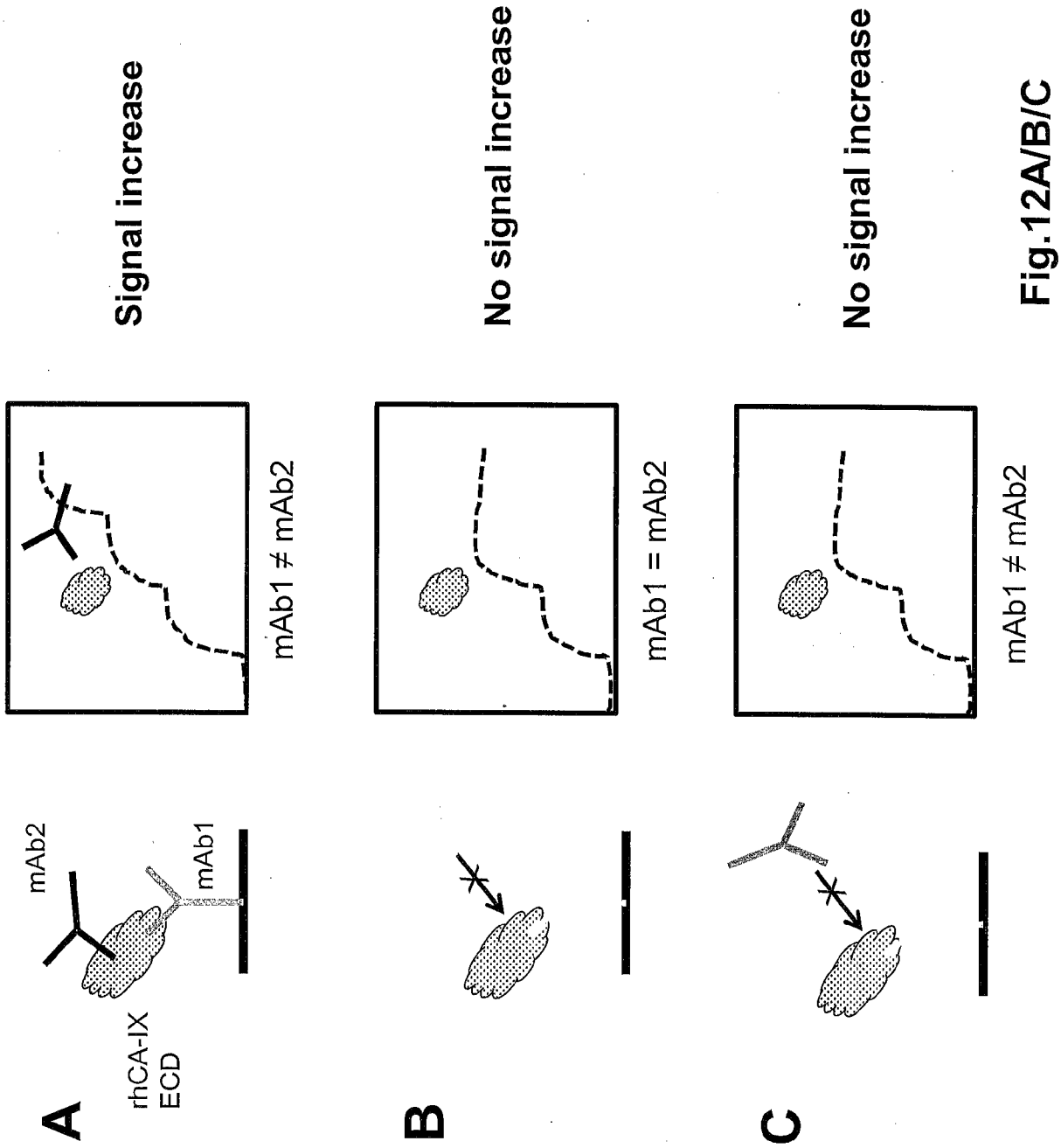

A
rhCA-IX
ECD
mAb2
mAb1
Signal increase
mAb1 ≠ mAb2
B
No signal increase
mAb1 = mAb2
C
No signal increase
mAb1 ≠ mAb2

Fig.12A/B/C

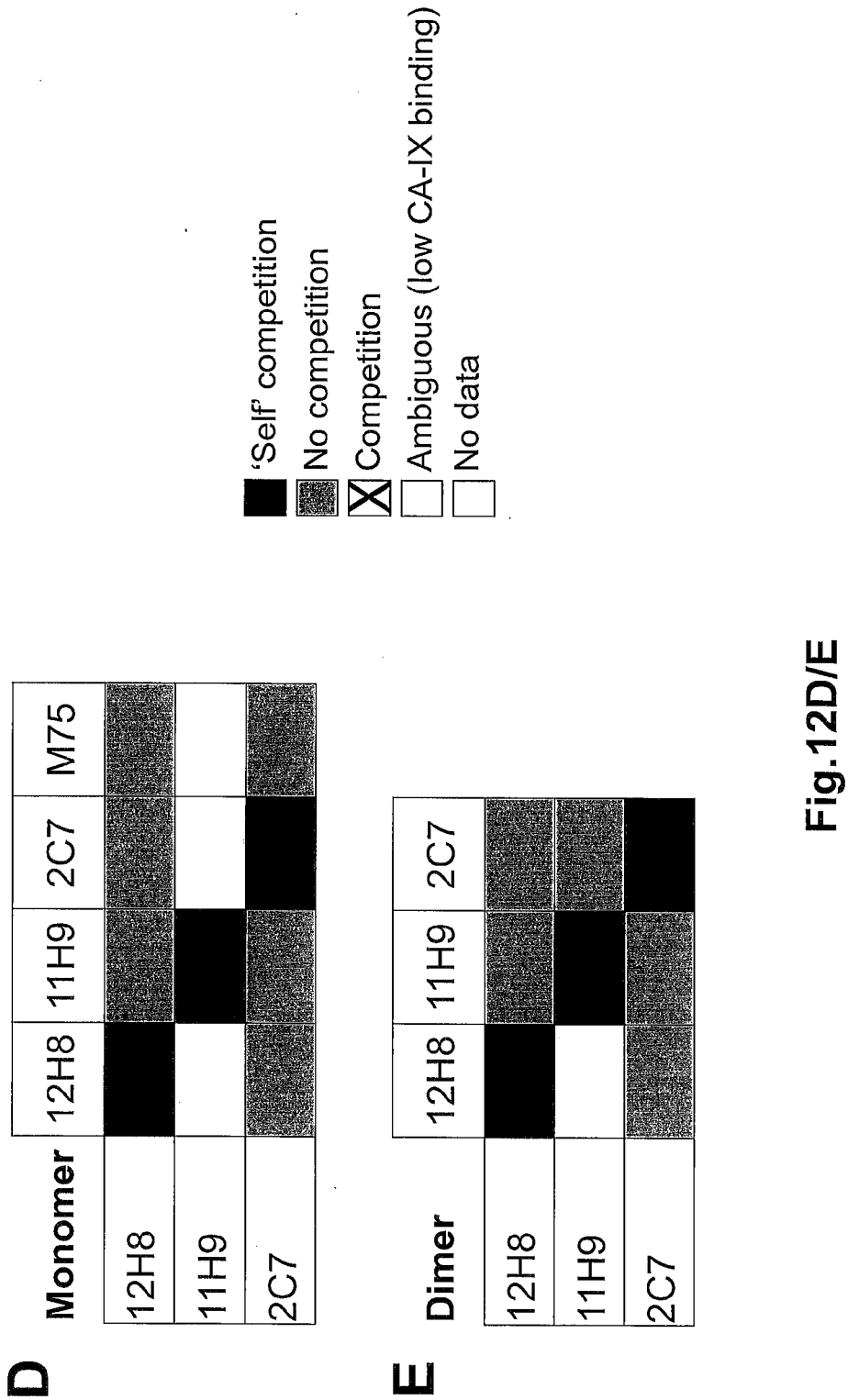

'Self' competition
No competition
Competition
Ambiguous (low CA-IX binding)
No data
D
Monomer
12H8
11H9
2C7
12H8
11H9
2C7
M75
E
Dimer
12H8
11H9
2C7
12H8
11H9
2C7

Fig.12D/E

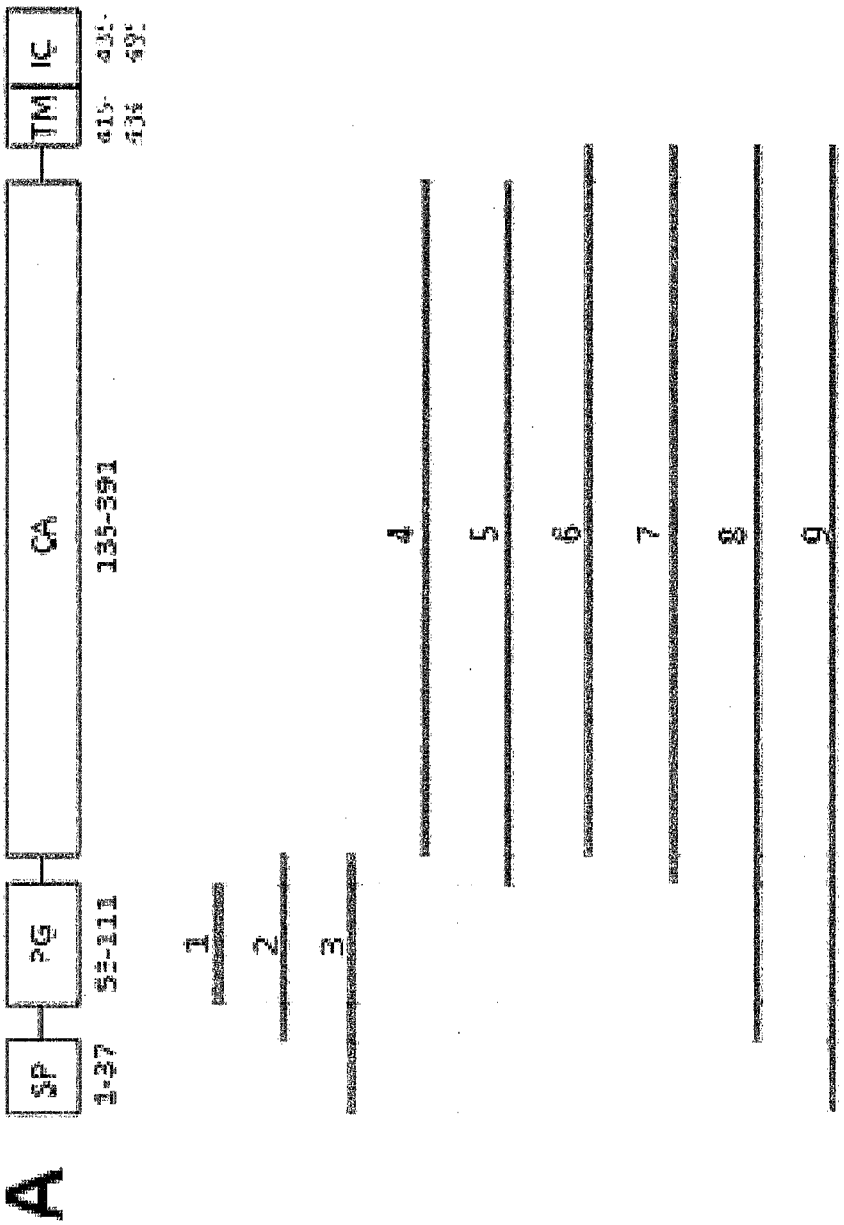


FIG. 13

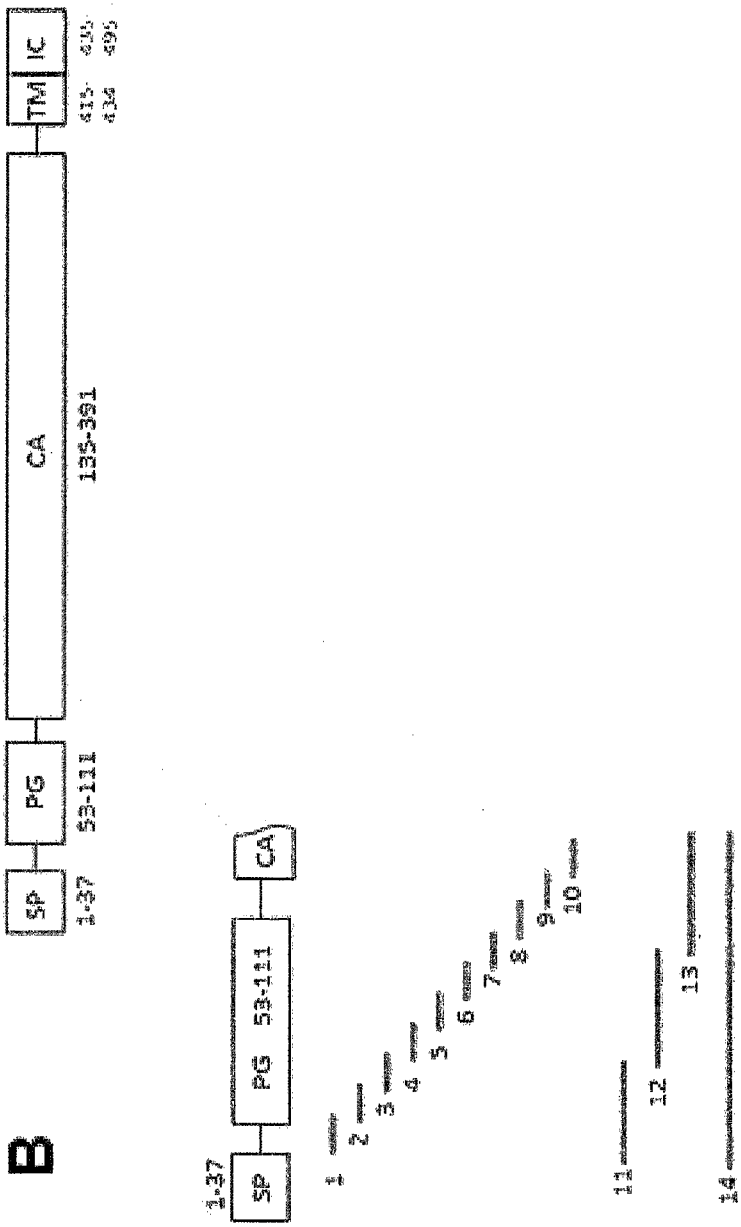
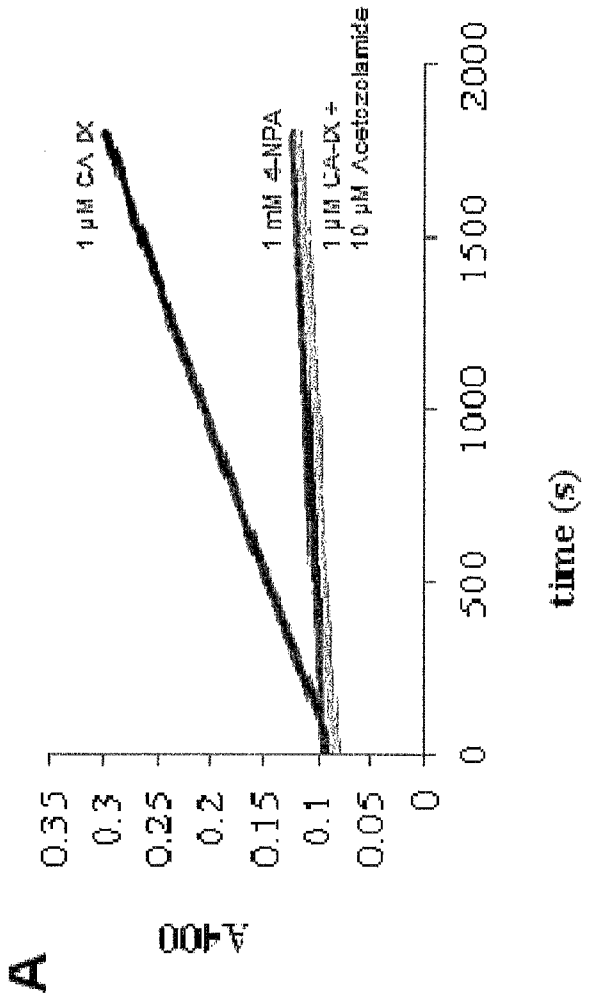

B
SP
PG
CA
TM
IC
1-37
53-111
135-391
415-434
435-495
1-37
SP
PG 53-111
CA
1
2
3
4
5
6
7
8
9
10
11
12
13
14

FIG. 13


A
A400
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0
500
1000
1500
2000
time (s)
1 µM CA IX
1 mM 4-NPA
1 µM CA-IX +
10 µM Acetazolamide

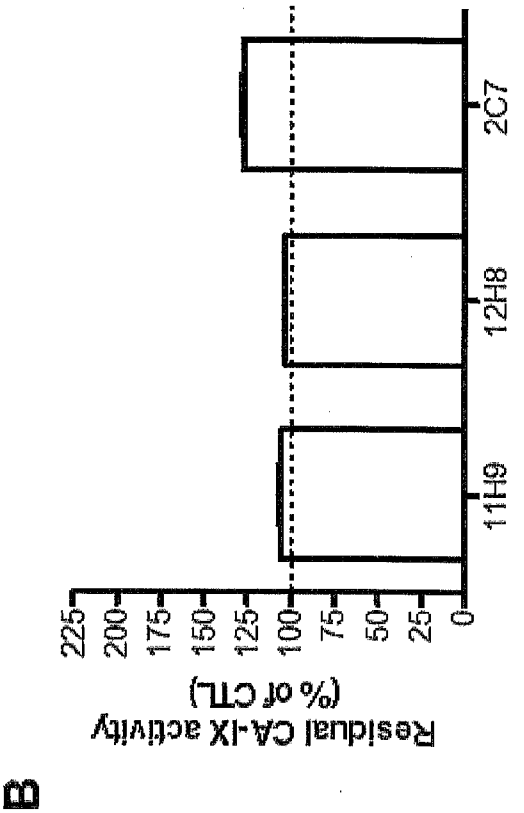

B
Residual CA-IX activity
(% of CTL)
225
200
175
150
125
100
75
50
25
0
11H9
12H8
2C7

FIG. 14

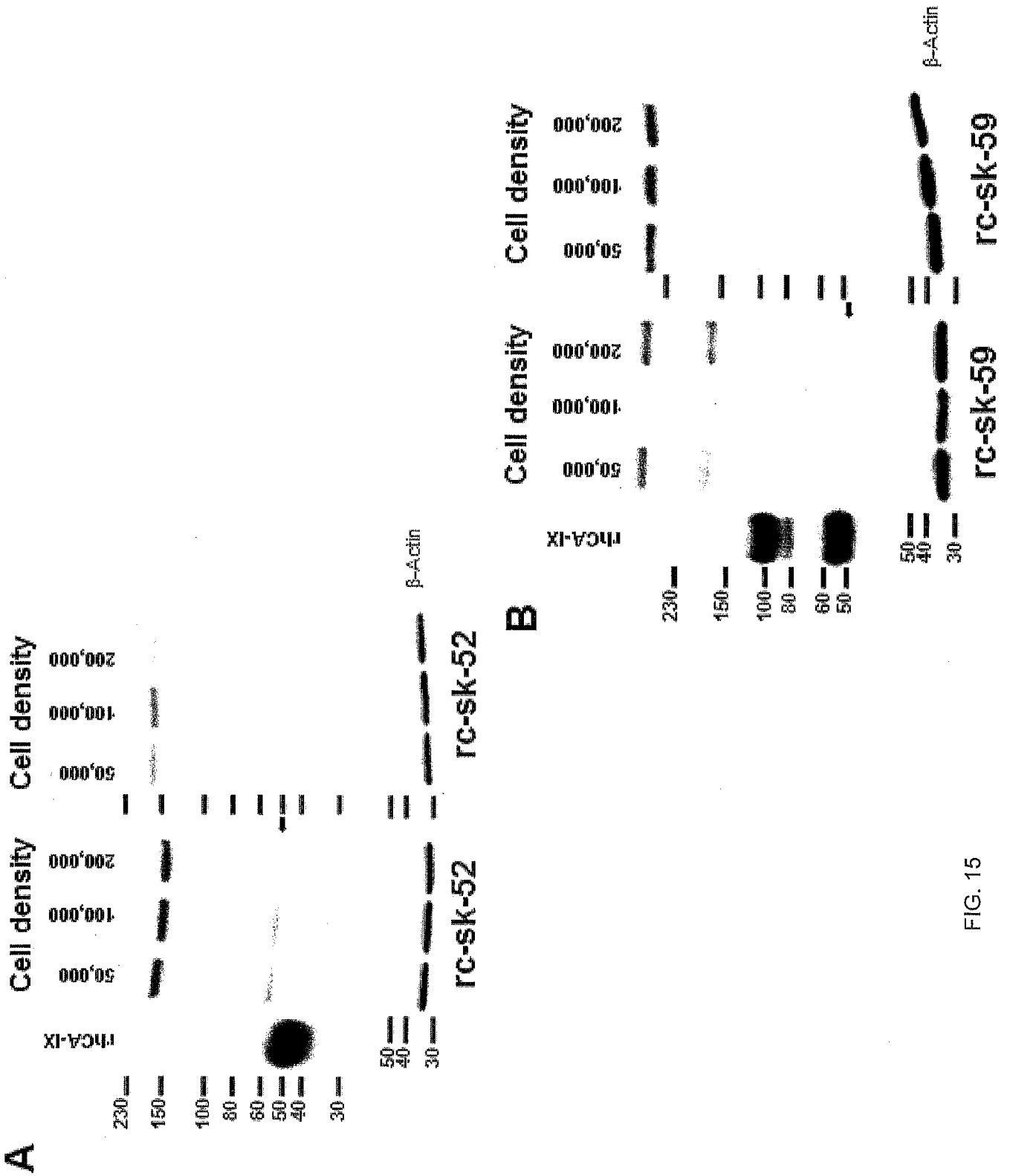

A
Cell density
50,000
100,000
200,000
rhCA-IX
230
150
100
80
60
50
40
30
50
40
30
β-Actin
rc-sk-52
rc-sk-52
B
Cell density
50,000
100,000
200,000
rhCA-IX
230
150
100
80
60
50
50
40
30
β-Actin
rc-sk-59
rc-sk-59

FIG. 15

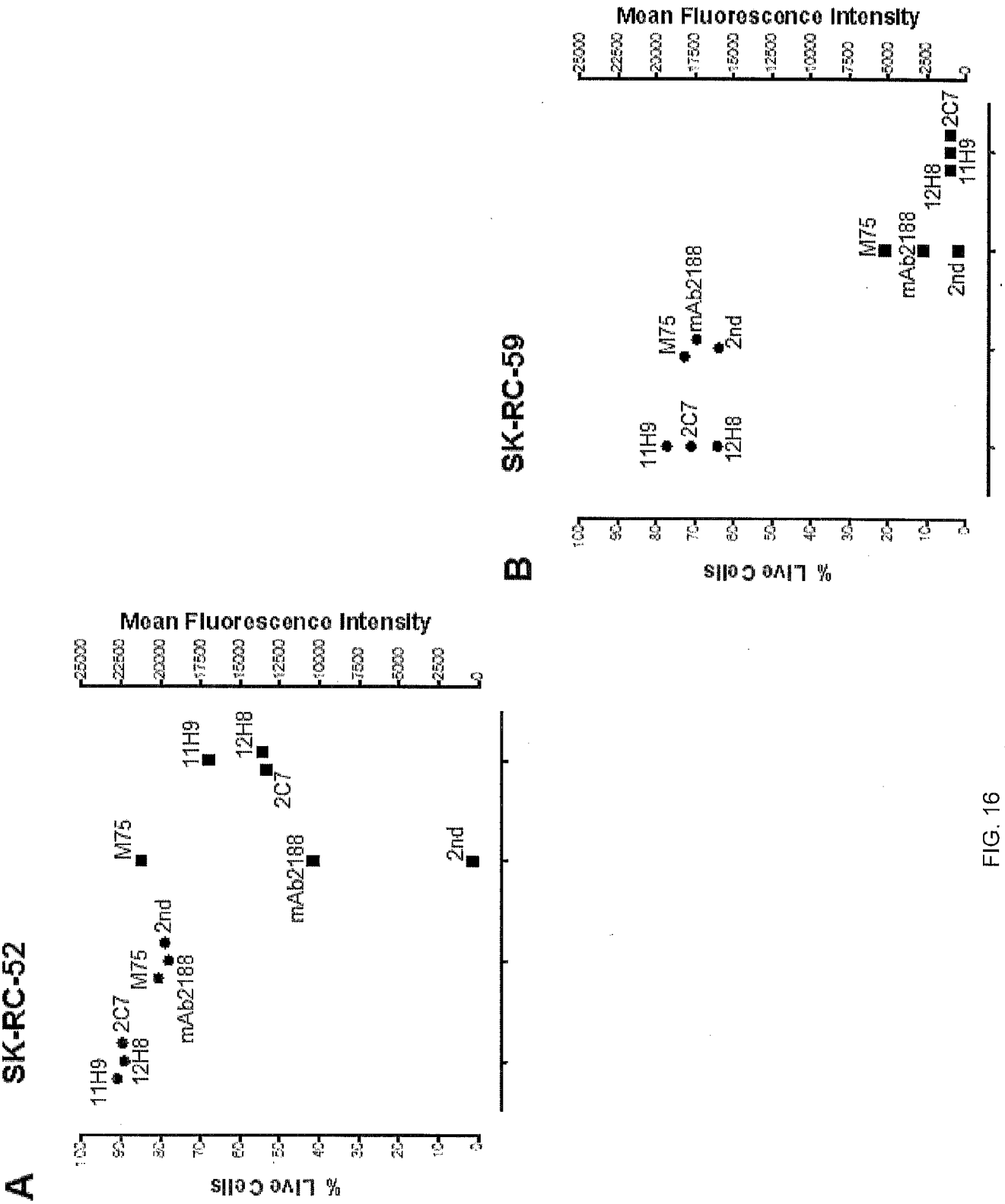

A
SK-RC-52
Mean Fluorescence Intensity
% Live Cells
11H9
12H8
2C7
M75
mAb2188
2nd
B
SK-RC-59
Mean Fluorescence Intensity
% Live Cells
11H9
12H8
2C7
M75
mAb2188
2nd

FIG. 16

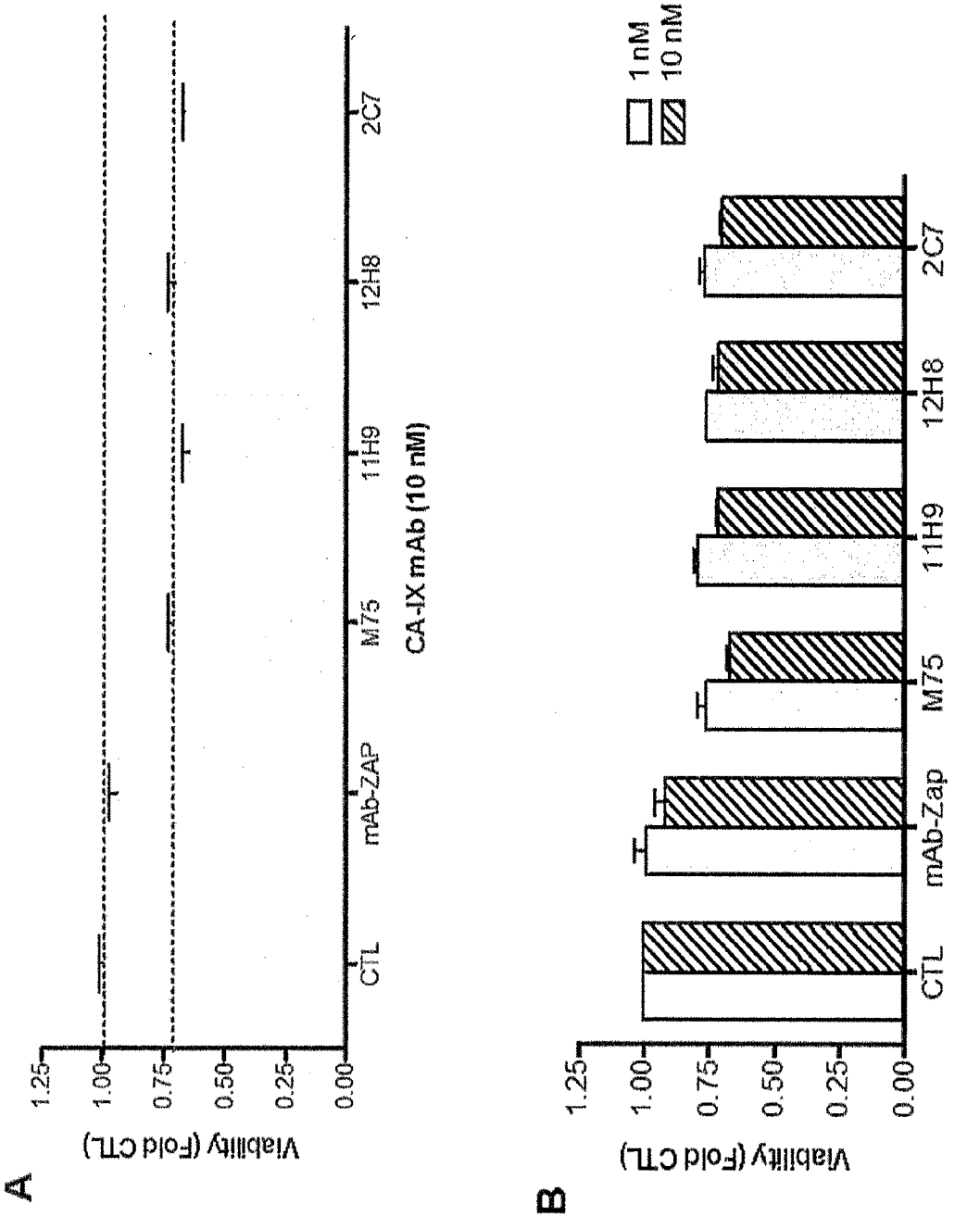

A
Viability (Fold CTL)
1.25
1.00
0.75
0.50
0.25
0.00
CTL
mAb-ZAP
M75
11H9
12H8
2C7
CA-IX mAb (10 nM)
B
1 nM
10 nM
Viability (Fold CTL)
1.25
1.00
0.75
0.50
0.25
0.00
CTL
mAb-Zap
M75
11H9
12H8
2C7
CA-IX mAb

FIG. 17

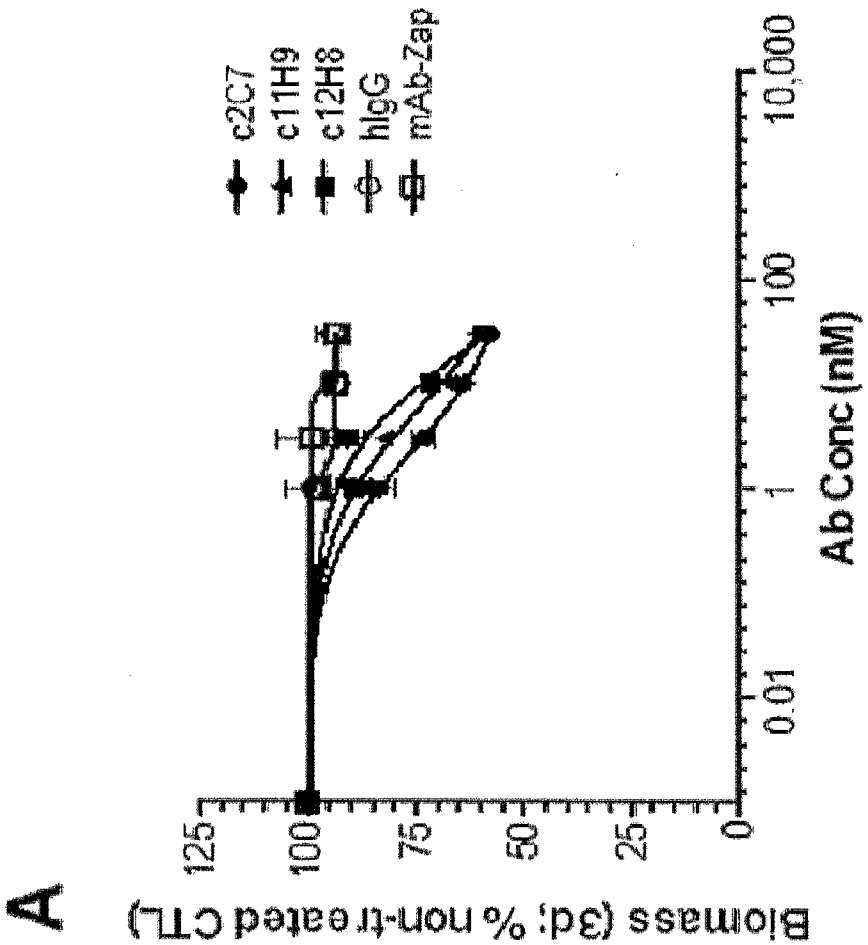

A
Biomass (3d; % non-treated CTL)
125
100
75
50
25
0
0.01
1
100
10,000
Ab Conc (nM)
c2C7
c11H9
c12H8
hIgG
mAb-Zap

FIG. 18

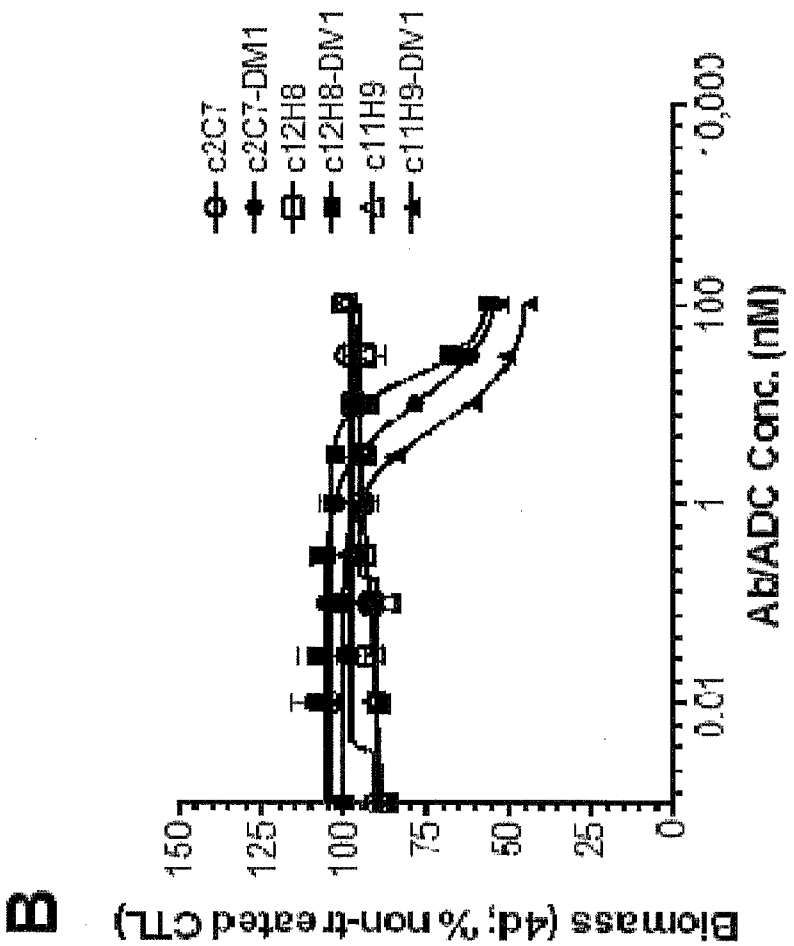

B
Biomass (4d; % non-treated CTL)
150
125
100
75
50
25
0
0.01
1
100
0,003
Ab/ADC Conc. (nM)
c2C7
c2C7-DM1
c12H8
c12H8-DM1
c11H9
c11H9-DM1

FIG. 18

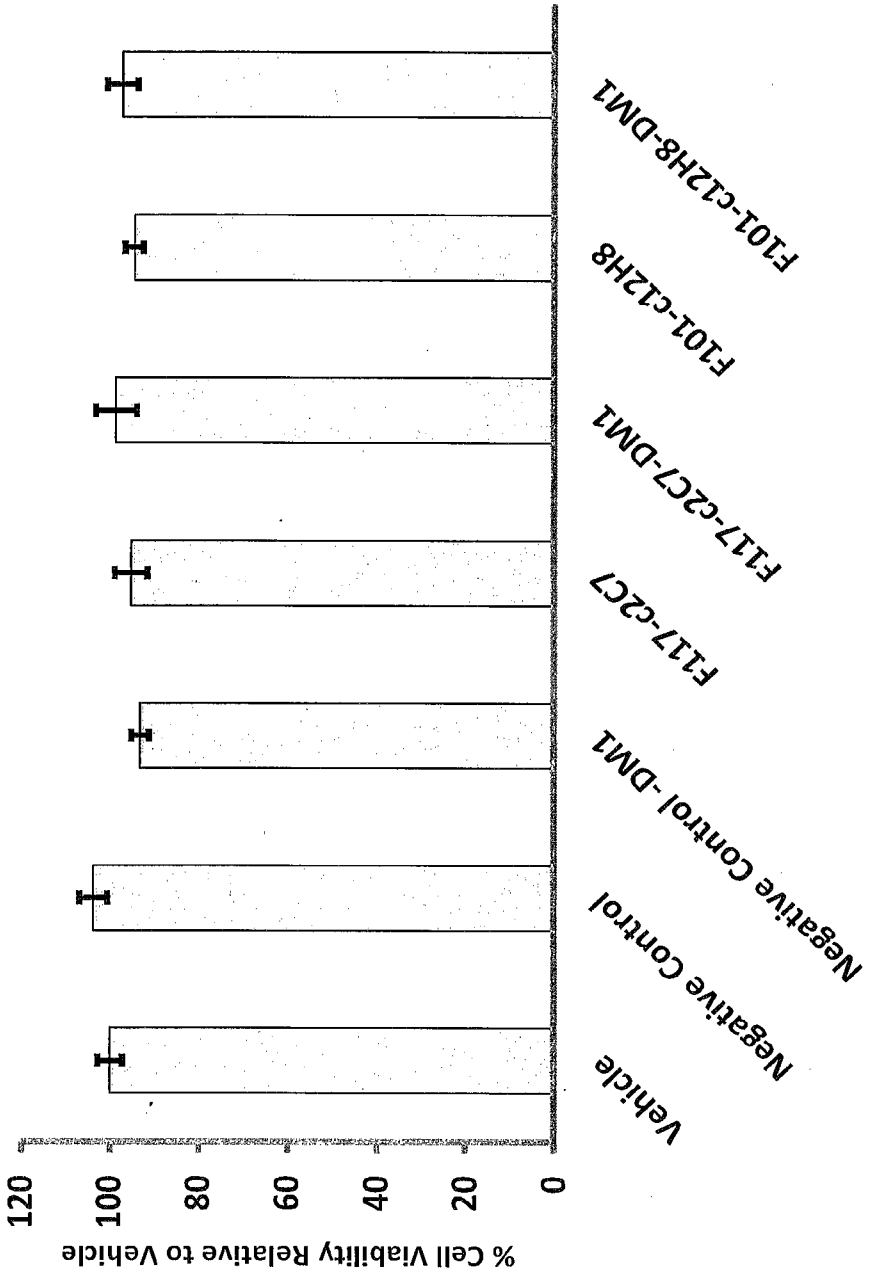
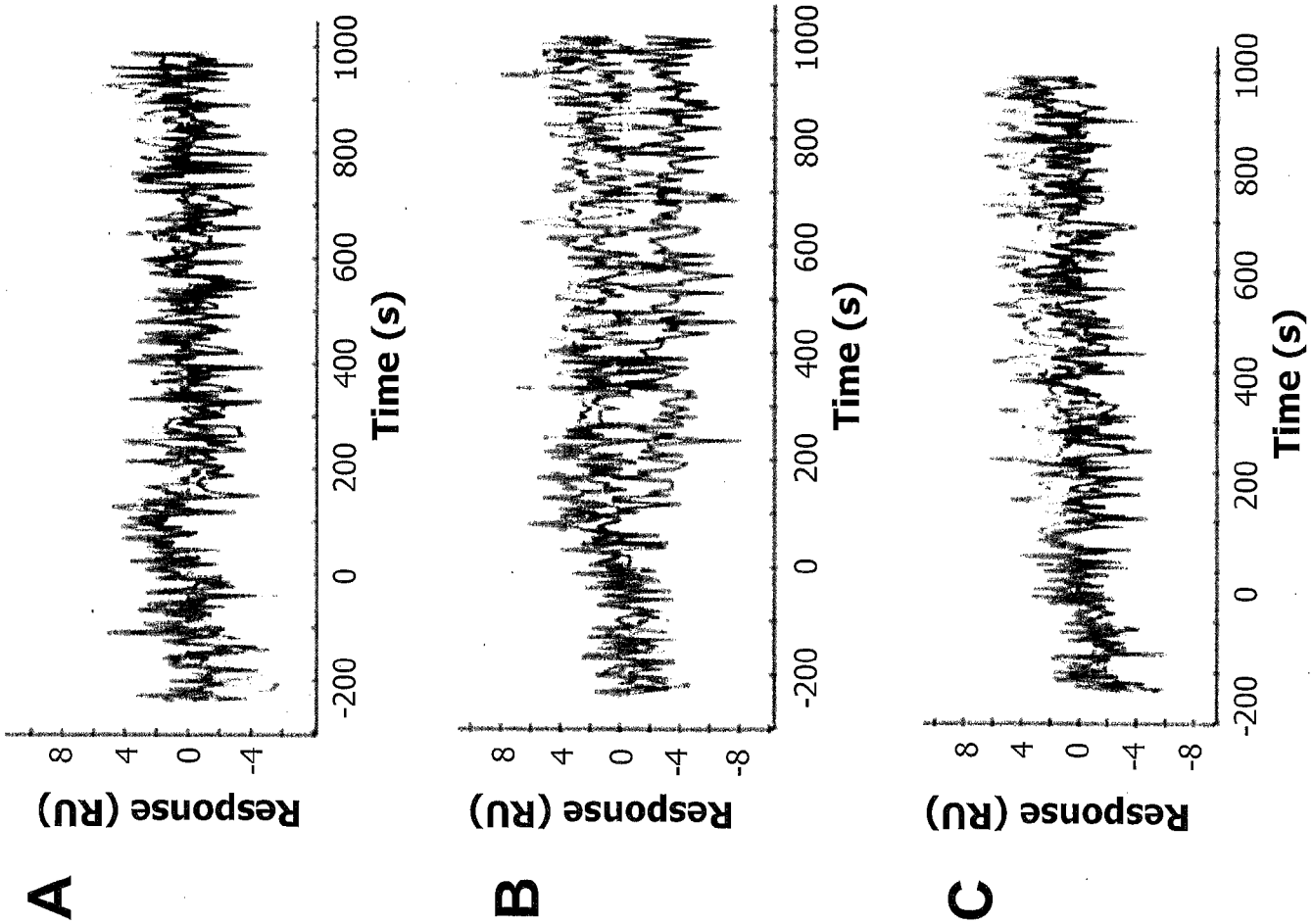
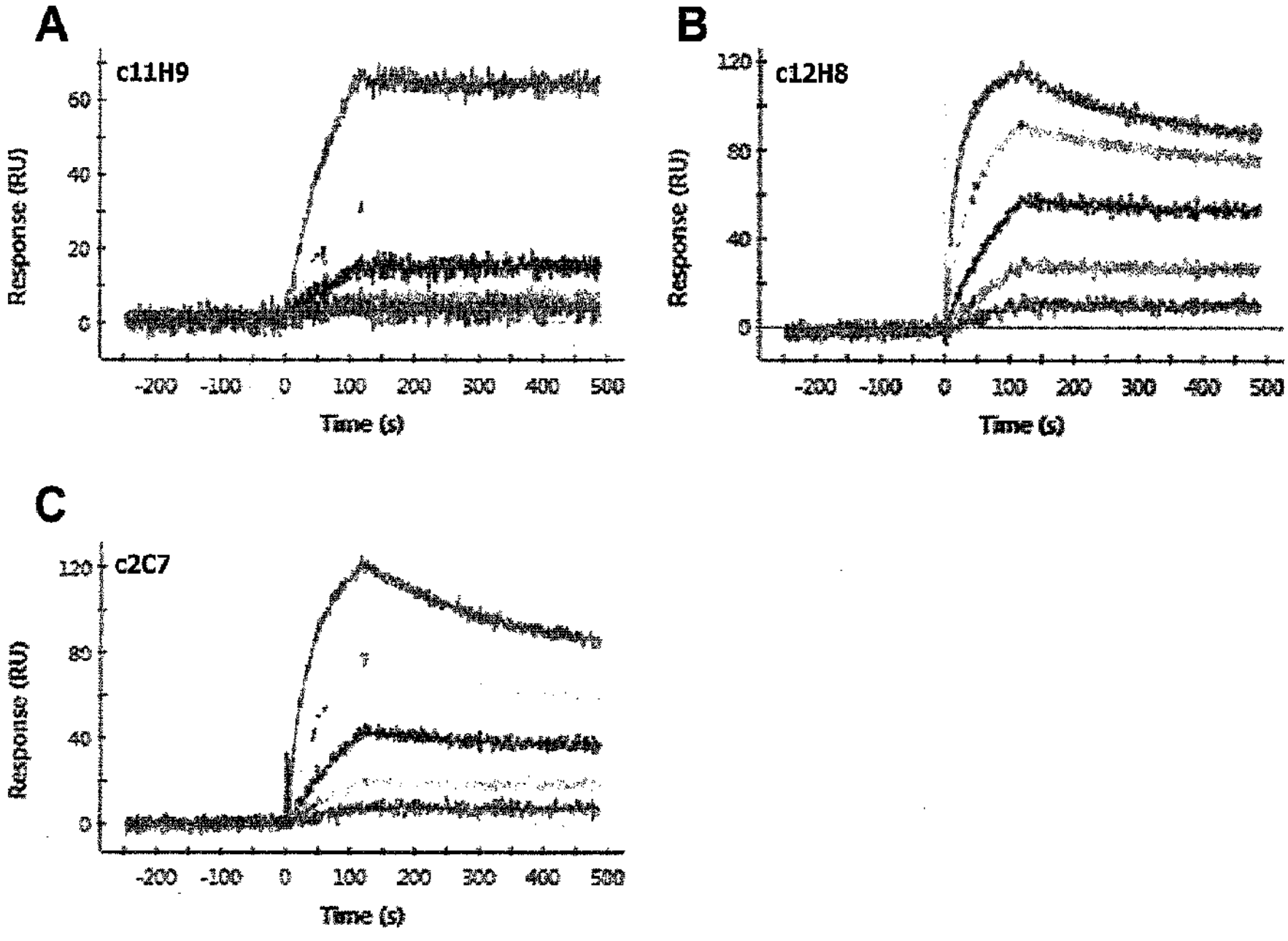

% Cell Viability Relative to Vehicle
120
100
80
60
40
20
0
Vehicle
Negative Control
Negative Control-DM1
F117-c2C7
F117-c2C7-DM1
F101-c12H8
F101-c12H8-DM1

FIG. 19

Fig.20A/B/C




A
c11H9
Response (RU)
60
40
20
0
-200
-100
0
100
200
300
400
500
Time (s)
B
c12H8
Response (RU)
120
80
40
0
-200
-100
0
100
200
300
400
500
Time (s)
C
c2C7
Response (RU)
120
80
40
0
-200
-100
0
100
200
300
400
500
Time (s)