Cross-species-specific PSCAxCD3, CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPalpha xCD3 bispecific single chain antibody

The present invention relates to a bispecific single chain antibody molecule comprising a first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3 epsilon chain, wherein the epitope is part of an amino acid sequence comprised in the group consisting of SEQ ID NOs. 2, 4, 6, and 8, and a second binding domain capable of binding to an antigen selected from the group consisting of Prostate Stem Cell Antigen (PSCA), B-Lymphocyte antigen CD19 (CD19), hepatocyte growth factor receptor (C-MET), Endosialin, the EGF-like domain 1 of EpCAM, encoded by exon 2, Fibroblast activation protein alpha (FAP alpha) and Insulin-like growth factor I receptor (IGF-IR or IGF-1R). The invention also provides nucleic acids encoding said bispecific single chain antibody molecule as well as vectors and host cells and a process for its production. The invention further relates to pharmaceutical compositions comprising said bispecific single chain antibody molecule and medical uses of said bispecific single chain antibody molecule.

T cell recognition is mediated by clonotypically distributed alpha beta and gamma delta T cell receptors (TcR) that interact with the peptide-loaded molecules of the peptide MHC (pMHC) (Davis & Bjorkman, Nature 334 (1988), 395-402). The antigen-specific chains of the TcR do not possess signalling domains but instead are coupled to the conserved multisubunit signalling apparatus CD3 (Call, Cell 111 (2002), 967-979, Alarcon, Immunol. Rev. 191 (2003), 38-46, Malissen Immunol. Rev. 191 (2003), 7-27). The mechanism by which TcR ligation is directly communicated to the signalling apparatus remains a fundamental question in T cell biology (Alarcon, loc. cit.; Davis, Cell 110 (2002), 285-287). It seems clear that sustained T cell responses involve coreceptor engagement, TcR oligomerization, and a higher order arrangement of TcR–pMHC complexes in the immunological synapse (Davis & van der Merwe, Curr. Biol. 11 (2001), R289-R291, Davis, Nat. Immunol. 4 (2003), 217-224). However very early TcR signalling occurs in the absence of these events and may involve a ligand-induced conformational change in CD3 epsilon (Alarcon, loc. cit., Davis (2002), loc. cit., Gil, J. Biol. Chem. 276 (2001), 11174-11179, Gil, Cell 109

(2002), 901-912). The epsilon, gamma, delta and zeta subunits of the signalling complex associate with each other to form a CD3 epsilon-gamma heterodimer, a CD3 epsilon-delta heterodimer, and a CD3 zeta-zeta homodimer (Call, loc. cit.). Various studies have revealed that the CD3 molecules are important for the proper cell surface expression of the alpha beta TcR and normal T cell development (Berkhout, J. Biol. Chem. 263 (1988), 8528-8536, Wang, J. Exp. Med. 188 (1998), 1375-1380, Kappes, Curr. Opin. Immunol. 7 (1995), 441-447). The solution structure of the ectodomain fragments of the mouse CD3 epsilon gamma heterodimer showed that the epsilon gamma subunits are both C2-set Ig domains that interact with each other to form an unusual side-to-side dimer configuration (Sun, Cell 105 (2001), 913-923). Although the cysteine-rich stalk appears to play an important role in driving CD3 dimerization (Su, loc. cit., Borroto, J. Biol. Chem. 273 (1998), 12807-12816), interaction by means of the extracellular domains of CD3 epsilon and CD3 gamma is sufficient for assembly of these proteins with TcR beta (Manolios, Eur. J. Immunol. 24 (1994), 84-92, Manolios & Li, Immunol. Cell Biol. 73 (1995), 532-536). Although still controversial, the dominant stoichiometry of the TcR most likely comprises one alpha beta TcR, one CD3 epsilon gamma heterodimer, one CD3 epsilon delta heterodimer and one CD3 zeta zeta homodimer (Call, loc. cit.). Given the central role of the human CD3 epsilon gamma heterodimer in the immune response, the crystal structure of this complex bound to the therapeutic antibody OKT3 has recently been elucidated (Kjer-Nielsen, PNAS 101, (2004), 7675-7680).

A number of therapeutic strategies modulate T cell immunity by targeting TcR signalling, particularly the anti-human CD3 monoclonal antibodies (mAbs) that are widely used clinically in immunosuppressive regimes. The CD3-specific mouse mAb OKT3 was the first mAb licensed for use in humans (Sgro, Toxicology 105 (1995), 23-29) and is widely used clinically as an immunosuppressive agent in transplantation (Chatenoud, Clin. Transplant 7 (1993), 422-430, Chatenoud, Nat. Rev. Immunol. 3 (2003), 123-132, Kumar, Transplant. Proc. 30 (1998), 1351-1352), type 1 diabetes (Chatenoud (2003), loc. cit.), and psoriasis (Utset, J. Rheumatol. 29 (2002), 1907-1913). Moreover, anti-CD3 mAbs can induce partial T cell signalling and clonal anergy (Smith, J. Exp. Med. 185 (1997), 1413-1422). OKT3 has been described in the literature as a potent T cell mitogen (Van Wauve, J. Immunol. 124 (1980), 2708-18) as well as a potent T cell killer (Wong, Transplantation 50 (1990),

683-9). OKT3 exhibits both of these activities in a time-dependent fashion; following early activation of T cells leading to cytokine release, upon further administration OKT3 later blocks all known T cell functions. It is due to this later blocking of T cell function that OKT3 has found such wide application as an immunosuppressant in therapy regimens for reduction or even abolition of allograft tissue rejection.

OKT3 reverses allograft tissue rejection most probably by blocking the function of all T cells, which play a major role in acute rejection. OKT3 reacts with and blocks the function of the CD3 complex in the membrane of human T cells, which is associated with the antigen recognition structure of T cells (TCR) and is essential for signal transduction. Which subunit of the TCR/CD3 is bound by OKT3 has been the subject of multiple studies. Though some evidence has pointed to a specificity of OKT3 for the epsilon-subunit of the TCR/CD3 complex (Tunnacliffe, Int. Immunol. 1 (1989), 546-50; Kjer-Nielsen, PNAS 101, (2004), 7675-7680). Further evidence has shown that OKT3 binding of the TCR/CD3 complex requires other subunits of this complex to be present (Salmeron, J. Immunol. 147 (1991), 3047-52).

Other well known antibodies specific for the CD3 molecule are listed in Tunnacliffe, Int. Immunol. 1 (1989), 546-50. As indicated above, such CD3 specific antibodies are able to induce various T cell responses such as lymphokine production (Von Wussow, J. Immunol. 127 (1981), 1197; Palacious, J. Immunol. 128 (1982), 337), proliferation (Van Wauve, J. Immunol. 124 (1980), 2708-18) and suppressor-T cell induction (Kunicka, in "Lymphocyte Typing II" 1 (1986), 223). That is, depending on the experimental conditions, CD3 specific monoclonal antibody can either inhibit or induce cytotoxicity (Leewenberg, J. Immunol. 134 (1985), 3770; Phillips, J. Immunol. 136 (1986) 1579; Platsoucas, Proc. Natl. Acad. Sci. USA 78 (1981), 4500; Itoh, Cell. Immunol. 108 (1987), 283-96; Mentzer, J. Immunol. 135 (1985), 34; Landegren, J. Exp. Med. 155 (1982), 1579; Choi (2001), Eur. J. Immunol. 31, 94-106; Xu (2000), Cell Immunol. 200, 16-26; Kimball (1995), Transpl. Immunol. 3, 212-221).

Although many of the CD3 antibodies described in the art have been reported to recognize the CD3 epsilon subunit of the CD3 complex, most of them bind in fact to conformational epitopes and, thus, only recognize CD3 epsilon in the native context of the TCR. Conformational epitopes are characterized by the presence of two or

more discrete amino acid residues which are separated in the primary sequence, but come together on the surface of the molecule when the polypeptide folds into the native protein/antigen (Sela, (1969) Science 166, 1365 and Laver, (1990) Cell 61, 553-6). The conformational epitopes bound by CD3 epsilon antibodies described in the art may be separated in two groups. In the major group, said epitopes are being formed by two CD3 subunits, e.g. of the CD3 epsilon chain and the CD3 gamma or CD3 delta chain. For example, it has been found in several studies that the most widely used CD3 epsilon monoclonal antibodies OKT3, WT31, UCHT1, 7D6 and Leu-4 did not bind to cells singly transfected with the CD3-epsilon chain. However, these antibodies stained cells doubly transfected with a combination of CD3 epsilon plus either CD3 gamma or CD3 delta (Tunnacliffe, loc. cit.; Law, Int. Immunol. 14 (2002), 389-400; Salmeron, J. Immunol. 147 (1991), 3047-52; Coulie, Eur. J. Immunol. 21 (1991), 1703-9). In a second smaller group, the conformational epitope is being formed within the CD3 epsilon subunit itself. A member of this group is for instance mAb APA 1/1 which has been raised against denatured CD3 epsilon (Risueno, Blood 106 (2005), 601-8). Taken together, most of the CD3 epsilon antibodies described in the art recognize conformational epitopes located on two or more subunits of CD3. The discrete amino acid residues forming the three-dimensional structure of these epitopes may hereby be located either on the CD3 epsilon subunit itself or on the CD3 epsilon subunit and other CD3 subunits such as CD3 gamma or CD3 delta.

Another problem with respect to CD3 antibodies is that many CD3 antibodies have been found to be species-specific. Anti-CD3 monoclonal antibodies – as holds true generally for any other monoclonal antibodies - function by way of highly specific recognition of their target molecules. They recognize only a single site, or epitope, on their target CD3 molecule. For example, one of the most widely used and best characterized monoclonal antibodies specific for the CD3 complex is OKT-3. This antibody reacts with chimpanzee CD3 but not with the CD3 homolog of other primates, such as macaques, or with dog CD3 (Sandusky et al., J. Med. Primatol. 15 (1986), 441-451). Similarly, WO2005/118635 or WO2007/033230 describe human monoclonal CD3 epsilon antibodies which react with human CD3 epsilon but not with CD3 epsilon of mouse, rat, rabbit, or non-chimpanzee primates, such as rhesus monkey, cynomolgus monkey or baboon monkey. The anti-CD3 monoclonal antibody UCHT-1 is also reactive with CD3 from chimpanzee but not with CD3 from macaques

(own data). On the other hand, there are also examples of monoclonal antibodies, which recognize macaque antigens, but not their human counterparts. One example of this group is monoclonal antibody FN-18 directed to CD3 from macaques (Uda et al., J. Med. Primatol. 30 (2001), 141-147). Interestingly, it has been found that peripheral lymphocytes from about 12% of cynomolgus monkeys lacked reactivity with anti-rhesus monkey CD3 monoclonal antibody (FN-18) due to a polymorphism of the CD3 antigen in macaques. Uda et al. described a substitution of two amino acids in the CD3 sequence of cynomolgus monkeys, which are not reactive with FN-18 antibodies, as compared to CD3 derived from animals, which are reactive with FN-18 antibodies (Uda et al., J Med Primatol. 32 (2003), 105-10; Uda et al., J Med Primatol. 33 (2004), 34-7).

The discriminatory ability, i.e. the species specificity, inherent not only to CD3 monoclonal antibodies (and fragments thereof), but to monoclonal antibodies in general, is a significant impediment to their development as therapeutic agents for the treatment of human diseases. In order to obtain market approval any new candidate medication must pass through rigorous testing. This testing can be subdivided into preclinical and clinical phases: Whereas the latter – further subdivided into the generally known clinical phases I, II and III – is performed in human patients, the former is performed in animals. The aim of pre-clinical testing is to prove that the drug candidate has the desired activity and most importantly is safe. Only when the safety in animals and possible effectiveness of the drug candidate has been established in preclinical testing this drug candidate will be approved for clinical testing in humans by the respective regulatory authority. Drug candidates can be tested for safety in animals in the following three ways, (i) in a relevant species, i.e. a species where the drug candidates can recognize the ortholog antigens, (ii) in a transgenic animal containing the human antigens and (iii) by use of a surrogate for the drug candidate that can bind the ortholog antigens present in the animal. Limitations of transgenic animals are that this technology is typically limited to rodents. Between rodents and man there are significant differences in the physiology and the safety results cannot be easily extrapolated to humans. The limitations of a surrogate for the drug candidate are the different composition of matter compared to the actual drug candidate and often the animals used are rodents with the limitation as discussed above. Therefore, preclinical data generated in rodents are of limited

predictive power with respect to the drug candidate. The approach of choice for safety testing is the use of a relevant species, preferably a lower primate. The limitation now of monoclonal antibodies suitable for therapeutic intervention in man described in the art is that the relevant species are higher primates, in particular chimpanzees. Chimpanzees are considered as endangered species and due to their human-like nature, the use of such animals for drug safety testing has been banned in Europe and is highly restricted elsewhere. CD3 has also been successfully used as a target for bispecific single chain antibodies in order to redirect cytotoxic T cells to pathological cells, resulting in the depletion of the diseased cells from the respective organism (WO 99/54440; WO 04/106380). For example, Bargou et al. (Science 321 (2008): 974-7) have recently reported on the clinical activity of a CD19xCD3 bispecific antibody construct called blinatumomab, which has the potential to engage all cytotoxic T cells in human patients for lysis of cancer cells. Doses as low as 0.005 milligrams per square meter per day in non-Hodgkin's lymphoma patients led to an elimination of target cells in blood. Partial and complete tumor regressions were first observed at a dose level of 0.015 milligrams, and all seven patients treated at a dose level of 0.06 milligrams experienced a tumor regression. Blinatumomab also led to clearance of tumor cells from bone marrow and liver. Though this study established clincical proof of concept for the therapeutic potency of the bispecific single chain antibody format in treating blood-cell derived cancer, there is still need for successful concepts for therapies of other cancer types.

In 2008, an estimated 186,320 men will be newly diagnosed with prostate cancer in the United States and about 28,660 men will die from the disease. The most recent report available on cancer mortality shows that, in 2004, the overall death rate from prostate cancer among American men was 25 per 100,000. In the late 1980s, the widespread adoption of the prostate-specific antigen (PSA) test represented a major improvement in the management of prostate cancer. This test measures the amount of PSA protein in the blood, which is often elevated in patients with prostate cancer. In 1986, the U.S. Food and Drug Administration approved the use of the PSA test to monitor patients with prostate cancer and, in 1994, additionally approved its use as a screening test for this disease. Due to the widespread implementation of PSA testing in the United States, approximately 90 percent of all prostate cancers are currently diagnosed at an early stage, and, consequently, men are surviving longer after

diagnosis. However, the results of two ongoing clinical trials, the NCI-sponsored Prostate, Lung, Colorectal, and Ovarian (PLCO) screening trial and the European Study of Screening for Prostate Cancer (ERSPC) will be needed to determine whether PSA screening actually saves lives. Ongoing clinical trials over the past 25 years have investigated the effectiveness of natural and synthetic compounds in the prevention of prostate cancer. For example, the Prostate Cancer Prevention Trial (PCPT), which enrolled nearly 19,000 healthy men, found that finasteride, a drug approved for the treatment of benign prostatic hyperplasia (BPH), which is a noncancerous enlargement of the prostate, reduced the risk of developing prostate cancer by 25 percent. Another trial, the Selenium and Vitamin E Cancer Prevention Trial (SELECT), is studying more than 35,000 men to determine whether daily supplements of selenium and vitamin E can reduce the incidence of prostate cancer in healthy men. Other prostate cancer prevention trials are currently evaluating the protective potential of multivitamins, vitamins C and D, soy, green tea, and lycopene, which is a natural compound found in tomatoes. One study, reported in 2005, showed that specific genes were fused in 60 to 80 percent of the prostate tumors analyzed. This study represents the first observation of non-random gene rearrangements in prostate cancer. This genetic alteration may eventually be used as a biomarker to aid in the diagnosis and, possibly, treatment of this disease. Other studies have shown that genetic variations in a specific region of chromosome 8 can increase a man's risk of developing prostate cancer. These genetic variations account for approximately 25 percent of the prostate cancers that occur in white men. They are the first validated genetic variants that increase the risk of developing prostate cancer and may help scientists better understand the genetic causes of this disease. There is also ongoing research that examines how proteins circulating in a patient's blood can be used to improve the diagnosis of prostate and other cancers. In 2005, scientists identified a group of specific proteins that are produced by a patient's immune system in response to prostate tumors. These proteins, a type of autoantibody, were able to detect the presence of prostate cancer cells in blood specimens with greater than 90 percent accuracy. When used in combination with PSA, these and other blood proteins may eventually be used to reduce the number of false-positive results obtained with PSA testing alone and, therefore, reduce the large number of unnecessary prostate biopsies that are performed each year due to false-positive PSA test results.

Apart from PSA, several other markers for prostate cancer have been identified, including e.g. the six-transmembrane epithelial antigen of the prostate (STEAP) (Hubert et al., PNAS 96 (1999), 14523-14528), the prostate-specific membrane antigen (PSM/PSMA) (Israeli et al., Cancer Res. 53 (1993), 227-230) and the Prostate stem cell antigen (PSCA) (Reiter et al., Proc. Nat. Acad. Sci. 95: 1735-1740, 1998). Prostate stem cell antigen (PSCA) is a 123 amino acid protein first identifed when looking for genes upregulated during cancer progression in the LAPC-4 prostate xenograft model (Reiter et al., loc. cit.). It is a glycosyl phosphatidylinositol-anchored cell-surface protein that belongs to the family of Thy-1/Ly-6 surface antigens. PSCA bears 30% homology to stem cell antigen type 2. Although the function of PSCA is yet to be elucidated, homologues of PSCA have diverse activities, and have themselves been implicated in carcinogenesis. Stem cell antigen type 2 has been shown to prevent apoptosis in immature thymocytes (Classon and Coverdale, PNAS 91 (1994), 5296-5300). Thy-1 activates T cells by signalling through src tyrosine kinases (Amoui et al., Eur. J. Immunol. 27 (1997), 1881-86). Ly-6 genes have been implicated in tumorigenesis and cell adhesion (Schrijvers et al., Exp. Cell. Res. 196 (1991), 264-69). Initial messenger RNA studies and subsequent monoclonal antibody (mAb) staining have revealed that PSCA is expressed on the cell surface of normal and malignant prostate cells (Reiter et al., loc. cit.; Gu et al., Oncogene 19 (2000), 1288-96; Ross et al., Cancer Res. 62 (2002), 2546-53). In normal prostate, PSCA mRNA has been detected in a subset of basal and secretory cells. In prostate carcinoma, PSCA mRNA expression has been detected in approximately 50-80% of primary and approximately 70% of metastatic cancers (Reiter et al., loc. cit.). Immunohistochemistry has been reported on 112 primary prostate cancers and nine prostate cancers metastatic to bone (Gu et al., loc. cit.). PSCA expression was detected in 94% and overexpressed in 40% of clinically localized prostate cancers. High levels of PSCA protein expression were also detected in nine out of nine prostate cancer bone metastases examined. Outside the prostate, PSCA is detected in the umbrella cell layer of the transitional epithelium, some renal collecting ducts, neuroendocrine cells of the stomach, and placental trophoblasts. Importantly, recent studies have reported an overexpression of PSCA in a large proportion of pancreatic cancers and invasive and non-invasive transitional cell carcinomas (Amara et al., Cancer Res. 61 (2001), 4660-4665; Argani et al.,

Cancer Res. 61 (2001), 4320-24). Because of its cell surface expression and its overexpression in a substantial proportion of various cancers, PSCA has been discussed as target for treatment strategies in cancer. However, future clinical correlation will be required to validate this possibility.

The expression of certain CD antigens is highly restricted to specific lineage lymphohematopoietic cells and over the past several years, antibodies directed against lymphoid-specific antigens have been used to develop treatments that were effective either in vitro or in animal models. In this respect CD19 has proved to be a very useful target. CD19 is expressed in the whole B lineage from the pro B cell to the mature B cell, it is not shed, is uniformly expressed on all lymphoma cells, and is absent from stem cells (Haagen, Clin Exp Immunol 90 (1992), 368-75, 14; Uckun, Proc. Natl. Acad. Sci. USA 85 (1988), 8603-7). The CD19 is involved in the development of certain B-cell mediated diseases such as various forms of non-Hodgkin lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells.

A further example for a molecule which is involved in the progression and spread of numerous human cancer types is the hepatocyte growth factor receptor MET (C-MET). The *MET* oncogene, encoding the receptor tyrosin kinase (RTK) for hepatocyte growth factor (HGF) and Scatter Factor (SF), controls genetic programs leading to cell growth, invasion, and protection from apoptosis. Deregulated activation of MET is critical not only for the acquisition of tumorigenic properties but also for the achievement of the invasive phenotype (Trusolino, L. & Comoglio, P. M. (2002) Nat. Rev. Cancer 2, 289–300). The role of *MET* in human tumors emerged from several experimental approaches and was unequivocally proven by the discovery of *MET*-activating mutations in inherited forms of carcinomas (Schmidt et al., Nat. Genet. 16 (1997), 68–73; Kim et al., J. Med. Genet. 40 (2003), e97). MET constitutive activation is frequent in sporadic cancers, and several studies have shown that the *MET* oncogene is overexpressed in tumors of specific histotypes or is activated through autocrine mechanisms (for a list see http://www.vai.org/met/). Besides, the *MET* gene is amplified in hematogenous metastases of colorectal carcinomas (Di Renzo et al., Clin. Cancer Res. 1 (1995), 147–154).

The Scatter Factor (SF) secreted in culture by fibroblasts, that has the ability to induce intercellular dissociation of epithelial cells, and the Hepatocyte Growth Factor (HGF), a potent mitogen for hepatocytes in culture derived from platelets or from blood of patients with acute liver failure, independently identified as Met ligands turned out to be the same molecule. Met and SF/HGF are widely expressed in a variety of tissues. The expression of Met (the receptor) is normally confined to cells of epithelial origin, while the expression of SF/HGF (the ligand) is restricted to cells of mesenchymal origin.

Met is a transmembrane protein produced as a single-chain precursor. The precursor is proteolytically cleaved at a furin site to produce a highly glycosylated and entirely extracellular α-subunit of 50 kd and a β-subunit of 145 kd with a large extracellular region (involved in binding the ligand), a membrane spanning segment, and an intracellular region (containing the catalytic activity) (Giordano (1989) 339: 155-156). The α and β chains are disulphide linked. The extracellular portion of Met contains a region of homology to semaphorins (Sema domain, which includes the full α chain and the N-terminal part of the β chain of Met), a cysteine-rich Met Related Sequence (MRS) followed by glycineproline- rich (G-P) repeats, and four Immunoglobuline-like structures (Birchmeier et al., Nature Rev. 4 (2003), 915-25). The intracellular region of Met contains three regions: (1) a juxtamembrane segment that contains: (a) a serine residue (Ser 985) that, when phosphorylated by protein kinase C or by Ca^{2+}calmodulin-dependent kinases downregulates the receptor kinase activity Gandino et al., J. Biol. Chem. 269 (1994), 1815-20); and (b) a tyrosine (Tyr 1003) that binds the ubiquitin ligase Cbl responsible for Met polyubiquitination, endocytosis and degradation (Peschard et al., Mol. Cell 8 (2001), 995-1004); (2) the tyrosine kinase domain that, upon receptor activation, undergoes transphosphorylation on Tyr1234 and Tyr1235; (3) the C-terminal region, which comprises two crucial tyrosines (Tyr1349 and Tyr1356) inserted in a degenerate motif that represents a multisubstrate docking site capable of recruiting several downstream adaptors containing Src homology-2 (SH2) domains Met receptor, as most Receptor Tyrosine Kinases (RTKs) use different tyrosines to bind specific signaling molecules. The two tyrosines of the docking sites have been demonstrated to be necessary and sufficient for the signal transduction both in vitro and in vivo (Maina et al., Cell 87 (1996), 531-542; Ponzetto et al., Cell 77 (1994), 261-71).

Though potent and selective preclinical drug candidates have been developed using C-MET as a tumor target, follow-up clinical trials have to reveal whether these drugs are indeed safe and show therapeutic efficacy in humans. In light of these uncertainties, there is still need for novel therapeutic concepts for cancer.

Cancer has surpassed heart disease as the top killer of Americans under 85, in 2005. Today, cancer ranks behind cardiovascular diseases as the second leading cause of death in Germany. Unless dramatic breakthroughs are achieved in cancer prevention in the next few years comparable to those achieved for cardiovascular disease, cancer will become the leading cause of death in Germany within 15-20 years. Inhibition of tumor angiogenesis is one of the anticancer strategies which has generated much excitement among clinicians and cancer research scientists in the last few years. In the course of these research efforts, several tumor endothelial markers have been identified. Tumor endothelial markers (TEMs) like Endosialin (= TEM1 or CD248) are overexpressed during tumor angiogenesis (St. Croix et al., Science 289 (2000), 1197-1202). Despite the fact that their functions have not been characterized in detail so far, it is well established that they are strongly expressed on vascular endothelial cells in developing embryos and tumors studies (Carson-Walter et al., Cancer Res. 61: 6649-6655, 2001). Accordingly, Endosialin, a 165-kDa type I transmembrane protein, is expressed on the cell surface of tumor blood vessel endothelium in a broad range of human cancers but not detected in blood vessels or other cell types in many normal tissues. It is a C-type lectin-like molecule of 757 amino acids composed of a signal leader peptide, five globular extracellular domains (including a C-type lectin domain, one domain with similarity to the Sushi/ccp/scr pattern, and three EGF repeats), followed by a mucin like region, a transmembrane segment, and a short cytoplasmic tail (Christian et al., J. Biol. Chem. 276: 7408-7414, 2001). The Endosialin core protein carries abundantly sialylated, O-linked oligosaccharides and is sensitive to *O*-sialoglycoprotein endopeptidase, placing it in the group of sialomucin-like molecules. The N-terminal 360 amino acids of Endosialin show homology to thrombomodulin, a receptor involved in regulating blood coagulation, and to complement receptor C1qRp. This structural relationship indicates a function for Endosialin as a tumor endothelial receptor. Although Endosialin mRNA is ubiquitously expressed on endothelial cells in normal human and murine somatic tissues, Endosialin protein is largely restricted to the corpus luteum

and highly angiogenic tissues such as the granular tissue of healing wounds or tumors (Opavsky et al., J. Biol. Chem. 276 (2001, 38795-38807; Rettig et al., PNAS 89 (1992), 10832-36). Endosialin protein expression is upregulated on tumor endothelial cells of carcinomas (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), sarcomas, and neuroectodermal tumors (melanoma, glioma, neuroblastoma) (Rettig et al., loc. cit.). In addition, Endosialin is expressed at a low level on a subset of tumor stroma fibroblasts (Brady et al., J. Neuropathol. Exp. Neurol. 63 (2004), 1274-83; Opavsky et al., loc. cit.). Because of its restricted normal tissue distribution and abundant expression on tumor endothelial cells of many different types of solid tumors, Endosialin has been discussed as a target for antibody-based antiangiogenic treatment strategies of cancer. However, so far, there are no effective therapeutic approaches using Endosialin as a tumor endothelial target.

A molecule which is very frequently and highly expressed on the majority of human adenocarcinoma and several squamous cell carcinoma cells is EpCAM (CD326) (Went et al., Br. J. Cancer 94 (20006), 128-135). Recent studies have shown that EpCAM is a signalling molecule that can upregulate nuclear expression of the proto-oncogene c-Myc and cyclins (Munz et al., Oncogene 23 (2004), 5748-58). When overexpressed in quiescent cells, EpCAM induces cell proliferation, growth factor independence and growth of colonies in soft agar, which are hallmarks of oncogenic proteins. When EpCAM expression is knocked down by small interfering RNA (siRNA) in breast cancer cells, such cells cease to proliferate, migrate and be invasive (Osta et al., Cancer Res. 64 (2004), 5818-24). This oncogenic signalling of EpCAM may explain why EpCAM overexpression correlates with poor overall survival in a number of human malignancies, including breast and ovarian cancer (Spizzo et al., Gynecol. Oncol. 103 (2006), 483-8). EpCAM has already been employed as a target antigen in several antibody-based therapeutic approaches, including a human antibody (Oberneder et al., Eur. J. Cancer 42 (2006), 2530-8) and an EpCAMxCD3 single chain bispecific antibody called MT110. The characteristics of MT110 have recently been desribed in detail (Brischwein et al., 43 (2006), 1129-43). This antibody is active against a variety of human carcinoma lines expressing the target antigen and is currently being tested in a phase I study for safety and early signs of efficacy.

More specifically, cancer has surpassed heart disease as the top killer of Americans under 85 in 2005. Today, cancer ranks behind cardiovascular diseases as the second leading cause of death in Germany. Unless dramatic breakthroughs are achieved in cancer prevention in the next few years comparable to those achieved for cardiovascular disease, cancer will become the leading cause of death in Germany within 15-20 years. Among the more than 100 types of different cancers, epithelial cancer is the leading cause of cancer deaths in Germany. In epithelial cancer, invasion and metastasis of malignant epithelial cells into normal tissues is accompanied by adaptive changes in the mesenchyme-derived supporting stroma of the target organs. Altered gene expression in these non-transformed stromal cells has been discussed to provide potential targets for therapy. The cell surface protease fibroblast activation protein alpha (FAP alpha) is one example for such a target of activated tumor fibroblasts. Fibroblast activation protein alpha is an inducible cell surface glycoprotein that has originally been identified in cultured fibroblasts using monoclonal antibody F19. Immunohistochemical studies have shown that FAP alpha is transiently expressed in certain normal fetal mesenchymal tissues but that normal adult tissues as well as malignant epithelial, neural, and hematopoietic cells are generally FAP alpha-negative. However, most of the common types of epithelial cancers contain abundant FAP alpha-reactive stromal fibroblasts. Scanlan et al. (Proc. Nat. Acad. Sci. 91: 5657-5661, 1994) cloned a FAP alpha cDNA from a WI-38 human fibroblast cDNA expression library by immunoselection using antibody F19. The predicted 760-amino acid human FAP alpha protein is a type II integral membrane protein with a large C-terminal extracellular domain, which contains 6 potential N-glycosylation sites, 13 cysteine residues, and 3 segments that correspond to highly conserved catalytic domains of serine proteases; a hydrophobic transmembrane segment; and a short cytoplasmic tail. FAP-alpha shows 48% amino acid identity with dipeptidyl peptidase IV (DPP4) and 30% identity with DPP4-related protein (DPPX). Northern blot analysis detected a 2.8-kb FAP alpha mRNA in fibroblasts. Seprase is a 170-kD integral membrane gelatinase whose expression correlates with the invasiveness of human melanoma and carcinoma cells. Goldstein et al. (Biochim. Biophys. Acta 1361: 11-19, 1997) cloned and characterized the corresponding seprase cDNA. The authors found that seprase and FAP alpha are the same protein and products of the same gene. Pineiro-Sanchez et al. (J. Biol. Chem. 272: 7595-7601, 1997) isolated seprase/FAP alpha protein from the cell

membranes and shed vesicles of human melanoma LOX cells. Serine protease inhibitors blocked the gelatinase activity of seprase/FAP alpha, suggesting that seprase/FAP alpha contains a catalytically active serine residue(s). The authors found that seprase/FAP alpha is composed of monomeric, N-glycosylated 97-kD subunits that are proteolytically inactive. They concluded that seprase/FAP alpha is similar to DPP4 in that their proteolytic activities are dependent upon subunit association. Due to its degrading activity of gelatine and heat-denatured type-I and type-IV collagen, a role for seprase/FAP alpha in extracellular matrix remodeling, tumor growth, and metastasis of cancers has been suggested. Moreover, seprase/FAP alpha shows a restricted expression pattern in normal tissues and a uniform expression in the supporting stroma of many malignant tumors. Therefore, seprase/FAP alpha may be used as a target for exploring the concept of tumor stroma targeting for immunotherapy of human epithelial cancer. However, though several clinical trials have been initiated to investigate seprase's/FAP alpha's role as a tumor antigen target, conventional immunotherapy approaches or inhibition of seprase/FAP alpha enzymatic activity so far did not yet result in therapeutic efficacy (see e.g. Welt et al., J. Clin. Oncol. 12:1193-203, 1994; Narra et al., Cancer Biol. Ther. 6, 1691-9, 2007; Henry et al., Clinical Cancer Research 13, 1736-1741, 2007).

Insulin-like growth factor I receptor (IGF-IR or IGF-1R) is a receptor with tyrosine kinase activity having 70% homology with the insulin receptor IR. IGF-1R is a glycoprotein of molecular weight approximately 350,000. It is a hetero-tetrameric receptor of which each half-linked by disulfide bridges-is composed of an extracellular a-subunit and of a transmembrane [beta]-subunit. IGF-1R binds IGF 1 and IGF 2 with a very high affinity but is equally capable of binding to insulin with an affinity 100 to 1000 times less. Conversely, the 1R binds insulin with a very high affinity although the ICFs only bind to the insulin receptor with a 100 times lower affinity. The tyrosine kinase domain of IGF-1R and of 1R has a very high sequence homology although the zones of weaker homology respectively concern the cysteine-rich region situated on the alpha-subunit and the C-terminal part of the [beta]-subunit. The sequence differences observed in the a-subunit are situated in the binding zone of the ligands and are therefore at the origin of the relative affinities of IGF-1R and of 1R for the IGFs and insulin respectively. The differences in the C-terminal part of the [beta]-subunit result in a divergence in the signalling pathways of the two receptors;

IGF-1R mediating mitogenic, differentiation and antiapoptosis effects, while the activation of the IR principally involves effects at the level of the metabolic pathways (Baserga et al., Biochim. Biophys. Acta, 1332: F105-126, 1997; Baserga R., Exp. Cell. Res., 253:1-6, 1999). The cytoplasmic tyrosine kinase proteins are activated by the binding of the ligand to the extracellular domain of the receptor. The activation of the kinases in its turn involves the stimulation of different intra-cellular substrates, including IRS-1, IRS-2, Shc and Grb 10 (Peruzzi F. et al., J. Cancer Res. Clin. Oncol., 125:166-173, 1999). The two major substrates of IGF-IR are IRS and Shc which mediate, by the activation of numerous effectors downstream, the majority of the growth and differentiation effects connected with the attachment of the IGFs to this receptor. The availability of substrates can consequently dictate the final biological effect connected with the activation of the IGF-1R. When IRS-1 predominates, the cells tend to proliferate and to transform. When Shc dominates, the cells tend to differentiate (Valentinis B. et al.; J. Biol. Chem. 274:12423-12430, 1999). It seems that the route principally involved for the effects of protection against apoptosis is the phosphatidyl-inositol 3-kinases (PI 3-kinases) route (Prisco M. et al., Horm. Metab. Res., 31:80-89, 1999; Peruzzi F. et al., J. Cancer Res. Clin. Oncol., 125:166-173, 1999). The role of the IGF system in carcinogenesis has become the subject of intensive research in the last ten years. This interest followed the discovery of the fact that in addition to its mitogenic and antiapoptosis properties, IGF-1R seems to be required for the establishment and the maintenance of a transformed phenotype. In fact, it has been well established that an overexpression or a constitutive activation of IGF-1R leads, in a great variety of cells, to a growth of the cells independent of the support in media devoid of fetal calf serum, and to the formation of tumors in nude mice. This in itself is not a unique property since a great variety of products of overexpressed genes can transform cells, including a good number of receptors of growth factors. However, the crucial discovery which has clearly demonstrated the major role played by, IGF-1R in the transformation has been the demonstration that the R-cells, in which the gene coding for IGF-1R has been inactivated, are totally refractory to transformation by different agents which are usually capable of transforming the cells, such as the E5 protein of bovine papilloma virus, an overexpression of EGFR or of PDGFR, the T antigen of SV 40, activated ras or the combination of these two last factors (Sell C. et al., Proc. Natl. Acad. Sci., USA, 90: 11217-11221, 1993; Sell C. et al., Mol. Cell. Biol., 14:3604-3612, 1994;

Morrione A. J., Virol., 69:5300-5303, 1995; Coppola D. et al., Mol. Cell. Biol., 14:458a-4595, 1994; DeAngelis T et al., J. Cell. Physiol., 164:214-221, 1995). IGF-1R is expressed in a great variety of tumors and of tumor lines and the IGFs amplify the tumor growth via their attachment to IGF-1R. Other arguments in favor of the role of IGF-IR in carcinogenesis come from studies using murine monoclonal antibodies directed against the receptor or using negative dominants of IGF-IR. In effect, murine monoclonal antibodies directed against IGF-1R inhibit the proliferation of numerous cell lines in culture and the growth of tumor cells in vivo (Arteaga C. et al., Cancer Res., 49:6237-6241, 1989 Li et al., Biochem. Biophys. Res. Com., 196:92-98, 1993; Zia F et al., J. Cell. Biol., 24:269-275, 1996; Scotlandi K et al., Cancer Res., 58:4127-4131, 1998). It has likewise been shown in the works of Jiang et al. (Oncogene, 18:6071-6077, 1999) that a negative dominant of IGF-1R is capable of inhibiting tumor proliferation.

Though there has been put much effort in identifying novel targets for therapeutic approaches for cancer, cancer is yet one of the most frequently diagnosed diseases. In light of this, there is still need for effective treatments for cancer.

The present invention provides for a bispecific single chain antibody molecule comprising a first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε (epsilon) chain, wherein the epitope is part of an amino acid sequence comprised in the group consisting of SEQ ID NOs. 2, 4, 6, and 8; and a second binding domain capable of binding to an antigen selected from the group consisting of Prostate stem cell antigen (PSCA), B-Lymphocyte antigen CD19 (CD19), hepatocyte growth factor receptor (C-MET), Endosialin, the EGF-like domain 1 of EpCAM, encoded by exon 2, Fibroblast Activation Protein Alpha (FAP alpha) and Insulin-like growth factor I receptor (IGF-IR or IGF-1R).

Though T cell-engaging bispecific single chain antibodies described in the art have great therapeutic potential for the treatment of malignant diseases, most of these bispecific molecules are limited in that they are species specific and recognize only human antigen, and - due to genetic similarity - likely the chimpanzee counterpart. The advantage of the present invention is the provision of a bispecific single chain antibody comprising a binding domain exhibiting cross-species specificity to human

and non-chimpanzee primate of the CD3 epsilon chain.

In the present invention, an N-terminal 1-27 amino acid residue polypeptide fragment of the extracellular domain of CD3 epsilon was surprisingly identified which – in contrast to all other known epitopes of CD3 epsilon described in the art – maintains its three-dimensional structural integrity when taken out of its native environment in the CD3 complex (and optionally fused to a heterologous amino acid sequence such as EpCAM or an immunoglobulin Fc part).

The present invention, therefore, provides for a bispecific single chain antibody molecule comprising a first binding domain capable of binding to an epitope of an N-terminal 1-27 amino acid residue polypeptide fragment of the extracellular domain of CD3 epsilon (which CD3 epsilon is, for example, taken out of its native environment and/or comprised by (presented on the surface of) a T-cell) of human and at least one non-chimpanzee primate CD3 epsilon chain, wherein the epitope is part of an amino acid sequence comprised in the group consisting of SEQ ID NOs. 2, 4, 6, and 8; and a second binding domain capable of binding to prostate-specific membrane antigen (PSMA). Preferred non-chimpanzee primates are mentioned herein elsewhere. At least one (or a selection thereof or all) primate(s) selected from Callithrix jacchus; Saguinus oedipus, Saimiri sciureus, and Macaca fascicularis (either SEQ ID 2225 or 2226 or both), is (are) particularily preferred. Macaca mulatta, also known as Rhesus Monkey is also envisaged as another preferred primate. It is thus envisaged that antibodies of the invention bind to (are capable of binding to) the context independent epitope of an N-terminal 1-27 amino acid residue polypeptide fragment of the extracellular domain of CD3 epsilon of human and Callithrix jacchus, Saguinus oedipus, Saimiri sciureus, and Macaca fascicularis (either SEQ ID 2225 or 2226 or both), and optionally also to Macaca mulatta. A bispecific single chain antibody molecule comprising a first binding domain as defined herein can be obtained (is obtainable by) or can be manufactured in accordance with the protocol set out in the appended Examples (in particular Example 2). To this end, it is envisaged to (a) immunize mice with an N-terminal 1-27 amino acid residue polypeptide fragment of the extracellular domain of CD3 epsilon of human and/or Saimiri sciureus; (b) generation of an immune murine antibody scFv library; (c) identification of CD3 epsilon specific binders by testing the capability to bind to at least SEQ ID NOs. 2, 4, 6, and 8.

The context-independence of the CD3 epitope provided in this invention corresponds to the first 27 N-terminal amino acids of CD3 epsilon or functional fragments of this 27 amino acid stretch. The phrase "context-independent," as used herein in relation to the CD3 epitope means that binding of the herein described inventive binding molecules/antibody molecules does not lead to a change or modification of the conformation, sequence, or structure surrounding the antigenic determinant or epitope. In contrast, the CD3 epitope recognized by a conventional CD3 binding molecule (e.g. as disclosed in WO 99/54440 or WO 04/106380) is localized on the CD3 epsilon chain C-terminally to the N-terminal 1-27 amino acids of the context-independent epitope, where it only takes the correct conformation if it is embedded within the rest of the epsilon chain and held in the right sterical position by heterodimerization of the epsilon chain with either the CD3 gamma or delta chain.
Anti-CD3 binding molecules/domains as part of a bispecific single chain antibody molecule as provided herein and generated (and directed) against a context-independent CD3 epitope provide for a surprising clinical improvement with regard to T cell redistribution and, thus, a more favourable safety profile. Without being bound by theory, since the CD3 epitope is context-independent, forming an autonomous selfsufficient subdomain without much influence on the rest of the CD3 complex, the CD3 binding molecules/domains provided herein induce less allosteric changes in CD3 conformation than the conventional CD3 binding molecules, which recognize context-dependent CD3 epitopes (e.g. as disclosed in WO 99/54440 or WO 04/106380).

The context-independence of the CD3 epitope which is recognized by the CD3 binding domain of the bispecific single chain antibody of the invention (PSCAxCD3, CD19xCD3, C-METxCD3. EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) is associated with less or no T cell redistribution (T cell redistribution equates with an initial episode of drop and subsequent recovery of absolute T cell counts) during the starting phase of treatment with said bispecific single chain antibodies of the invention. This results in a better safety profile of the bispecific single chain antibodies of the invention compared to conventional CD3 binding molecules known in the art, which recognize context-dependent CD3 epitopes. Particularly, because T cell redistribution during the starting phase of treatment with CD3 binding molecules is a major risk factor for adverse events, like CNS adverse events, the bispecific single chain antibodies of the invention has a substantial safety

advantage over the CD3 binding molecules known in the art by recognizing a context-independent rather than a context-dependent CD3 epitope. Patients with such CNS adverse events related to T cell redistribution during the starting phase of treatment with conventional CD3 binding molecules usually suffer from confusion and disorientation, in some cases also from urinary incontinence. Confusion is a change in mental status in which the patient is not able to think with his or her usual level of clarity. The patient usually has difficulties to concentrate and thinking is not only blurred and unclear but often significantly slowed down. Patients with CNS adverse events related to T cell redistribution during the starting phase of treatment with conventional CD3 binding molecules may also suffer from loss of memory. Frequently, the confusion leads to the loss of ability to recognize people, places, time or dates. Feelings of disorientation are common in confusion, and the decision-making ability is impaired. CNS adverse events related to T cell redistribution during the starting phase of treatment with conventional CD3 binding molecules may further comprise blurred speech and/or word finding difficulties. This disorder may impair both, the expression and understanding of language as well as reading and writing. Besides urinary incontinence, vertigo and dizziness may also accompany CNS adverse events related to T cell redistribution during the starting phase of treatment with conventional CD3 binding molecules in some patients.

The maintenance of the three-dimensional structure within the mentioned 27 amino acid N-terminal polypeptide fragment of CD3 epsilon can be used for the generation of, preferably human, binding domains which are capable of binding to the N-terminal CD3 epsilon polypeptide fragment *in vitro* and to the native (CD3 epsilon subunit of the) CD3 complex on T cells *in vivo* with the same binding affinity. These data strongly indicate that the N-terminal fragment as described herein forms a tertiary conformation, which is similar to its structure normally existing *in vivo*. A very sensitive test for the importance of the structural integrity of the amino acids 1-27 of the N-terminal polypeptide fragment of CD3 epsilon was performed. Individual amino acids of amino acids 1-27 of the N-terminal polypeptide fragment of CD3 epsilon were changed to alanine (alanine scanning) to test the sensitivity of the amino acids 1-27 of the N-terminal polypeptide fragment of CD3 epsilon for minor disruptions. The CD3 binding domains as part of the bispecific single chain antibodies of the invention were used to test for binding to the alanine-mutants of amino acids 1-27 of the N-terminal polypeptide fragment of CD3 epsilon (see appended Example 5). Individual

exchanges of the first five amino acid residues at the very N-terminal end of the fragment and two of the amino acids at positions 23 and 25 of the amino acids 1-27 of the N-terminal polypeptide fragment of CD3 epsilon were critical for binding of the antibody molecules. The substitution of amino acid residues in the region of position 1-5 comprising the residues Q (Glutamine at position 1), D (Aspartic acid at position 2), G (Glycine at position 3), N (Asparagine at position 4), and E (Glutamic acid at position 5) to Alanine abolished binding of the, preferably human, bispecific single chain antibodies of the invention to said fragment. While, for at least some of the, preferably human bispecific single chain antibodies of the invention, two amino acid residues at the C-terminus of the mentioned fragment T (Threonine at position 23) and I (Isoleucine at position 25) reduced the binding energy to the, preferably human, bispecific single chain antibodies of the invention.

Unexpectedly, it has been found that the thus isolated, preferably human, bispecific single chain antibodies of the invention not only recognize the human N-terminal fragment of CD3 epsilon, but also the corresponding homologous fragments of CD3 epsilon of various primates, including New-World Monkeys (Marmoset, Callithrix jacchus; Saguinus oedipus; Saimiri sciureus) and Old-World Monkeys (Macaca fascicularis, also known as Cynomolgus Monkey; or Macaca mulatta, also known as Rhesus Monkey). Thus, multi-primate specificity of the bispecific single chain antibodies of the invention was detected. The following sequence analyses confirmed that human and primates share a highly homologous sequence stretch at the N-terminus of the extracellular domain of CD3 epsilon.
The amino acid sequence of the aformentioned N-terminal fragments of CD3 epsilon are depicted in SEQ ID No. 2 (human), SEQ ID No. 4 (Callithrix jacchus); SEQ ID No. 6 (Saguinus oedipus); SEQ ID No. 8 (Saimiri sciureus); SEQ ID No. 2225 QDGNEEMGSITQTPYQVSISGTTILTC or SEQ ID No. 2226 QDGNEEMGSITQTPYQVSISGTTVILT (Macaca fascicularis, also known as Cynomolgus Monkey), and SEQ ID No. 2227 QDGNEEMGSITQTPYHVSISGTTVILT (Macaca mulatta, also known as Rhesus Monkey).

In one embodiment of the invention the second binding domain of the PSCAxCD3 bispecific single chain antibody of the invention binds to the Prostate stem cell antigen (PSCA). In alternative embodiments the second binding domain binds to

CD19, C-MET, Endosialin (CD248), EpCAM, FAPα or IGF-1R. As shown in the following examples, the second binding domain of the EpCAMxCD3 bispecific single chain antibody of the invention binds to amino acid residues 26 to 61 of the EGF-like domain 1 of EpCAM which is encoded by Exon 2 of the EpCAM gene. Said amino acid residues 26 to 61 of the EGF-like domain 1 of human EpCAM are shown in SEQ ID NO. 571. Thus, the EpCAM-directed bispecific single chain molecules of this invention form a unique own class of EpCAM-binding molecules, that is clearly differentiated from EpCAM-binding molecules based on the EpCAM-binder HD69 described earlier. Said EpCAM-binder HD69 bind to a different epitope (i.e. an epitope not localized in the EGF-like domain 1 of human EpCAM).

Preferably, the second binding domain of the PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody binds to the human PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) or a non-chimpanzee primate PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα); more preferred it binds to the human PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) and a non-chimpanzee primate PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) and therefore is cross-species specific; even more preferred to the human PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) and the macaque PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) (and therefore is cross-species specific as well). Particularly preferred, the macaque PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) is the Cynomolgus monkey PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) and/or the Rhesus monkey PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα). It is to be understood, that the second binding domain of the EpCAMxCD3 bispecific single chain antibody of the invention preferably binds to the EGF-like domain 1 of the non-chimpanzee primate EpCAM which is encoded by Exon 2 of the non-chimpanzee primate EpCAM gene. As indicated above, the non-chimpanzee primate EpCAM is preferably a macaque EpCAM, more preferably the Cynomolgus monkey EpCAM and/or the Rhesus monkey EpCAM.

However, it is not excluded from the scope of the present invention, that the second binding domain may also bind to PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) homologs of other species, such as to the chimpanzee

PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) or the PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) homolog in rodents.

It will be understood that in a preferred embodiment, the cross-species specificity of the first and second binding domain of the antibodies of the invention is identical.

Prostate cancer is the second most cancer in men. For 2008, it is estimated that 186,320 men will be newly diagnosed with prostate cancer in the United States and about 28,660 men will die from the disease (see e.g. http://www.cancer.gov/cancertopics/types/prostate). Prostate cancer risk is strongly related to age: very few cases are registered in men under 50 and three-quarters of cases occur in men over 65 years. The largest number of cases is diagnosed in those aged 70-74. Currently, the growth rate of the older population is significantly higher than that of the total population. By 2025-2030, projections indicate that the population over 60 will be growing 3.5 times as rapidly as the total population. The proportion of older persons is projected to more than double worldwide over the next half century, which means that a further increase in incidence of diagnosed prostate cancer has to be expected. However, PSCA is not only a prostate cancer target. Rather, overexpression of PSCA has also been found in bladder cancer (Amara et al., Cancer Res 61 (2001): 4660-4665) and in pancreatic cancer (Argani et al., Cancer Res 61 (2001): 4320-4324). In light of the above, the PSCAxCD3 bispecific single chain antibody of the invention provides an advantageous tool in order to kill PSCA-expressing cancer cells of, including, but not limited to, prostate cancer, bladder cancer or pancreatic cancer in human. As shown in the following Examples, the cytotoxic activity of the PSCAxCD3 bispecific single chain antibody of the invention is higher than the cytotoxic activity of antibodies described in the art.

Advantageously, the present invention provides also PSCAxCD3 bispecific single chain antibodies comprising a second binding domain which binds both to the human PSCA and to the macaque PSCA homolog, i.e. the homolog of a non-chimpanzee primate. In a preferred embodiment, the bispecific single chain antibody thus comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate Prostate stem cell antigen (PSCA). In this case, the identical bispecific single chain antibody molecule can be used both for preclinical

evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drugs in humans. Put in other words, the same molecule can be used in preclinical animal studies as well as in clinical studies in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since both the CD3 and the PSCA binding domain of the PSCAxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates, it can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drugs in humans.

CD19 is a cell surface molecule expressed only by B lymphocytes and follicular dendritic cells of the hematopoietic system. It is the earliest of the B-lineage-restricted antigens to be expressed and is present on most pre-B cells and most non-T-cell acute lymphocytic leukemia cells and B-cell type chronic lymphocytic leukemia cells.

In a preferred embodiment, the bispecific single chain antibody of the invention comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate CD19. In this case, the identical bispecific single chain antibody molecule can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drug in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since in this embodiment both the CD3 and the CD19 binding domain of the CD19xCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates, it can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drug in humans.

As described herein above, the *MET* oncogene, encoding the receptor tyrosin kinase (RTK) for hepatocyte growth factor (HGF), and Scatter Factor (SF), controls genetic programs leading to cell growth, invasion, and protection from apoptosis. As shown in the following Examples, the C-METxCD3 bispecific single chain antibody of the invention thus provides an advantageous tool in order to kill C-MET-expressing

cancer cells, as exemplified by the human C-MET positive breast cancer cell line MDA-MB-231. The cytotoxic activity of the C-METxCD3 bispecific single chain antibody of the invention is higher than the cytotoxic activity of antibodies described in the art. Since preferably both the CD3 and the C-MET binding domain of the C-METxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates' antigens, the C-METxCD3 bispecific single chain antibody of the invention can be used for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drugs in humans.

Advantageously, the present invention provides in a further alternative embodiment C-METxCD3 bispecific single chain antibodies comprising a second binding domain which binds both to the human C-MET and to the macaque C-MET homolog, i.e. the homolog of a non-chimpanzee primate. In a preferred embodiment, the bispecific single chain antibody thus comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate C-MET. In this case, the identical bispecific single chain antibody molecule can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drugs in humans. Put in other words, the same molecule can be used in preclinical animal studies as well as in clinical studies in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since both the CD3 and the C-MET binding domain of the C-METxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates' antigens, it can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drugs in humans.

Angiogenesis, i.e. the formation of new capillaries, is essential to a number of important physiological events, both normal and pathological. Recently, increased attention has focused on the purification and characterization of inhibitors of this process, because of the potential therapeutic value of angiogenesis inhibitors in controlling solid tumors. Because of its restricted normal tissue distribution and abundant expression on tumor endothelial cells of many different types of solid

tumors, Endosialin can be used as a target for antibody-based anti-angiogenic treatment strategies of cancer. In particular, targeting of tumor endothelial cells instead of the cancer cells has the advantage that target expression on the untransformed endothelial cells of tumor blood vessels is more stable than target expression on the genetically unstable cancer cells. The EndosialinxCD3 bispecific single chain antibody of the invention provides an advantageous tool in order to inhibit the formation of new capillaries in solid tumors which plays a major role in supporting the growth of the tumors. In this novel and inventive therapeutic approach, it is not the tumor cells which are targeted but tumor blood vessels. The EndosialinxCD3 bispecific single chain antibody of the invention recruits cytotoxic T cells to the Endosialin-positive endothelial cells in tumors, including, but not limited to, carcinomas (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), sarcomas, and neuroectodermal tumors (melanoma, glioma, neuroblastoma), resulting in the depletion of the Endosialin-expressing endothelial cells from the tumor. In this way, tumor angegiogenesis is inhibited resulting in tumor regression or even depletion. As shown in the following Examples, the cytotoxic activity of the EndosialinxCD3 bispecific single chain antibody of the invention is higher than the activity of antibodies described in the art. Since the growth of solid neoplasms requires the recruitment of supporting blood vessels, the therapeutic use of the EndosialinxCD3 bispecific single chain antibody of the invention provides a novel and inventive approach for tumor endothelial targeting and killing.

Advantageously, the present invention provides also EndosialinxCD3 bispecific single chain antibodies comprising a second binding domain which binds both to the human Endosialin and to the macaque Endosialin homolog, i.e. the homolog of a non-chimpanzee primate. In a preferred embodiment, the bispecific single chain antibody thus comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate Endosialin. In this case, the identical bispecific single chain antibody molecule can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drug in humans. Put in other words, the same molecule can be used in preclinical animal studies as well as in clinical studies in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since both the CD3 and the

Endosialin binding domain of the EndosialinxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates, it can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drug in humans.

EpCAM has recently been found to be expressed on so called "cancer stem cells" (Dalerba et al., PNAS 104 (2007), 10158-63; Dalerba et al., Ann. Rev. Med. 58 (2007), 267-84). In light of this, the EpCAMxCD3 bispecific single chain antibody of the invention not only provides an advantageous tool in order to kill EpCAM-expressing cancer cells in epithelial cancer or minimal residual cancer, but may also be useful for the elimination of the presumed culprits responsible for tumor relapse after therapy. In addition, the cytotoxic activity of the EpCAMxCD3 bispecific single chain antibody of the invention is higher than the cytotoxic activity of antibodies described in the art.

In a preferred embodiment, the bispecific single chain antibody of the invention comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate EpCAM. In this case, the identical bispecific single chain antibody molecule can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drug in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since in this embodiment both the CD3 and the EpCAM binding domain of the EpCAMxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates, it can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drug in humans.

The FAPalphaxCD3 bispecific single chain antibody of the invention provides an advantageous tool in order to attack the stroma of solid tumors, such as epithelial tumors, which plays a major role in supporting the growth and neovascularisation of tumors. In this novel and inventive therapeutic approach, it is not the tumor cells which are targeted but activated stromal fibroblasts. Previous study have shown that

most of the common types of epithelial cancers, including more than 90% of primary and malignant breast, lung and colorectal carcinomas, contain abundant FAP alpha-reactive stromal fibroblasts (Scanlan et al., PNAS 91 (1994), 5657-5661 and references cited therein). In contrast, normal tissues and benign and premalignant epithelial lesions only rarely contain FAP alpha-positive stromal cells. The FAPalphaxCD3 bispecific single chain antibody of the invention recruits cytotoxic T cells to the FAP alpha-positive activated stromal fibroblasts in primary and malignant epithelial tumors resulting in the depletion of the stromal cells from the tumor. In particular, targeting of tumor stromal cells instead of the cancer cells has the advantage that target expression on the untransformed stromal cells is more stable than target expression on the genetically unstable cancer cells. As shown in the following Examples, the cytotoxic activity of the FAPalphaxCD3 bispecific single chain antibody of the invention is higher than the activity of antibodies described in the art. Since the growth of solid neoplasms requires the recruitment of a supporting stroma, the therapeutic use of the FAPalphaxCD3 bispecific single chain antibody of the invention provides a novel and inventive approach for tumor stromal targeting and killing.

Advantageously, the present invention provides also FAPalphaxCD3 bispecific single chain antibodies comprising a second binding domain which binds both to the human FAP alpha and to the macaque FAP alpha homolog, i.e. the homolog of a non-chimpanzee primate. In a preferred embodiment, the bispecific single chain antibody thus comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate FAP alpha. In this case, the identical bispecific single chain antibody molecule can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drugs in humans. Put in other words, the same molecule can be used in preclinical animal studies as well as in clinical studies in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since both the CD3 and the FAP alpha binding domain of the FAPalphaxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates, it can be used both for preclinical evaluation of safety, activity

and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drugs in humans.

As described herein above, IGF-1R is a receptor (and, thus a cell surface antigen) with tyrosine kinase activity having 70% homology with the insulin receptor 1R. IGF-1R is expressed in a great variety of tumors and of tumor lines and the IGFs amplify the tumor growth via their attachment to IGF-1R.

In a preferred embodiment, the bispecific single chain antibody of the invention comprises a second binding domain exhibiting cross-species specificity to the human and a non-chimpanzee primate IGF-1R. In this case, the identical bispecific single chain antibody molecule can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and as drug in humans. This leads to highly comparable results and a much-increased predictive power of the animal studies compared to species-specific surrogate molecules. Since in this embodiment both the CD3 and the IGF-1R binding domain of the IGF-1RxCD3 bispecific single chain antibody of the invention are cross-species specific, i.e. reactive with the human and non-chimpanzee primates, it can be used both for preclinical evaluation of safety, activity and/or pharmacokinetic profile of these binding domains in primates and – in the identical form - as drug in humans.

It has been found in the present invention that it is possible to generate a, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody wherein the identical molecule can be used in preclinical animal testing, as well as clinical studies and even in therapy in human. This is due to the unexpected identification of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody, which, in addition to binding to human CD3 epsilon and PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα), respectively, (and due to genetic similarity likely to the chimpanzee counterpart), also binds to the homologs of said antigens of non-chimpanzee primates, including New-World Monkeys and Old-

World Monkeys. As shown in the following Examples, said preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention can be used as therapeutic agent or drug against various diseases, including, but not limited, to cancer.

The PSCAxCD3 bispecific single chain antibody is particularly advantageous for the therapy of prostate cancer, bladder cancer or pancreatic cancer.

Said preferably human CD19xCD3 bispecific single chain antibody of the invention can be used as therapeutic agent against various diseases, including but not limited to cancer, preferably B-cell malignancies, such as non-Hodgkin Lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells.

Said preferably human c-METxCD3 bispecific single chain antibody of the invention can be used as therapeutic agent against various diseases, including but not limited to cancer, preferably carcinoma, sarcoma, glioblastoma/astrocytoma, melanoma, mesothelioma, Wilms tumor or a hematopoietic malignancy such as leukemia, lymphoma or multiple myeloma.

Said preferably human EndosialinxCD3 bispecific single chain antibody of the invention provides a novel and inventive approach for tumor endothelium targeting and killing for including (but not limited to) carcinomas (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), sarcomas, and neuroectodermal tumors (melanoma, glioma, neuroblastoma). The EndosialinxCD3 bispecific single chain antibody of the invention can deprive solid tumors of their supporting blood vessels, thereby inhibiting angiogenesis and consequently the growth of said neoplasms.

Said preferably human EpCAMxCD3 bispecific single chain antibody of the invention can be used as therapeutic agent against various diseases, including but not limited to cancer, preferably epthelial cancer.

Said preferably human IGF-1RxCD3 bispecific single chain antibody of the invention can be used as therapeutic agent against various diseases, including but not limited to cancer, preferably bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer. IGF-1RxCD3 bispecific single chain antibody of the invention can be used as therapeutic agent against autoimmune diseases, preferably psoriasis.

In view of the above, the need to construct a surrogate PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody for testing in a phylogenetic distant (from humans) species disappears. As a result, the identical molecule can be used in animal preclinical testing as is intended to be administered to humans in clinical testing as well as following market approval and therapeutic drug administration. The ability to use the same molecule for preclinical animal testing as in later administration to humans virtually eliminates, or at least greatly reduces, the danger that the data obtained in preclinical animal testing have limited applicability to the human case. In short, obtaining preclinical safety data in animals using the same molecule as will actually be administered to humans does much to ensure the applicability of the data to a human-relevant scenario. In contrast, in conventional approaches using surrogate molecules, said surrogate molecules have to be molecularly adapted to the animal test system used for preclinical safety assessment. Thus, the molecule to be used in human therapy in fact differs in sequence and also likely in structure from the surrogate molecule used in preclinical testing in pharmacokinetic parameters and/or biological activity, with the consequence that data obtained in preclinical animal testing have limited applicability / transferability to the human case. The use of surrogate molecules requires the construction, production, purification and characterization of a completely new construct. This leads to additional development costs and time necessary to obtain that molecule. In sum, surrogates have to be developed separately in addition to the actual drug to be used in human therapy, so that two lines of development for two molecules have to be carried out. Therefore, a major advantage of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention exhibiting cross-species specificity described herein is that the identical molecule can be used for therapeutics in humans and in preclinical animal testing.

It is preferred that at least one of said first or second binding domains of the bispecific single chain antibody of the invention is CDR-grafted, humanized or human, as set forth in more detail below. Preferably, both the first and second binding domains of the bispecific single chain antibody of the invention are CDR-grafted, humanized or human. For the preferably human, PSCAxCD3 (respectively CD19xCD3, C-

METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention, the generation of an immune reaction against said binding molecules is excluded to the maximum possible extent upon administration of the molecule to human patients.

Another major advantage of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention is its applicability for preclinical testing in various primates. The behavior of a drug candidate in animals should ideally be indicative of the expected behavior of this drug candidate upon administration to humans. As a result, the data obtained from such preclinical testing should therefore generally have a highly predictive power for the human case. However, as learned from the tragic outcome of the recent Phase I clinical trial on TGN1412 (a CD28 monoclonal antibody), a drug candidate may act differently in a primate species than in humans: Whereas in preclinical testing of said antibody no or only limited adverse effects have been observed in animal studies performed with cynomolgus monkeys, six human patients developed multiple organ failure upon administration of said antibody (Lancet 368 (2006), 2206-7). The results of these dramatic, non-desired negative events suggest that it may not be sufficient to limit preclinical testing to only one (non-chimpanzee primate) species. The fact that the PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention binds to a series of New-World and Old-World Monkeys may help to overcome the problems faced in the case mentioned above. Accordingly, the present invention provides means and methods for minimizing species differences in effects when drugs for human therapy are being developed and tested.

With the, preferably human, cross-species specific PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention it is also no longer necessary to adapt the test animal to the drug candidate intended for administration to humans, such as e.g. the creation of transgenic animals. The, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention

exhibiting cross-species specificity according to the uses and the methods of invention can be directly used for preclinical testing in non-chimpanzee primates, without any genetic manipulation of the animals. As well known to those skilled in the art, approaches in which the test animal is adapted to the drug candidate always bear the risk that the results obtained in the preclinical safety testing are less representative and predictive for humans due to the modification of the animal. For example, in transgenic animals, the proteins encoded by the transgenes are often highly over-expressed. Thus, data obtained for the biological activity of an antibody against this protein antigen may be limited in their predictive value for humans in which the protein is expressed at much lower, more physiological levels.

A further advantage of the uses of the preferably human PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention exhibiting cross-species specificity is the fact that chimpanzees as an endangered species are avoided for animal testing. Chimpanzees are the closest relatives to humans and were recently grouped into the family of hominids based on the genome sequencing data (Wildman et al., PNAS 100 (2003), 7181). Therefore, data obtained with chimpanzee is generally considered to be highly predictive for humans. However, due to their status as endangered species, the number of chimpanzees, which can be used for medical experiments, is highly restricted. As stated above, maintenance of chimpanzees for animal testing is therefore both costly and ethically problematic. The uses of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention avoid both ethical objections and financial burden during preclinical testing without prejudicing the quality, i.e. applicability, of the animal testing data obtained. In light of this, the uses of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention provide for a reasonable alternative for studies in chimpanzees.

A still further advantage of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention is the ability of extracting

multiple blood samples when using it as part of animal preclinical testing, for example in the course of pharmacokinetic animal studies. Multiple blood extractions can be much more readily obtained with a non-chimpanzee primate than with lower animals, e.g. a mouse. The extraction of multiple blood samples allows continuous testing of blood parameters for the determination of the biological effects induced by the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention. Furthermore, the extraction of multiple blood samples enables the researcher to evaluate the pharmacokinetic profile of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention as defined herein. In addition, potential side effects, which may be induced by said, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention reflected in blood parameters can be measured in different blood samples extracted during the course of the administration of said antibody. This allows the determination of the potential toxicity profile of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention as defined herein.

The advantages of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention as defined herein exhibiting cross-species specificity may be briefly summarized as follows:

First, the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention as defined herein used in preclinical testing is the same as the one used in human therapy. Thus, it is no longer necessary to develop two independent molecules, which may differ in their pharmacokinetic properties and biological activity. This is highly advantageous in that e.g. the pharmacokinetic results are more directly transferable and applicable to the human setting than e.g. in conventional surrogate approaches.

Second, the uses of the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention as defined herein for the preparation of therapeutics in human is less cost- and labor-intensive than surrogate approaches.

Third, the, preferably human, PSCAxCD3 (respectively CD19xCD3, C-METxCD3, EndosialinxCD3, EpCAMxCD3, IGF-1RxCD3 or FAPαxCD3) bispecific single chain antibody of the invention as defined herein can be used for preclinical testing not only in one primate species, but in a series of different primate species, thereby limiting the risk of potential species differences between primates and human.

Fourth, chimpanzee as an endangered species for animal testing can be avoided if desired.

Fifth, multiple blood samples can be extracted for extensive pharmacokinetic studies.

Sixth, due to the human origin of the, preferably human, binding molecules according to a preferred embodiment of the invention the generation of an immune reaction against said binding molecules is minimalized when administered to human patients. Induction of an immune response with antibodies specific for a drug candidate derived from a non-human species as e.g. a mouse leading to the development of human-anti-mouse antibodies (HAMAs) against therapeutic molecules of murine origin is excluded.

Last but not least:

- the therapeutic use of the PSCAxCD3 bispecific single chain antibody of the invention provides a novel and inventive therapeutic approach for cancer, including, but not limited to, prostate cancer, bladder cancer or pancreatic cancer. The following examples clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector cells against cells positive for PSCA.
- the therapeutic use of the CD19xCD3 bispecific single chain antibody of the invention provides a novel and inventive therapeutic approach for cancer, preferably B-cell malignancies, such as non-Hodgkin lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells. As shown in the following Examples, the cytotoxic activity of the CD19xCD3 bispecific single chain antibody of the invention is higher than the activity of antibodies described in the art.
- the therapeutic use of the C-METxCD3 bispecific single chain antibody of the invention provides a novel and inventive therapeutic approach for cancer,

preferably carcinoma, sarcoma, glioblastoma/astrocytoma, melanoma, mesothelioma, Wilms tumor or a hematopoietic malignancy such as leukemia, lymphoma or multiple myeloma. As shown in the following Examples, the cytotoxic activity of the C-METxCD3 bispecific single chain antibody of the invention is higher than the activity of antibodies described in the art.

- the therapeutic use of the EndosialinxCD3 bispecific single chain antibody of the invention provides a novel and inventive approach for tumor endothelium targeting and killing for including (but not limited to) carcinomas (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), sarcomas, and neuroectodermal tumors (melanoma, glioma, neuroblastoma). The EndosialinxCD3 bispecific single chain antibody of the invention can deprive solid tumors of their supporting blood vessels, thereby inhibiting angiogenesis and consequently the growth of said neoplasms.
- the therapeutic use of the EpCAMxCD3 bispecific single chain antibody of the invention provides a novel and inventive therapeutic approach for cancer, preferably epithelial cancer and/or a minimal residual cancer. The EpCAMxCD3 bispecific single chain antibody of the invention not only provides an advantageous tool in order to kill EpCAM-expressing cancer cells in cancer, preferably epithelial cancer or a minimal residual cancer, but may also be useful for the elimination of the presumed culprits responsible for tumor relapse after therapy. In addition, the cytotoxic activity of the EpCAMxCD3 bispecific single chain antibody of the invention is higher than the cytotoxic activity of antibodies described in the art.
- the therapeutic use of the FAPalphaxCD3 bispecific single chain antibody of the invention provides a novel and inventive approach for tumor stromal targeting and killing: The FAPalphaxCD3 bispecific single chain antibody of the invention deprives solid tumors, such as epithelial tumors, of their supporting stroma, thereby inhibiting the growth and neovascularisation of solid neoplasms.
- the therapeutic use of the IGF-1RxCD3 bispecific single chain antibody of the invention provides a novel and inventive approach for cancer (preferably bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer) or autoimmune diseases (preferably psoriasis).

As noted herein above, the present invention provides polypeptides, i.e. bispecific single chain antibodies, comprising a first binding domain capable of binding to an

epitope of human and non-chimpanzee primate CD3ε chain and a second binding domain capable of binding to PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα), wherein the second binding domain preferably also binds to PSCA (respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα) of a human and a non-chimpanzee primate. The advantage of bispecific single chain antibody molecules as drug candidates fulfilling the requirements of the preferred bispecific single chain antibody of the invention is the use of such molecules in preclinical animal testing as well as in clinical studies and even for therapy in human. In a preferred embodiment of the cross-species specific bispecific single chain antibodies of the invention the second binding domain binding to a cell surface antigen is human. In a cross-species specific bispecific molecule according to the invention the binding domain binding to an epitope of human and non-chimpanzee primate CD3 epsilon chain is located in the order VH-VL or VL-VH at the N-terminus or the C-terminus of the bispecific molecule. Examples for cross-species specific bispecific molecules according to the invention in different arrangements of the VH- and the VL-chain in the first and the second binding domain are described in the appended examples.

As used herein, a "bispecific single chain antibody" denotes a single polypeptide chain comprising two binding domains. Each binding domain comprises one variable region from an antibody heavy chain ("VH region"), wherein the VH region of the first binding domain specifically binds to the CD3ε molecule, and the VH region of the second binding domain specifically binds to PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα. The two binding domains are optionally linked to one another by a short polypeptide spacer. A non-limiting example for a polypeptide spacer is Gly-Gly-Gly-Gly-Ser (G-G-G-G-S) and repeats thereof. Each binding domain may additionally comprise one variable region from an antibody light chain ("VL region"), the VH region and VL region within each of the first and second binding domains being linked to one another via a polypeptide linker, for example of the type disclosed and claimed in EP 623679 B1, but in any case long enough to allow the VH region and VL region of the first binding domain and the VH region and VL region of the second binding domain to pair with one another such that, together, they are able to specifically bind to the respective first and second binding domains.

The term "protein" is well known in the art and describes biological compounds. Proteins comprise one or more amino acid chains (polypeptides), whereby the amino acids are bound among one another via a peptide bond. The term "polypeptide" as used herein describes a group of molecules, which consists of more than 30 amino acids. In accordance with the invention, the group of polypeptides comprises "proteins" as long as the proteins consist of a single polypeptide chain. Also in line with the definition the term "polypeptide" describes fragments of proteins as long as these fragments consist of more than 30 amino acids. Polypeptides may further form multimers such as dimers, trimers and higher oligomers, i.e. consisting of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding higher order structures of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a hereteromultimer is an antibody molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms "polypeptide" and "protein" also refer to naturally modified polypeptides/proteins wherein the modification is effected e.g. by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. Such modifications are well known in the art.

The term "binding domain" characterizes in connection with the present invention a domain of a polypeptide which specifically binds to/interacts with a given target structure/antigen/epitope. Thus, the binding domain is an "antigen-interaction-site". The term "antigen-interaction-site" defines, in accordance with the present invention, a motif of a polypeptide, which is able to specifically interact with a specific antigen or a specific group of antigens, e.g. the identical antigen in different species. Said binding/interaction is also understood to define a "specific recognition". The term "specifically recognizing" means in accordance with this invention that the antibody molecule is capable of specifically interacting with and/or binding to at least two, preferably at least three, more preferably at least four amino acids of an antigen, e.g. the human CD3 antigen as defined herein. Such binding may be exemplified by the specificity of a "lock-and-key-principle". Thus, specific motifs in the amino acid sequence of the binding domain and the antigen bind to each other as a result of their primary, secondary or tertiary structure as well as the result of secondary modifications of said structure. The specific interaction of the antigen-interaction-site

with its specific antigen may result as well in a simple binding of said site to the antigen. Moreover, the specific interaction of the binding domain/antigen-interaction-site with its specific antigen may alternatively result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc. A preferred example of a binding domain in line with the present invention is an antibody. The binding domain may be a monoclonal or polyclonal antibody or derived from a monoclonal or polyclonal antibody.

The term "antibody" comprises derivatives or functional fragments thereof which still retain the binding specificity. Techniques for the production of antibodies are well known in the art and described, e.g. in Harlow and Lane "Antibodies, A Laboratory Manual", Cold Spring Harbor Laboratory Press, 1988 and Harlow and Lane "Using Antibodies: A Laboratory Manual" Cold Spring Harbor Laboratory Press, 1999. The term "antibody" also comprises immunoglobulins (Ig's) of different classes (i.e. IgA, IgG, IgM, IgD and IgE) and subclasses (such as IgG1, IgG2 etc.).

The definition of the term "antibody" also includes embodiments such as chimeric, single chain and humanized antibodies, as well as antibody fragments, like, inter alia, Fab fragments. Antibody fragments or derivatives further comprise $F(ab')_2$, Fv, scFv fragments or single domain antibodies, single variable domain antibodies or immunoglobulin single variable domain comprising merely one variable domain, which might be VH or VL, that specifically bind to an antigen or epitope independently of other V regions or domains; see, for example, Harlow and Lane (1988) and (1999), loc. cit. Such immunoglobulin single variable domain encompasses not only an isolated antibody single variable domain polypeptide, but also larger polypeptides that comprise one or more monomers of an antibody single variable domain polypeptide sequence.

Various procedures are known in the art and may be used for the production of such antibodies and/or fragments. Thus, the (antibody) derivatives can also be produced by peptidomimetics. Further, techniques described for the production of single chain antibodies (see, inter alia, US Patent 4,946,778) can be adapted to produce single chain antibodies specific for elected polypeptide(s). Also, transgenic animals may be used to express humanized antibodies specific for polypeptides and fusion proteins of this invention. For the preparation of monoclonal antibodies, any technique, providing antibodies produced by continuous cell line cultures can be used.

Examples for such techniques include the hybridoma technique (Köhler and Milstein Nature 256 (1975), 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96). Surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of a target polypeptide, such as CD3 epsilon, PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13). It is also envisaged in the context of this invention that the term "antibody" comprises antibody constructs, which may be expressed in a host as described herein below, e.g. antibody constructs which may be transfected and/or transduced via, inter alia, viruses or plasmid vectors.

The term "specific interaction" as used in accordance with the present invention means that the binding domain does not or does not significantly cross-react with polypeptides which have similar structure as those bound by the binding domain, and which might be expressed by the same cells as the polypeptide of interest. Cross-reactivity of a panel of binding domains under investigation may be tested, for example, by assessing binding of said panel of binding domains under conventional conditions (see, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1988 and Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1999). Examples for the specific interaction of a binding domain with a specific antigen comprise the specificity of a ligand for its receptor. Said definition particularly comprises the interaction of ligands, which induce a signal upon binding to its specific receptor. Examples for said interaction, which is also particularly comprised by said definition, is the interaction of an antigenic determinant (epitope) with the binding domain (antigenic binding site) of an antibody.

The term "cross-species specificity" or "interspecies specificity" as used herein means binding of a binding domain described herein to the same target molecule in humans and non-chimpanzee primates. Thus, "cross-species specificity" or "interspecies specificity" is to be understood as an interspecies reactivity to the same

molecule "X" (i.e. the homolog) expressed in different species, but not to a molecule other than "X". Cross-species specificity of a monoclonal antibody recognizing e.g. human CD3 epsilon, to a non-chimpanzee primate CD3 epsilon, e.g. macaque CD3 epsilon, can be determined, for instance, by FACS analysis. The FACS analysis is carried out in a way that the respective monoclonal antibody is tested for binding to human and non-chimpanzee primate cells, e.g. macaque cells, expressing said human and non-chimpanzee primate CD3 epsilon antigens, respectively. An appropriate assay is shown in the following examples. The above-mentioned subject matter applies mutatis mutandis for the PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R and FAPα antigen: Cross-species specificity of a monoclonal antibody recognizing e.g. human PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, to a non-chimpanzee primate PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, e.g. macaque PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, can be determined, for instance, by FACS analysis. The FACS analysis is carried out in a way that the respective monoclonal antibody is tested for binding to human and non-chimpanzee primate cells, e.g. macaque cells, expressing said human and non-chimpanzee primate PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα antigens, respectively.

As used herein, CD3 epsilon denotes a molecule expressed as part of the T cell receptor and has the meaning as typically ascribed to it in the prior art. In human, it encompasses in individual or independently combined form all known CD3 subunits, for example CD3 epsilon, CD3 delta, CD3 gamma, CD3 zeta, CD3 alpha and CD3 beta. The non-chimpanzee primate, non-human CD3 antigens as referred to herein are, for example, *Macaca fascicularis* CD3 and *Macaca mulatta* CD3. In *Macaca fascicularis*, it encompasses CD3 epsilon FN-18 negative and CD3 epsilon FN-18 positive, CD3 gamma and CD3 delta. In *Macaca mulatta*, it encompasses CD3 epsilon, CD3 gamma and CD3 delta. Preferably, said CD3 as used herein is CD3 epsilon.

The human CD3 epsilon is indicated in GenBank Accession No.NM_000733 and comprises SEQ ID NO. 1. The human CD3 gamma is indicated in GenBank Accession NO. NM_000073. The human CD3 delta is indicated in GenBank Accession No. NM_000732.

The CD3 epsilon "FN-18 negative" of *Macaca fascicularis* (i.e. CD3 epsilon not

recognized by monoclonal antibody FN-18 due to a polymorphism as set forth above) is indicated in GenBank Accession No. AB073994.

The CD3 epsilon "FN-18 positive" of *Macaca fascicularis* (i.e. CD3 epsilon recognized by monoclonal antibody FN-18) is indicated in GenBank Accession No. AB073993. The CD3 gamma of *Macaca fascicularis* is indicated in GenBank Accession No. AB073992. The CD3 delta of *Macaca fascicularis* is indicated in GenBank Accession No. AB073991.

The nucleic acid sequences and amino acid sequences of the respective CD3 epsilon, gamma and delta homologs of *Macaca mulatta* can be identified and isolated by recombinant techniques described in the art (Sambrook et al. Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press, 3rd edition 2001). This applies mutatis mutandis to the CD3 epsilon, gamma and delta homologs of other non-chimpanzee primates as defined herein. The identification of the amino acid sequence of Callithrix jacchus, Saimiri sciureus und Saguinus oedipus is described in the appended examples. The amino acid sequence of the extracellular domain of the CD3 epsilon of *Callithrix jacchus* is depicted in SEQ ID NO: 3, the one of *Saguinus oedipus* is depicted in SEQ ID NO: 5 and the one of *Saimiri sciureus* is depicted in SEQ ID NO: 7.

The human PSCA is indicated in GenBank Accession No.NM_005672. The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 444 and 443, respectively. The cloning of the PSCA homolog of macaque is demonstrated in the following examples, the corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 446 and 445, respectively.

The human CD19 is indicated in GenBank Accession No. NM_001770. On the basis of this sequence information it is possible for the person skilled in the art without any inventive ado to clone (and express) the macaque CD19 molecule. For example, the human CD19 cDNA or a fragment thereof indicated in GenBank Accession No. NM_001770 can be used as a hybridization probe in order to screen a macaque cDNA library (e.g. a cDNA library of Cynomolgus monkey or Rhesus monkey) under appropriate hybridization conditions. Recombinant techniques and screening methods (including hybridization approaches) in molecular biology are described e.g. in Sambrook et al. Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press, 3rd edition 2001.

The human C-MET is indicated in GenBank Accession No.NM_000245. The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 776 and 777, respectively. The cloning of the C-MET homolog of macaque is demonstrated in the following examples, the corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 788 and 789, respectively.

The human Endosialin is indicated in GenBank Accession No. NM_020404. The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 913 and 914, respectively. The cloning of the Endosialin homolog of macaque is demonstrated in the following examples, the corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 915 and 916, respectively.

The human EpCAM is indicated in GenBank Accession No. NM_002354. The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 1029 and 1028, respectively. As demonstrated in the following examples, the second binding domain of the EpCAMxCD3 bispecific single chain antibody of the invention binds to an epitope localized in amino acid residues 26 to 61 of the EGF-like domain 1 of EpCAM which is encoded by Exon 2 of the EpCAM gene. Said amino acids residues 26 to 61 of the EGF-like domain 1 of human EpCAM are shown in SEQ ID NO. 1130. On the basis of this sequence information it is possible for the person skilled in the art without any inventive ado to clone (and express) the macaque EpCAM molecule. For example, the human EpCAM cDNA or a fragment thereof indicated in GenBank Accession No. NM_002354 can be used as a hybridization probe in order to screen a macaque cDNA library (e.g. a cDNA library of Cynomolgus monkey or Rhesus monkey) under appropriate hybridization conditions. Recombinant techniques and screening methods (including hybridization approaches) in molecular biology are described e.g. in Sambrook et al. Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press, 3rd edition 2001.

The human FAP alpha is indicated in GenBank Accession No. NM_004460. The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 1149 and 1150, respectively. The cloning of the FAP alpha homolog of macaque is demonstrated in the following examples, the corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 1151 and 1152, respectively.

The human IGF-1R is indicated in GenBank Accession No. NM_000875. The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 1988 and 1989, respectively. The coding sequence of macaque IGF-1R as published in

GenBank (Accession number XM_001100407). The corresponding cDNA and amino acid sequences are shown in SEQ ID NOs. 1998 and 1999, respectively.

In line with the above, the term "epitope" defines an antigenic determinant, which is specifically bound/identified by a binding domain as defined herein. The binding domain may specifically bind to/interact with conformational or continuous epitopes, which are unique for the target structure, e.g. the human and non-chimpanzee primate CD3 epsilon chain or the human and non-chimpanzee primate PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα. A conformational or discontinuous epitope is characterized for polypeptide antigens by the presence of two or more discrete amino acid residues which are separated in the primary sequence, but come together on the surface of the molecule when the polypeptide folds into the native protein/antigen (Sela, (1969) Science 166, 1365 and Laver, (1990) Cell 61, 553-6). The two or more discrete amino acid residues contributing to the epitope are present on separate sections of one or more polypeptide chain(s). These residues come together on the surface of the molecule when the polypeptide chain(s) fold(s) into a three-dimensional structure to constitute the epitope. In contrast, a continuous or linear epitope consists of two or more discrete amino acid residues, which are present in a single linear segment of a polypeptide chain. Within the present invention, a "context-dependent" CD3 epitope refers to the conformation of said epitope. Such a context-dependent epitope, localized on the epsilon chain of CD3, can only develop its correct conformation if it is embedded within the rest of the epsilon chain and held in the right position by heterodimerization of the epsilon chain with either CD3 gamma or delta chain. In contrast, a context-independent CD3 epitope as provided herein refers to an N-terminal 1-27 amino acid residue polypeptide or a functional fragment thereof of CD3 epsilon. This N-terminal 1-27 amino acid residue polypeptide or a functional fragment thereof maintains its three-dimensional structural integrity and correct conformation when taken out of its native environment in the CD3 complex. The context-independency of the N-terminal 1-27 amino acid residue polypeptide or a functional fragment thereof, which is part of the extracellular domain of CD3 epsilon, represents, thus, an epitope which is completely different to the epitopes of CD3 epsilon described in connection with a method for the preparation of human binding molecules in WO 2004/106380. Said method used solely expressed recombinant CD3 epsilon. The conformation of this solely

expressed recombinant CD3 epsilon differed from that adopted in its natural form, that is, the form in which the CD3 epsilon subunit of the TCR/CD3 complex exists as part of a noncovalent complex with either the CD3 delta or the CD3-gamma subunit of the TCR/CD3 complex. When such solely expressed recombinant CD3 epsilon protein is used as an antigen for selection of antibodies from an antibody library, antibodies specific for this antigen are identified from the library although such a library does not contain antibodies with specificity for self-antigens/autoantigens. This is due to the fact that solely expressed recombinant CD3 epsilon protein does not exist in vivo; it is not an autoantigen. Consequently, subpopulations of B cells expressing antibodies specific for this protein have not been depleted in vivo; an antibody library constructed from such B cells would contain genetic material for antibodies specific for solely expressed recombinant CD3 epsilon protein.

However, since the context-independent N-terminal 1-27 amino acid residue polypeptide or a functional fragment thereof is an epitope, which folds in its native form, binding domains in line with the present invention cannot be identified by methods based on the approach described in WO 2004/106380. Therefore, it could be verified in tests that binding molecules as disclosed in WO 2004/106380 are not capable of binding to the N-terminal 1-27 amino acid residues of the CD3 epsilon chain. Hence, conventional anti-CD3 binding molecules or anti-CD3 antibody molecules (e.g. as disclosed in WO 99/54440) bind CD3 epsilon chain at a position which is more C-terminally located than the context-independent N-terminal 1-27 amino acid residue polypeptide or a functional fragment provided herein. Prior art antibody molecules OKT3 and UCHT-1 have also a specificity for the epsilon-subunit of the TCR/CD3 complex between amino acid residues 35 to 85 and, accordingly, the epitope of these antibodies is also more C-terminally located. In addition, UCHT-1 binds to the CD3 epsilon chain in a region between amino acid residues 43 to 77 (Tunnacliffe, Int. Immunol. 1 (1989), 546-50; Kjer-Nielsen, PNAS 101, (2004), 7675-7680; Salmeron, J. Immunol. 147 (1991), 3047-52). Therefore, prior art anti-CD3 molecules do not bind to and are not directed against the herein defined context-independent N-terminal 1-27 amino acid residue epitope (or a functional fragment thereof). In particular, the state of the art fails to provide anti-CD3 molecules which specifically binds to the context-independent N-terminal 1-27 amino acid residue epitope and which are cross-species specific, i.e. bind to human and non-chimpanzee primate CD3 epsilon.

For the generation of a, preferably human, binding domain comprised in a bispecific single chain antibody molecule of the invention, e.g. monoclonal antibodies binding to both the human and non-chimpanzee primate CD3 epsilon (e.g. macaque CD3 epsilon) or monoclonal antibodies binding to the human and/or non-chimpanzee primate PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, can be used.

As used herein, "human" and "man" refers to the species *Homo sapiens*. As far as the medical uses of the constructs described herein are concerned, human patients are to be treated with the same molecule.

It is preferred that at least one of said first or second binding domains of the bispecific single chain antibody of the invention is CDR-grafted, humanized or human. Preferably, both the first and second binding domains of the bispecific single chain antibody of the invention are CDR-grafted, humanized or human.
The term "human" antibody as used herein is to be understood as meaning that the bispecific single chain antibody as defined herein, comprises (an) amino acid sequence(s) contained in the human germline antibody repertoire. For the purposes of definition herein, said bispecific single chain antibody may therefore be considered human if it consists of such (a) human germline amino acid sequence(s), i.e. if the amino acid sequence(s) of the bispecific single chain antibody in question is (are) identical to (an) expressed human germline amino acid sequence(s). A bispecific single chain antibody as defined herein may also be regarded as human if it consists of (a) sequence(s) that deviate(s) from its (their) closest human germline sequence(s) by no more than would be expected due to the imprint of somatic hypermutation. Additionally, the antibodies of many non-human mammals, for example rodents such as mice and rats, comprise VH CDR3 amino acid sequences which one may expect to exist in the expressed human antibody repertoire as well. Any such sequence(s) of human or non-human origin which may be expected to exist in the expressed human repertoire would also be considered "human" for the purposes of the present invention.

As used herein, the term "humanized", "humanization", "human-like" or grammatically related variants thereof are used interchangeably to refer to a bispecific single chain antibody comprising in at least one of its binding domains at least one complementarity determining region ("CDR") from a non-human antibody or fragment thereof. Humanization approaches are described for example in WO 91/09968 and US 6,407,213. As non-limiting examples, the term encompasses the case in which a variable region of at least one binding domain comprises a single CDR region, for example the third CDR region of the VH (CDRH3), from another non-human animal, for example a rodent, as well as the case in which a or both variable region/s comprise at each of their respective first, second and third CDRs the CDRs from said non-human animal. In the event that all CDRs of a binding domain of the bispecific single chain antibody have been replaced by their corresponding equivalents from, for example, a rodent, one typically speaks of "CDR-grafting", and this term is to be understood as being encompassed by the term "humanized" or grammatically related variants thereof as used herein. The term "humanized" or grammatically related variants thereof also encompasses cases in which, in addition to replacement of one or more CDR regions within a VH and/or VL of the first and/or second binding domain further mutation/s (e.g. substitutions) of at least one single amino acid residue/s within the framework ("FR") regions between the CDRs has/have been effected such that the amino acids at that/those positions correspond/s to the amino acid/s at that/those position/s in the animal from which the CDR regions used for replacement is/are derived. As is known in the art, such individual mutations are often made in the framework regions following CDR-grafting in order to restore the original binding affinity of the non-human antibody used as a CDR-donor for its target molecule. The term "humanized" may further encompass (an) amino acid substitution(s) in the CDR regions from a non-human animal to the amino acid(s) of a corresponding CDR region from a human antibody, in addition to the amino acid substitutions in the framework regions as described above.

As used herein, the term "homolog" or "homology" is to be understood as follows: Homology among proteins and DNA is often concluded on the basis of sequence similarity, especially in bioinformatics. For example, in general, if two or more genes have highly similar DNA sequences, it is likely that they are homologous. But sequence similarity may arise from different ancestors: short sequences may be similar by chance, and sequences may be similar because both were selected to bind

to a particular protein, such as a transcription factor. Such sequences are similar but not homologous. Sequence regions that are homologous are also called conserved. This is not to be confused with conservation in amino acid sequences in which the amino acid at a specific position has changed but the physio-chemical properties of the amino acid remain unchanged. Homologous sequences are of two types: orthologous and paralogous. Homologous sequences are orthologous if they were separated by a speciation event: when a species diverges into two separate species, the divergent copies of a single gene in the resulting species are said to be orthologous. Orthologs, or orthologous genes, are genes in different species that are similar to each other because they originated from a common ancestor. The strongest evidence that two similar genes are orthologous is the result of a phylogenetic analysis of the gene lineage. Genes that are found within one clade are orthologs, descended from a common ancestor. Orthologs often, but not always, have the same function. Orthologous sequences provide useful information in taxonomic classification studies of organisms. The pattern of genetic divergence can be used to trace the relatedness of organisms. Two organisms that are very closely related are likely to display very similar DNA sequences between two orthologs. Conversely, an organism that is further removed evolutionarily from another organism is likely to display a greater divergence in the sequence of the orthologs being studied. Homologous sequences are paralogous if they were separated by a gene duplication event: if a gene in an organism is duplicated to occupy two different positions in the same genome, then the two copies are paralogous. A set of sequences that are paralogous are called paralogs of each other. Paralogs typically have the same or similar function, but sometimes do not: due to lack of the original selective pressure upon one copy of the duplicated gene, this copy is free to mutate and acquire new functions. An example can be found in rodents such as rats and mice. Rodents have a pair of paralogous insulin genes, although it is unclear if any divergence in function has occurred. Paralogous genes often belong to the same species, but this is not necessary: for example, the hemoglobin gene of humans and the myoglobin gene of chimpanzees are paralogs. This is a common problem in bioinformatics: when genomes of different species have been sequenced and homologous genes have been found, one can not immediately conclude that these genes have the same or similar function, as they could be paralogs whose function has diverged.

As used herein, a "non-chimpanzee primate" or "non-chimp primate" or grammatical variants thereof refers to any primate animal (i.e. not human) other than chimpanzee, i.e. other than an animal of belonging to the genus *Pan*, and including the species *Pan paniscus* and *Pan troglodytes*, also known as *Anthropopithecus troglodytes* or *Simia satyrus*. It will be understood, however, that it is possible that the antibodies of the invention can also bind with their first and/or second binding domain to the respective epitopes/fragments etc. of said chimpanzees. The intention is merely to avoid animal tests which are carried out with chimpanzees, if desired. It is thus also envisaged that in another embodiment the antibodies of the present invention also bind with their first and/or second binding domain to the respective epitopes of chimpanzees. A "primate", "primate species", "primates" or grammatical variants thereof denote/s an order of eutherian mammals divided into the two suborders of prosimians and anthropoids and comprising apes, monkeys and lemurs. Specifically, "primates" as used herein comprises the suborder *Strepsirrhini* (non-tarsier prosimians), including the infraorder *Lemuriformes* (itself including the superfamilies *Cheirogaleoidea* and *Lemuroidea*), the infraorder *Chiromyiformes* (itself including the family *Daubentoniidae*) and the infraorder *Lorisiformes* (itself including the families *Lorisidae* and *Galagidae*). "Primates" as used herein also comprises the suborder *Haplorrhini*, including the infraorder *Tarsiiformes* (itself including the family *Tarsiidae*), the infraorder *Simiiformes* (itself including the *Platyrrhini*, or New-World monkeys, and the *Catarrhini*, including the *Cercopithecidea*, or Old-World Monkeys).

The non-chimpanzee primate species may be understood within the meaning of the invention to be a lemur, a tarsier, a gibbon, a marmoset (belonging to New-World Monkeys of the family *Cebidae*) or an Old-World Monkey (belonging to the superfamily *Cercopithecoidea*).

As used herein, an "Old-World Monkey" comprises any monkey falling in the superfamily *Cercopithecoidea*, itself subdivided into the families: the *Cercopithecinae*, which are mainly African but include the diverse genus of macaques which are Asian and North African; and the *Colobinae*, which include most of the Asian genera but also the African colobus monkeys.
Specifically, within the subfamily *Cercopithecinae*, an advantageous non-chimpanzee primate may be from the Tribe *Cercopithecini*, within the genus *Allenopithecus*

(Allen's Swamp Monkey, *Allenopithecus nigroviridis*); within the genus *Miopithecus* (Angolan Talapoin, *Miopithecus talapoin*; Gabon Talapoin, *Miopithecus ogouensis*); within the genus *Erythrocebus* (Patas Monkey, *Erythrocebus patas*); within the genus *Chlorocebus* (Green Monkey, *Chlorocebus sabaceus*; Grivet, *Chlorocebus aethiops*; Bale Mountains Vervet, *Chlorocebus djamdjamensis*; Tantalus Monkey, *Chlorocebus tantalus*; Vervet Monkey, *Chlorocebus pygerythrus*; Malbrouck, *Chlorocebus cynosuros*); or within the genus *Cercopithecus* (Dryas Monkey or Salongo Monkey, *Cercopithecus dryas*; Diana Monkey, *Cercopithecus diana*; Roloway Monkey, *Cercopithecus roloway*; Greater Spot-nosed Monkey, *Cercopithecus nictitans*; Blue Monkey, *Cercopithecus mitis*; Silver Monkey, *Cercopithecus doggetti*; Golden Monkey, *Cercopithecus kandti*; Sykes's Monkey, *Cercopithecus albogularis*; Mona Monkey, *Cercopithecus mona*; Campbell's Mona Monkey, *Cercopithecus campbelli*; Lowe's Mona Monkey, *Cercopithecus lowei*; Crested Mona Monkey, *Cercopithecus pogonias*; Wolf's Mona Monkey, *Cercopithecus wolfi*; Dent's Mona Monkey, *Cercopithecus denti*; Lesser Spot-nosed Monkey, *Cercopithecus petaurista*; White-throated Guenon, *Cercopithecus erythrogaster*; Sclater's Guenon, *Cercopithecus sclateri*; Red-eared Guenon, *Cercopithecus erythrotis*; Moustached Guenon, *Cercopithecus cephus*; Red-tailed Monkey, *Cercopithecus ascanius*; L'Hoest's Monkey, *Cercopithecus lhoesti*; Preuss's Monkey, *Cercopithecus preussi*; Sun-tailed Monkey, *Cercopithecus solatus*; Hamlyn's Monkey or Owl-faced Monkey, *Cercopithecus hamlyni*; De Brazza's Monkey, *Cercopithecus neglectus*).

Alternatively, an advantageous non-chimpanzee primate, also within the subfamily *Cercopithecinae* but within the Tribe *Papionini*, may be from within the genus *Macaca* (Barbary Macaque, *Macaca sylvanus*; Lion-tailed Macaque, *Macaca silenus*; Southern Pig-tailed Macaque or Beruk, *Macaca nemestrina*; Northern Pig-tailed Macaque, *Macaca leonina*; Pagai Island Macaque or Bokkoi, *Macaca pagensis*; Siberut Macaque, *Macaca siberu*; Moor Macaque, *Macaca maura*; Booted Macaque, *Macaca ochreata*; Tonkean Macaque, *Macaca tonkeana*; Heck's Macaque, *Macaca hecki*; Gorontalo Macaque, *Macaca nigriscens*; Celebes Crested Macaque or Black "Ape", *Macaca nigra*; Cynomolgus monkey or Crab-eating Macaque or Long-tailed Macaque or Kera, *Macaca fascicularis*; Stump-tailed Macaque or Bear Macaque, *Macaca arctoides*; Rhesus Macaque, *Macaca mulatta*; Formosan Rock Macaque, *Macaca cyclopis*; Japanese Macaque, *Macaca fuscata*; Toque Macaque, *Macaca sinica*; Bonnet Macaque, *Macaca radiata*; Barbary Macaque, *Macaca sylvanmus*;

Assam Macaque, *Macaca assamensis*; Tibetan Macaque or Milne-Edwards' Macaque, *Macaca thibetana*; Arunachal Macaque or Munzala, *Macaca munzala*); within the genus *Lophocebus* (Gray-cheeked Mangabey, *Lophocebus albigena*; *Lophocebus albigena albigena*; *Lophocebus albigena osmani*; *Lophocebus albigena johnstoni*; Black Crested Mangabey, *Lophocebus aterrimus*; Opdenbosch's Mangabey, *Lophocebus opdenboschi*; Highland Mangabey, *Lophocebus kipunji*); within the genus *Papio* (Hamadryas Baboon, *Papio hamadryas*; Guinea Baboon, *Papio papio*; Olive Baboon, *Papio anubis*; Yellow Baboon, *Papio cynocephalus*; Chacma Baboon, *Papio ursinus*); within the genus *Theropithecus* (Gelada, *Theropithecus gelada*); within the genus *Cercocebus* (Sooty Mangabey, *Cercocebus atys*; *Cercocebus atys atys*; *Cercocebus atys lunulatus*; Collared Mangabey, *Cercocebus torquatus*; Agile Mangabey, *Cercocebus agilis*; Golden-bellied Mangabey, *Cercocebus chrysogaster*; Tana River Mangabey, *Cercocebus galeritus*; Sanje Mangabey, *Cercocebus sanjei*); or within the genus *Mandrillus* (Mandrill, *Mandrillus sphinx*; Drill, *Mandrillus leucophaeus*).

Most preferred is *Macaca fascicularis* (also known as Cynomolgus monkey and, therefore, in the Examples named "Cynomolgus") and *Macaca mulatta* (rhesus monkey, named "rhesus").

Within the subfamily *Colobinae*, an advantageous non-chimpanzee primate may be from the African group, within the genus *Colobus* (Black Colobus, *Colobus satanas*; Angola Colobus, *Colobus angolensis*; King Colobus, *Colobus polykomos*; Ursine Colobus, *Colobus vellerosus*; Mantled Guereza, *Colobus guereza*); within the genus *Piliocolobus* (Western Red Colobus, *Piliocolobus badius*; *Piliocolobus badius badius*; *Piliocolobus badius temminckii*; *Piliocolobus badius waldronae*; Pennant's Colobus, *Piliocolobus pennantii*; *Piliocolobus pennantii pennantii*; *Piliocolobus pennantii epieni*; *Piliocolobus pennantii bouvieri*; Preuss's Red Colobus, *Piliocolobus preussi*; Thollon's Red Colobus, *Piliocolobus tholloni*; Central African Red Colobus, *Piliocolobus foai*; *Piliocolobus foai foai*; *Piliocolobus foai ellioti*; *Piliocolobus foai oustaleti*; *Piliocolobus foai semlikiensis*; *Piliocolobus foai parmentierorum*; Ugandan Red Colobus, *Piliocolobus tephrosceles*; Uzyngwa Red Colobus, *Piliocolobus gordonorum*; Zanzibar Red Colobus, *Piliocolobus kirkii*; Tana River Red Colobus, *Piliocolobus rufomitratus*); or within the genus *Procolobus* (Olive Colobus, *Procolobus verus*).

Within the subfamily *Colobinae*, an advantageous non-chimpanzee primate may alternatively be from the Langur (leaf monkey) group, within the genus

Semnopithecus (Nepal Gray Langur, *Semnopithecus schistaceus*; Kashmir Gray Langur, *Semnopithecus ajax*; Tarai Gray Langur, *Semnopithecus hector*; Northern Plains Gray Langur, *Semnopithecus entellus*; Black-footed Gray Langur, *Semnopithecus hypoleucos*; Southern Plains Gray Langur, *Semnopithecus dussumieri*; Tufted Gray Langur, *Semnopithecus priam*); within the *T. vetulus* group or the genus *Trachypithecus* (Purple-faced Langur, *Trachypithecus vetulus*; Nilgiri Langur, *Trachypithecus johnii*); within the *T. cristatus* group of the genus *Trachypithecus* (Javan Lutung, *Trachypithecus auratus*; Silvery Leaf Monkey or Silvery Lutung, *Trachypithecus cristatus*; Indochinese Lutung, *Trachypithecus germaini*; Tenasserim Lutung, *Trachypithecus barbei*); within the *T. obscurus* group of the genus *Trachypithecus* (Dusky Leaf Monkey or Spectacled Leaf Monkey, *Trachypithecus obscurus*; Phayre's Leaf Monkey, *Trachypithecus phayrei*); within the *T. pileatus* group of the genus *Trachypithecus* (Capped Langur, *Trachypithecus pileatus*; Shortridge's Langur, *Trachypithecus shortridgei*; Gee's Golden Langur, *Trachypithecus geei*); within the *T. francoisi* group of the genus *Trachypithecus* (Francois' Langur, *Trachypithecus francoisi*; Hatinh Langur, *Trachypithecus hatinhensis*; White-headed Langur, *Trachypithecus poliocephalus*; Laotian Langur, *Trachypithecus laotum*; Delacour's Langur, *Trachypithecus delacouri*; Indochinese Black Langur, *Trachypithecus ebenus*); or within the genus *Presbytis* (Sumatran Surili, *Presbytis melalophos*; Banded Surili, *Presbytis femoralis*; Sarawak Surili, *Presbytis chrysomelas*; White-thighed Surili, *Presbytis siamensis*; White-fronted Surili, *Presbytis frontata*; Javan Surili, *Presbytis comata*; Thomas's Langur, *Presbytis thomasi*; Hose's Langur, *Presbytis hosei*; Maroon Leaf Monkey, *Presbytis rubicunda*; Mentawai Langur or Joja, *Presbytis potenziani*; Natuna Island Surili, *Presbytis natunae*).

Within the subfamily *Colobinae*, an advantageous non-chimpanzee primate may alternatively be from the Odd-Nosed group, within the genus *Pygathrix* (Red-shanked Douc, *Pygathrix nemaeus*; Black-shanked Douc, *Pygathrix nigripes*; Gray-shanked Douc, *Pygathrix cinerea*); within the genus *Rhinopithecus* (Golden Snub-nosed Monkey, *Rhinopithecus roxellana*; Black Snub-nosed Monkey, *Rhinopithecus bieti*; Gray Snub-nosed Monkey, *Rhinopithecus brelichi*; Tonkin Snub-nosed Langur, *Rhinopithecus avunculus*); within the genus *Nasalis* (Proboscis Monkey, *Nasalis larvatus*); or within the genus *Simias* (Pig-tailed Langur, *Simias concolor*).

As used herein, the term "marmoset" denotes any New-World Monkeys of the genus *Callithrix*, for example belonging to the Atlantic marmosets of subgenus *Callithrix* (sic!) (Common Marmoset, *Callithrix (Callithrix) jacchus*; Black-tufted Marmoset, *Callithrix (Callithrix) penicillata*; Wied's Marmoset, *Callithrix (Callithrix) kuhlii*; White-headed Marmoset, *Callithrix (Callithrix) geoffroyi*; Buffy-headed Marmoset, *Callithrix (Callithrix) flaviceps*; Buffy-tufted Marmoset, *Callithrix (Callithrix) aurita*); belonging to the Amazonian marmosets of subgenus *Mico* (Rio Acari Marmoset, *Callithrix (Mico) acariensis*; Manicore Marmoset, *Callithrix (Mico) manicorensis*; Silvery Marmoset, *Callithrix (Mico) argentata*; White Marmoset, *Callithrix (Mico) leucippe*; Emilia's Marmoset, *Callithrix (Mico) emiliae*; Black-headed Marmoset, *Callithrix (Mico) nigriceps*; Marca's Marmoset, *Callithrix (Mico)marcai*; Black-tailed Marmoset, *Callithrix (Mico) melanura*; Santarem Marmoset, *Callithrix (Mico) humeralifera*; Maués Marmoset, *Callithrix (Mico) mauesi*; Gold-and-white Marmoset, *Callithrix (Mico) chrysoleuca*; Hershkovitz's Marmoset, *Callithrix (Mico) intermedia*; Satéré Marmoset, *Callithrix (Mico) saterei*); Roosmalens' Dwarf Marmoset belonging to the subgenus Callibella (*Callithrix (Callibella) humilis*); or the Pygmy Marmoset belonging to the subgenus Cebuella (*Callithrix (Cebuella) pygmaea*).
Other genera of the New-World Monkeys comprise tamarins of the genus *Saguinus* (comprising the *S. oedipus*-group, the *S. midas* group, the *S. nigricollis* group, the *S. mystax* group, the *S. bicolor* group and the *S. inustus* group) and squirrel monkeys of the genus *Samiri* (e.g. *Saimiri sciureus, Saimiri oerstedii, Saimiri ustus, Saimiri boliviensis, Saimiri vanzolini*)

In a preferred embodiment of the bispecific single chain antibody molecule of the invention, the non-chimpanzee primate is an old world monkey. In a more preferred embodiment of the polypeptide, the old world monkey is a monkey of the Papio genus Macaque genus. Most preferably, the monkey of the Macaque genus is Assamese macaque (*Macaca assamensis*), Barbary macaque (*Macaca sylvanus*), Bonnet macaque (*Macaca radiata*), Booted or Sulawesi-Booted macaque (*Macaca ochreata*), Sulawesi-crested macaque (*Macaca nigra*), Formosan rock macaque (*Macaca cyclopsis*), Japanese snow macaque or Japanese macaque (*Macaca fuscata*), Cynomologus monkey or crab-eating macaque or long-tailed macaque or Java macaque (*Macaca fascicularis*), Lion-tailed macaque (*Macaca silenus*), Pigtailed macaque (*Macaca nemestrina*), Rhesus macaque (*Macaca mulatta*),

Tibetan macaque (*Macaca thibetana*), Tonkean macaque (*Macaca tonkeana*), Toque macaque (*Macaca sinica*), Stump-tailed macaque or Red-faced macaque or Bear monkey (*Macaca arctoides*), or Moor macaque (*Macaca maurus*). Most preferably, the monkey of the Papio genus is *Hamadryas Baboon, Papio hamadryas; Guinea Baboon, Papio papio; Olive Baboon, Papio anubis; Yellow Baboon, Papio cynocephalus; Chacma Baboon, Papio ursinus.*

In an alternatively preferred embodiment of the bispecific single chain antibody molecule of the invention, the non-chimpanzee primate is a new world monkey. In a more preferred embodiment of the polypeptide, the new world monkey is a monkey of the Callithrix genus (marmoset), the Saguinus genus or the Samiri genus. Most preferably, the monkey of the Callithrix genus is *Callithrix jacchus*, the monkey of the Saguinus genus is *Saguinus oedipus* and the monkey of the Samiri genus is *Saimiri sciureus*.

The term "cell surface antigen" as used herein denotes a molecule, which is displayed on the surface of a cell. In most cases, this molecule will be located in or on the plasma membrane of the cell such that at least part of this molecule remains accessible from outside the cell in tertiary form. A non-limiting example of a cell surface molecule, which is located in the plasma membrane is a transmembrane protein comprising, in its tertiary conformation, regions of hydrophilicity and hydrophobicity. Here, at least one hydrophobic region allows the cell surface molecule to be embedded, or inserted in the hydrophobic plasma membrane of the cell while the hydrophilic regions extend on either side of the plasma membrane into the cytoplasm and extracellular space, respectively. Non-limiting examples of cell surface molecules which are located on the plasma membrane are proteins which have been modified at a cysteine residue to bear a palmitoyl group, proteins modified at a C-terminal cysteine residue to bear a farnesyl group or proteins which have been modified at the C-terminus to bear a glycosyl phosphatidyl inositol ("GPI") anchor. These groups allow covalent attachment of proteins to the outer surface of the plasma membrane, where they remain accessible for recognition by extracellular molecules such as antibodies. Examples of cell surface antigens are CD3 epsilon and PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα.

As described herein above, PSCA is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to prostate cancer, bladder cancer or pancreatic cancer.

As also described herein above, CD19 is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to B-cell malignancies such as non-Hodgkin Lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells.

As further described herein above, C-MET is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to carcinomas, sarcomas, glioblastomas/astrocytomas, melanomas, mesotheliomas, Wilms tumors or hematopoietic malignancies such as leukemias, lymphomas or multiple myelomas.

Moreover, as described herein above, Endosialin is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to carcinomas (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), sarcomas, and neuroectodermal tumors (melanoma, glioma, neuroblastoma).

As also described herein above, EpCAM is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to epithelial cancer or a minimal residual cancer.

Furthermore, as described herein above, FAP alpha is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to, epithelial cancer.

Moreover, as described herein above, IGF-1R is a cell surface antigen which is a target for therapy of various cancers, including, but not limited to, bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer, and autoimmune diseases, including, but not limited to, preferably psoriasis.

In light of this, PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα can also be characterized as a tumor antigen. The term „tumor antigen" as used herein may be understood as those antigens that are presented on tumor cells. These antigens can be presented on the cell surface with an extracellular part, which is often combined with a transmembrane and cytoplasmic part of the molecule. These antigens can sometimes be presented only by tumor cells and never by the normal ones. Tumor antigens can be exclusively expressed on tumor cells or might represent a tumor specific mutation compared to normal cells. In this case, they are

called tumor-specific antigens. More common are antigens that are presented by tumor cells and normal cells, and they are called tumor-associated antigens. These tumor-associated antigens can be overexpressed compared to normal cells or are accessible for antibody binding in tumor cells due to the less compact structure of the tumor tissue compared to normal tissue. Example for tumor antigens in line with the present invention are PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R and FAPα.

As described herein above the bispecific single chain antibody molecule of the invention binds with the first binding domain to an epitope of human and non-chimpanzee primate CD3ε (epsilon) chain, wherein the epitope is part of an amino acid sequence comprised in the group consisting of 27 amino acid residues as depicted in SEQ ID NOs. 2, 4, 6, or 8 or a functional fragment thereof.
In line with the present invention it is preferred for the bispecific single chain antibody molecule of the invention that said epitope is part of an amino acid sequence comprising 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6 or 5 amino acids.
More preferably, wherein said epitope comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu (Q-D-G-N-E).
Within the present invention, a functional fragment of the N-terminal 1-27 amino acid residues means that said functional fragment is still a context-independent epitope maintaining its three-dimensional structural integrity when taken out of its native environment in the CD3 complex (and fused to a heterologous amino acid sequence such as EpCAM or an immunoglobulin Fc part, e.g. as shown in Example 3.1). The maintenance of the three-dimensional structure within the 27 amino acid N-terminal polypeptide or functional fragment thereof of CD3 epsilon can be used for the generation of binding domains which bind to the N-terminal CD3 epsilon polypeptide fragment *in vitro* and to the native (CD3 epsilon subunit of the) CD3 complex on T cells *in vivo* with the same binding affinity. Within the present invention, a functional fragment of the N-terminal 1-27 amino acid residues means that CD3 binding domains provided herein can still bind to such functional fragments in a context-independent manner. The person skilled in the art is aware of methods for epitope mapping to determine which amino acid residues of an epitope are recognized by such anti-CD3 binding domains (e.g. alanine scanning; see appended examples).

In one embodiment of the invention, the bispecific single chain antibody molecule of the invention comprises a (first) binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε chain and a second binding domain capable of binding to the cell surface antigen PSCA. In alternative embodiments of the invention the said secong binding domain capable of binding to the cell surface antigen CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα

Within the present invention it is further preferred that the second binding domain binds to the human cell surface antigen PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα and/or a non-chimpanzee primate PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα. Particularly preferred, the second binding domain binds to the human cell surface antigen PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα and a non-chimpanzee primate PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, preferably a macaque PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα. It is to be understood, that the second binding domain binds to at least one non-chimpanzee primate PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, however, it may also bind to two, three or more, non-chimpanzee primate PSCA homologs, respectively CD19 homologs, C-MET homologs, Endosialin homologs, EpCAM homologs, IGF-1R homologs or FAPα homologs. For example, the second binding domain may bind to the Cynomogus monkey PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, and to the Rhesus monkey PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα.

For the generation of the second binding domain of the bispecific single chain antibody molecule of the invention, e.g. bispecific single chain antibodies as defined herein, monoclonal antibodies binding to both of the respective human and/or non-chimpanzee primate cell surface antigen such as PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα, can be utilized. Appropriate binding domains for the bispecific polypeptide as defined herein e.g. can be derived from cross-species specific monoclonal antibodies by recombinant methods described in the art. A monoclonal antibody binding to a human cell surface antigen and to the homolog of said cell surface antigen in a non-chimpanzee primate can be tested by FACS

assays as set forth above. It is evident to those skilled in the art that cross-species specific antibodies can also be generated by hybridoma techniques described in the literature (Milstein and Köhler, Nature 256 (1975), 495-7). For example, mice may be alternately immunized with human and non-chimpanzee primate cell surface antigen, such as PSCA, respectively CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα. From these mice, cross-species specific antibody-producing hybridoma cells are isolated via hybridoma technology and analysed by FACS as set forth above. The generation and analysis of bispecific polypeptides such as bispecific single chain antibodies exhibiting cross-species specificity as described herein is shown in the following examples. The advantages of the bispecific single chain antibodies exhibiting cross-species specificity include the points enumerated herein.

It is particularly preferred for the bispecific single chain antibody molecule of the invention that the first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε chain comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

(a) CDR-L1 as depicted in SEQ ID NO. 27, CDR-L2 as depicted in SEQ ID NO. 28 and CDR-L3 as depicted in SEQ ID NO. 29;

(b) CDR-L1 as depicted in SEQ ID NO. 117, CDR-L2 as depicted in SEQ ID NO. 118 and CDR-L3 as depicted in SEQ ID NO. 119; and

(c) CDR-L1 as depicted in SEQ ID NO. 153, CDR-L2 as depicted in SEQ ID NO. 154 and CDR-L3 as depicted in SEQ ID NO. 155.

The variable regions, i.e. the variable light chain ("L" or "VL") and the variable heavy chain ("H" or "VH") are understood in the art to provide the binding domain of an antibody. This variable regions harbor the complementary determining regions.
The term "complementary determining region" (CDR) is well known in the art to dictate the antigen specificity of an antibody. The term "CDR-L" or "L CDR" or "LCDR" refers to CDRs in the VL, whereas the term "CDR-H" or "H CDR" or "HCDR" refers to the CDRs in the VH.

In an alternatively preferred embodiment of the bispecific single chain antibody molecule of the invention the first binding domain capable of binding to an epitope of

human and non-chimpanzee primate CD3ε chain comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:

(a) CDR-H1 as depicted in SEQ ID NO. 12, CDR-H2 as depicted in SEQ ID NO. 13 and CDR-H3 as depicted in SEQ ID NO. 14;

(b) CDR-H1 as depicted in SEQ ID NO. 30, CDR-H2 as depicted in SEQ ID NO. 31 and CDR-H3 as depicted in SEQ ID NO. 32;

(c) CDR-H1 as depicted in SEQ ID NO. 48, CDR-H2 as depicted in SEQ ID NO. 49 and CDR-H3 as depicted in SEQ ID NO. 50;

(d) CDR-H1 as depicted in SEQ ID NO. 66, CDR-H2 as depicted in SEQ ID NO. 67 and CDR-H3 as depicted in SEQ ID NO. 68;

(e) CDR-H1 as depicted in SEQ ID NO. 84, CDR-H2 as depicted in SEQ ID NO. 85 and CDR-H3 as depicted in SEQ ID NO. 86;

(f) CDR-H1 as depicted in SEQ ID NO. 102, CDR-H2 as depicted in SEQ ID NO. 103 and CDR-H3 as depicted in SEQ ID NO. 104;

(g) CDR-H1 as depicted in SEQ ID NO. 120, CDR-H2 as depicted in SEQ ID NO. 121 and CDR-H3 as depicted in SEQ ID NO. 122;

(h) CDR-H1 as depicted in SEQ ID NO. 138, CDR-H2 as depicted in SEQ ID NO. 139 and CDR-H3 as depicted in SEQ ID NO. 140;

(i) CDR-H1 as depicted in SEQ ID NO. 156, CDR-H2 as depicted in SEQ ID NO. 157 and CDR-H3 as depicted in SEQ ID NO. 158; and

(j) CDR-H1 as depicted in SEQ ID NO. 174, CDR-H2 as depicted in SEQ ID NO. 175 and CDR-H3 as depicted in SEQ ID NO. 176.

It is further preferred that the binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε chain comprises a VL region selected from the group consisting of a VL region as depicted in SEQ ID NO. 35, 39, 125, 129, 161 or 165.

It is alternatively preferred that the first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε chain comprises a VH region selected from the group consisting of a VH region as depicted in SEQ ID NO. 15, 19, 33, 37, 51, 55, 69, 73, 87, 91, 105, 109, 123, 127, 141, 145, 159, 163, 177 or 181.

More preferably, the bispecific single chain antibody molecule of the invention is characterized by the first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε chain, which comprises a VL region and a VH region selected from the group consisting of:

(a) a VL region as depicted in SEQ ID NO. 17 or 21 and a VH region as depicted in SEQ ID NO. 15 or 19;

(b) a VL region as depicted in SEQ ID NO. 35 or 39 and a VH region as depicted in SEQ ID NO. 33 or 37;

(c) a VL region as depicted in SEQ ID NO. 53 or 57 and a VH region as depicted in SEQ ID NO. 51 or 55;

(d) a VL region as depicted in SEQ ID NO. 71 or 75 and a VH region as depicted in SEQ ID NO. 69 or 73;

(e) a VL region as depicted in SEQ ID NO. 89 or 93 and a VH region as depicted in SEQ ID NO. 87 or 91;

(f) a VL region as depicted in SEQ ID NO. 107 or 111 and a VH region as depicted in SEQ ID NO. 105 or 109;

(g) a VL region as depicted in SEQ ID NO. 125 or 129 and a VH region as depicted in SEQ ID NO. 123 or 127;

(h) a VL region as depicted in SEQ ID NO. 143 or 147 and a VH region as depicted in SEQ ID NO. 141 or 145;

(i) a VL region as depicted in SEQ ID NO. 161 or 165 and a VH region as depicted in SEQ ID NO. 159 or 163; and

(j) a VL region as depicted in SEQ ID NO. 179 or 183 and a VH region as depicted in SEQ ID NO. 177 or 181.

According to a preferred embodiment of the bispecific single chain antibody molecule of the invention the pairs of VH-regions and VL-regions in the first binding domain binding to CD3 epsilon are in the format of a single chain antibody (scFv). The VH and VL regions are arranged in the order VH-VL or VL-VH. It is preferred that the VH-region is positioned N-terminally to a linker sequence. The VL-region is positioned C-terminally of the linker sequence. Put in other words, the domain arrangement in the CD3 binding domain of the bispecific single chain antibody molecule of the invention is preferably VH-VL, with said CD3 binding domain located C-terminally to the second (cell surface antigen, such as PSCA, CD19, C-MET, Endosialin, EpCAM,

IGF-1R or FAPα) binding domain. Preferably the VH-VL comprises or is SEQ ID NO. 185.

A preferred embodiment of the above described bispecific single chain antibody molecule of the invention is characterized by the first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 23, 25, 41, 43, 59, 61, 77, 79, 95, 97, 113, 115, 131, 133, 149, 151, 167, 169, 185 or 187.

The invention further relates to an above described bispecific single chain antibody, wherein the second binding domain binds to the cell surface antigen PSCA, CD19, C-MET, Endosialin, EpCAM, IGF-1R or FAPα.

PSCAxCD3

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 382 – 384 and CDR L1-3 of SEQ ID NO: 377 – 379;

b) CDR H1-3 of SEQ ID NO: 400 – 402 and CDR L1-3 of SEQ ID NO: 395 – 397;

c) CDR H1-3 of SEQ ID NO: 414 – 416 and CDR L1-3 of SEQ ID NO: 409 – 411;

d) CDR H1-3 of SEQ ID NO: 432 – 434 and CDR L1-3 of SEQ ID NO: 427 – 429;

e) CDR H1-3 of SEQ ID NO: 1215 – 1217 and CDR L1-3 of SEQ ID NO: 1220 – 1222;

f) CDR H1-3 of SEQ ID NO: 1187 – 1189 and CDR L1-3 of SEQ ID NO: 1192 – 1194;

g) CDR H1-3 of SEQ ID NO: 1173 – 1175 and CDR L1-3 of SEQ ID NO: 1178 – 1180;

h) CDR H1-3 of SEQ ID NO: 1229 – 1231 and CDR L1-3 of SEQ ID NO: 1234 – 1236;

i) CDR H1-3 of SEQ ID NO: 1201 – 1203 and CDR L1-3 of SEQ ID NO: 1206 – 1208;

k) CDR H1-3 of SEQ ID NO: 1257 – 1259 and CDR L1-3 of SEQ ID NO: 1262 – 1264; and

l) CDR H1-3 of SEQ ID NO: 1243 – 1245 and CDR L1-3 of SEQ ID NO: 1248 – 1250.

The sequences of the corresponding VL- and VH-regions of the second binding domain of the bispecific single chain antibody molecule of the invention as well as of the respective scFvs are shown in the sequence listing.

In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH PSCA-VL PSCA-VH CD3-VL CD3 or VL PSCA-VH PSCA-VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs: 389, 421, 439, 391, 405, 423, 441, 1226, 1198, 1184, 1240, 1212, 1268 or 1254

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 390, 422, 440, 392, 406, 424, 442, 1227, 1199, 1185, 1241, 1213, 1269 or 1255; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 389, 421, 439, 391, 405, 423, 441, 1226, 1198, 1184, 1240, 1212, 1268 or 1254, as well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 %

identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 389, 421, 439, 391, 405, 423, 441, 1226, 1198, 1184, 1240, 1212, 1268 or 1254. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 390, 422, 440, 392, 406, 424, 442, 1227, 1199, 1185, 1241, 1213, 1269 or 1255 as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 390, 422, 440, 392, 406, 424, 442, 1227, 1199, 1185, 1241, 1213, 1269 or 1255. It is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence having e.g. 85% (90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid sequences of the bispecific single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid residue. Said hypothesis is well known to the person skilled in the art (see e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the PSCAxCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen PSCA recognized by their second binding domain.

CD19xCD3

According to an alternatively preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 478 - 480 and CDR L1-3 of SEQ ID NO: 473 - 475;

b) CDR H1-3 of SEQ ID NO: 530 - 532 and CDR L1-3 of SEQ ID NO: 525 - 527;

c) CDR H1-3 of SEQ ID NO: 518 - 520 and CDR L1-3 of SEQ ID NO: 513 - 515;

d) CDR H1-3 of SEQ ID NO: 506 - 508 and CDR L1-3 of SEQ ID NO: 501 – 503;

e) CDR H1-3 of SEQ ID NO: 494 – 496 and CDR L1-3 of SEQ ID NO: 489 – 491;

f) CDR H1-3 of SEQ ID NO: 542 – 544 and CDR L1-3 of SEQ ID NO: 537 – 539;

g) CDR H1-3 of SEQ ID NO: 554 – 556 and CDR L1-3 of SEQ ID NO: 549 – 551;

h) CDR H1-3 of SEQ ID NO: 566 – 568 and CDR L1-3 of SEQ ID NO: 561 – 563;

i) CDR H1-3 of SEQ ID NO: 578 – 580 and CDR L1-3 of SEQ ID NO: 573 – 575;

j) CDR H1-3 of SEQ ID NO: 590 – 592 and CDR L1-3 of SEQ ID NO: 585 – 587;

k) CDR H1-3 of SEQ ID NO: 602 – 604 and CDR L1-3 of SEQ ID NO: 597 – 599;

l) CDR H1-3 of SEQ ID NO: 614 – 616 and CDR L1-3 of SEQ ID NO: 609 – 611;

m) CDR H1-3 of SEQ ID NO: 626 – 628 and CDR L1-3 of SEQ ID NO: 621 – 623;

n) CDR H1-3 of SEQ ID NO: 638 – 640 and CDR L1-3 of SEQ ID NO: 633 – 635;

o) CDR H1-3 of SEQ ID NO: 650 – 652 and CDR L1-3 of SEQ ID NO: 645 – 647;

p) CDR H1-3 of SEQ ID NO: 662 – 664 and CDR L1-3 of SEQ ID NO: 657 – 659;

q) CDR H1-3 of SEQ ID NO: 674 – 676 and CDR L1-3 of SEQ ID NO: 669 – 671;

r) CDR H1-3 of SEQ ID NO: 686 – 688 and CDR L1-3 of SEQ ID NO: 681 – 683;

s) CDR H1-3 of SEQ ID NO: 698 – 700 and CDR L1-3 of SEQ ID NO: 693 – 695;

t) CDR H1-3 of SEQ ID NO: 710 – 712 and CDR L1-3 of SEQ ID NO: 705 – 707;

u) CDR H1-3 of SEQ ID NO: 722 – 724 and CDR L1-3 of SEQ ID NO: 717 – 719;

v) CDR H1-3 of SEQ ID NO: 734 – 736 and CDR L1-3 of SEQ ID NO: 729 – 731;

w) CDR H1-3 of SEQ ID NO: 746 – 748 and CDR L1-3 of SEQ ID NO: 741 – 743;

x) CDR H1-3 of SEQ ID NO: 758 – 760 and CDR L1-3 of SEQ ID NO: 753 – 755;

y) CDR H1-3 of SEQ ID NO: 1271 - 1273 and CDR L1-3 of SEQ ID NO: 1276 – 1278;

z) CDR H1-3 of SEQ ID NO: 1285 – 1287 and CDR L1-3 of SEQ ID NO: 1290 – 1292;

aa) CDR H1-3 of SEQ ID NO: 1299 – 1301 and CDR L1-3 of SEQ ID NO: 1304 – 1306;

ab) CDR H1-3 of SEQ ID NO: 1313 – 1315 and CDR L1-3 of SEQ ID NO: 1318 – 1320;

ac) CDR H1-3 of SEQ ID NO: 1327 – 1329 and CDR L1-3 of SEQ ID NO: 1332 – 1334;

ad) CDR H1-3 of SEQ ID NO: 1341 – 1343 and CDR L1-3 of SEQ ID NO: 1346 – 1348;

ae) CDR H1-3 of SEQ ID NO: 1355 – 1357 and CDR L1-3 of SEQ ID NO: 1360 – 1362;

af) CDR H1-3 of SEQ ID NO: 1369 – 1371 and CDR L1-3 of SEQ ID NO: 1374 – 1376; and

ag) CDR H1-3 of SEQ ID NO: 1383 – 1385 and CDR L1-3 of SEQ ID NO: 1388 – 1390.

The sequences of the corresponding VL- and VH-regions of the second binding domain of the bispecific single chain antibody molecule of the invention as well as of the respective scFvs are shown in the sequence listing.
In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH CD19-VL CD19-VH CD3-VL CD3 or VL CD19-VH CD19-VH CD3-VL CD3. More preferably, the binding domains are arranged in the order VL CD19-VH CD19-VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 481, 485, 483, 533, 521, 509, 497, 545, 557, 569, 581, 593, 605, 617, 629, 641, 653, 665, 677, 689, 701, 713, 725, 737, 749, 761, 1282, 1296, 1310, 1324, 1338, 1352, 1366, 1380 or 1394 ;

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 482, 486, 484, 534, 522, 510, 498, 546, 558, 570, 582, 594, 606, 618, 630, 642, 654, 666, 678, 690, 702, 714, 726, 738, 750, 762, 1283, 1297, 1311, 1325, 1339, 1353, 1367, 1381 or 1395; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 481, 485, 483, 533, 521, 509, 497, 545, 557, 569, 581, 593, 605, 617, 629, 641, 653, 665, 677, 689, 701, 713, 725, 737, 749, 761, 1282, 1296, 1310, 1324, 1338, 1352, 1366, 1380 or 1394, as

well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 481, 485, 483, 533, 521, 509, 497, 545, 557, 569, 581, 593, 605, 617, 629, 641, 653, 665, 677, 689, 701, 713, 725, 737, 749, 761, 1282, 1296, 1310, 1324, 1338, 1352, 1366, 1380 or 1394. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 482, 486, 484, 534, 522, 510, 498, 546, 558, 570, 582, 594, 606, 618, 630, 642, 654, 666, 678, 690, 702, 714, 726, 738, 750, 762, 1283, 1297, 1311, 1325, 1339, 1353, 1367, 1381 or 1395 as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 482, 486, 484, 534, 522, 510, 498, 546, 558, 570, 582, 594, 606, 618, 630, 642, 654, 666, 678, 690, 702, 714, 726, 738, 750, 762, 1283, 1297, 1311, 1325, 1339, 1353, 1367, 1381 or 1395. It is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence having e.g. 85% (90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid sequences of the bispecific single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid residue. Said hypothesis is well known to the person skilled in the art (see e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the CD19xCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen CD19 recognized by their second binding domain.

c-METxCD3

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 821 - 823 and CDR L1-3 of SEQ ID NO: 816 - 818;

b) CDR H1-3 of SEQ ID NO: 836 - 838 and CDR L1-3 of SEQ ID NO: 833 - 835;

c) CDR H1-3 of SEQ ID NO: 845 – 847 and CDR L1-3 of SEQ ID NO: 840 - 842;

d) CDR H1-3 of SEQ ID NO: 863 - 865 and CDR L1-3 of SEQ ID NO: 858 – 860;

e) CDR H1-3 of SEQ ID NO: 881 – 883 and CDR L1-3 of SEQ ID NO: 876 – 878;

f) CDR H1-3 of SEQ ID NO: 899 – 901 and CDR L1-3 of SEQ ID NO: 894 – 896;

g) CDR H1-3 of SEQ ID NO: 1401 – 1403 and CDR L1-3 of SEQ ID NO: 1406 – 1408;

h) CDR H1-3 of SEQ ID NO: 1415 – 1417 and CDR L1-3 of SEQ ID NO: 1420 – 1422;

i) CDR H1-3 of SEQ ID NO: 1429 – 1431 and CDR L1-3 of SEQ ID NO: 1434 – 1436;

j) CDR H1-3 of SEQ ID NO: 1443 – 1445 and CDR L1-3 of SEQ ID NO: 1448 – 1450;

k) CDR H1-3 of SEQ ID NO: 1457 – 1459 and CDR L1-3 of SEQ ID NO: 1462 – 1464;

l) CDR H1-3 of SEQ ID NO: 1471 – 1473 and CDR L1-3 of SEQ ID NO: 1476 – 1478;

m) CDR H1-3 of SEQ ID NO: 1639 – 1641 and CDR L1-3 of SEQ ID NO: 1644 – 1646;

n) CDR H1-3 of SEQ ID NO: 1625 – 1627 and CDR L1-3 of SEQ ID NO: 1630 – 1632;

o) CDR H1-3 of SEQ ID NO: 1611 – 1613 and CDR L1-3 of SEQ ID NO: 1616 – 1618;

p) CDR H1-3 of SEQ ID NO: 1597 – 1599 and CDR L1-3 of SEQ ID NO: 1602 – 1604;

q) CDR H1-3 of SEQ ID NO: 1569 – 1571 and CDR L1-3 of SEQ ID NO: 1574 – 1576;

r) CDR H1-3 of SEQ ID NO: 1555 – 1557 and CDR L1-3 of SEQ ID NO: 1560 – 1562;

s) CDR H1-3 of SEQ ID NO: 1583 – 1585 and CDR L1-3 of SEQ ID NO: 1588 – 1590;

t) CDR H1-3 of SEQ ID NO: 1541 – 1543 and CDR L1-3 of SEQ ID NO: 1546 – 1548;

u) CDR H1-3 of SEQ ID NO: 1513 – 1515 and CDR L1-3 of SEQ ID NO: 1518 – 1520;

v) CDR H1-3 of SEQ ID NO: 1527 – 1529 and CDR L1-3 of SEQ ID NO: 1532 – 1534;

w) CDR H1-3 of SEQ ID NO: 1499 – 1501 and CDR L1-3 of SEQ ID NO: 1504 – 1506; and

x) CDR H1-3 of SEQ ID NO: 1485 – 1487 and CDR L1-3 of SEQ ID NO: 1490 – 1492.

The sequences of the corresponding VL- and VH-regions of the second binding domain of the bispecific single chain antibody molecule of the invention as well as of the respective scFvs are shown in the sequence listing.

In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH C-MET-VL C-MET-VH CD3-VL CD3 or VL C-MET-VH C-MET-VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 829, 853, 871, 889, 831, 855, 873, 891, 905, 1412, 1426, 1440, 1454, 1468 or 1482;

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 830, 854, 872, 890, 832, 856, 874, 892, 906, 1413, 1427, 1441, 1455, 1469, or 1483; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 829, 853, 871, 889, 831, 855, 873, 891, 905, 1412, 1426, 1440, 1454, 1468 or 1482;, as well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 829, 853, 871, 889, 831, 855, 873, 891, 905, 1412, 1426, 1440, 1454, 1468 or 1482;. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 830, 854, 872, 890, 832, 856, 874, 892, 906, 1413, 1427, 1441, 1455, 1469, or 1483; as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 830, 854, 872, 890, 832, 856, 874, 892, 906, 1413, 1427, 1441, 1455, 1469, or 1483;. It is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence having e.g. 85% (90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid sequences of the bispecific

single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid residue. Said hypothesis is well known to the person skilled in the art (see e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the C-METxCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen C-MET recognized by their second binding domain.

EndosialinxCD3

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

CDR H1-3 of SEQ ID NO: 910 - 912 and CDR L1-3 of SEQ ID NO: 907 - 909.

Starting from these CDR sequences of the heavy and light chain for the second binding domain the person skilled in the art can produce a bispecific single chain antibody molecule of the invention without any further inventive ado. In particular, the CDR sequences can be positioned in a framework of a VL and a VH chain and arranged in form of a scFv.

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 1653 – 1655 and CDR L1-3 of SEQ ID NO: 1658 - 1660;

b) CDR H1-3 of SEQ ID NO: 1667 - 1669 and CDR L1-3 of SEQ ID NO: 1672 - 1674;

c) CDR H1-3 of SEQ ID NO: 1681 – 1683 and CDR L1-3 of SEQ ID NO: 1686 – 1688; and

d) CDR H1-3 of SEQ ID NO: 1695 – 1697 and CDR L1-3 of SEQ ID NO: 1700 – 1702;

e) CDR H1-3 of SEQ ID NO: 1709 – 1711 and CDR L1-3 of SEQ ID NO: 1714 – 1716; and

f) CDR H1-3 of SEQ ID NO: 1723 – 1725 and CDR L1-3 of SEQ ID NO: 1728 – 1730.

In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH Endosialin -VL Endosialin -VH CD3-VL CD3 or VL Endosialin -VH Endosialin -VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises an above characterized first binding domain capable of binding to an epitope of human and non-chimpanzee primate CD3ε and a second binding domain capable of binding to Endosialin and comprising the CDR H1, 2 and 3 of SEQ ID NOs: 910 – 912 and the CDR L1, 2 and 3 of SEQ ID NOs: 907 - 909, or CDR amino acid sequences at least 50%, 60%, 70%, 75%, 80%, 85%, or 90 % identical, more preferred at least 95% identical, most preferred at least 96%, 97%, 98%, or 99% identical to each of the respective amino acid sequences of the above defined CDRs. It is to be understood that the sequence identity is determined over the entire CDRH or CDRL amino acid sequence.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 1664, 1678, 1692, 1706, 1720, or 1734;

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 1665, 1679, 1693, 1707, 1721, or 1735; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 1664, 1678, 1692, 1706, 1720, or 1734, as well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 1664, 1678, 1692, 1706, 1720, or 1734. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 1665, 1679, 1693, 1707, 1721, or 1735; as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 1665, 1679, 1693, 1707, 1721, or 1735.

If not indicated otherwise, it is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence or CDR sequence having e.g. 50% (60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid or CDR sequences of the bispecific single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid residue. Said hypothesis is well known to the person skilled in the art (see

e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the EndosialinxCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen Endosialin recognized by their second binding domain.

EpCAMxCD3

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 940 – 942 and CDR L1-3 of SEQ ID NO: 935 - 937;

b) CDR H1-3 of SEQ ID NO: 956 – 958 and CDR L1-3 of SEQ ID NO: 951 - 953;

c) CDR H1-3 of SEQ ID NO: 968 – 970 and CDR L1-3 of SEQ ID NO: 963 - 965; and

d) CDR H1-3 of SEQ ID NO: 980 - 982 and CDR L1-3 of SEQ ID NO: 975-977;

e) CDR H1-3 of SEQ ID NO: 992 – 994 and CDR L1-3 of SEQ ID NO: 987 – 989;

f) CDR H1-3 of SEQ ID NO: 1004 – 1006 and CDR L1-3 of SEQ ID NO: 999 – 1001;

g) CDR H1-3 of SEQ ID NO: 1028 – 1030 and CDR L1-3 of SEQ ID NO: 1023 – 1025;

h) CDR H1-3 of SEQ ID NO: 1040 – 1042 and CDR L1-3 of SEQ ID NO: 1035 – 1037;

i) CDR H1-3 of SEQ ID NO: 1052 – 1054 and CDR L1-3 of SEQ ID NO: 1047 – 1049;

j) CDR H1-3 of SEQ ID NO: 1074 – 1076 and CDR L1-3 of SEQ ID NO: 1069 – 1071;

k) CDR H1-3 of SEQ ID NO: 1086 – 1088 and CDR L1-3 of SEQ ID NO: 1081 – 1083;

l) CDR H1-3 of SEQ ID NO: 1098 – 1000 and CDR L1-3 of SEQ ID NO: 1093 – 1095;

m) CDR H1-3 of SEQ ID NO: 1110 – 1112 and CDR L1-3 of SEQ ID NO: 1105 – 1107;

n) CDR H1-3 of SEQ ID NO: 1122 – 1124 and CDR L1-3 of SEQ ID NO: 1117 – 1119;

o) CDR H1-3 of SEQ ID NO: 1016 – 1018 and CDR L1-3 of SEQ ID NO: 1011 – 1013; and

p) CDR H1-3 of SEQ ID NO: 1765 – 1767 and CDR L1-3 of SEQ ID NO: 1770 – 1772.

The sequences of the corresponding VL- and VH-regions of the second binding domain of the bispecific single chain antibody molecule of the invention as well as of the respective scFvs are shown in the sequence listing.

In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH EpCAM-VL EpCAM-VH CD3-VL CD3 or VL EpCAM-VH EpCAM-VH CD3-VL CD3. More preferably, the binding domains are arranged in the order VL EpCAM-VH EpCAM-VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 944, 948, 946, 960, 972, 984, 996, 1008, 1032, 1044, 1056, 1078, 1090, 1102, 1114, 1126, 1020, or 1776;

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 945, 949, 947, 961, 973, 985, 979,

1009, 1033, 1045, 1057, 1079, 1091, 1103, 1115, 1127, 1021, or 1777; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 944, 948, 946, 960, 972, 984, 996, 1008, 1032, 1044, 1056, 1078, 1090, 1102, 1114, 1126, 1020, or 1776, as well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 944, 948, 946, 960, 972, 984, 996, 1008, 1032, 1044, 1056, 1078, 1090, 1102, 1114, 1126, 1020, or 1776. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 945, 949, 947, 961, 973, 985, 979, 1009, 1033, 1045, 1057, 1079, 1091, 1103, 1115, 1127, 1021, or 1777 as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 945, 949, 947, 961, 973, 985, 979, 1009, 1033, 1045, 1057, 1079, 1091, 1103, 1115, 1127, 1021, or 1777. It is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence having e.g. 85% (90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid sequences of the bispecific single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid residue. Said hypothesis is well known to

the person skilled in the art (see e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the EpCAMxCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen EpCAM recognized by their second binding domain.

FAPα xCD3

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from:

CDR H1-3 of SEQ ID NO: 1137 - 1139 and CDR L1-3 of SEQ ID NO: 1132 - 1134.

The sequences of the corresponding VL- and VH-regions of the second binding domain of the bispecific single chain antibody molecule of the invention as well as of the respective scFvs are shown in the sequence listing.
According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 1137 - 1139 and CDR L1-3 of SEQ ID NO: 1132 - 1134;

b) CDR H1-3 of SEQ ID NO: 1849 - 1851and CDR L1-3 of SEQ ID NO: 1854 - 1856;

c) CDR H1-3 of SEQ ID NO: 1835 - 1837and CDR L1-3 of SEQ ID NO: 1840 - 1842; and

d) CDR H1-3 of SEQ ID NO: 1779 - 1781and CDR L1-3 of SEQ ID NO: 1784 - 1786;

e) CDR H1-3 of SEQ ID NO: 1793 – 1795 and CDR L1-3 of SEQ ID NO: 1798 – 1800;

f) CDR H1-3 of SEQ ID NO: 1863 – 1865 and CDR L1-3 of SEQ ID NO: 1868 – 1870;

g) CDR H1-3 of SEQ ID NO: 1807 – 1809 and CDR L1-3 of SEQ ID NO: 1812 – 1814;

h) CDR H1-3 of SEQ ID NO: 1821 – 1823 and CDR L1-3 of SEQ ID NO: 1826 – 1828;

i) CDR H1-3 of SEQ ID NO: 1891 – 1893 and CDR L1-3 of SEQ ID NO: 1896 – 1898;

j) CDR H1-3 of SEQ ID NO: 1877 – 1879 and CDR L1-3 of SEQ ID NO: 1882 – 1884;

k) CDR H1-3 of SEQ ID NO: 1961 – 1963 and CDR L1-3 of SEQ ID NO: 1966 – 1968;

l) CDR H1-3 of SEQ ID NO: 1947 – 1949 and CDR L1-3 of SEQ ID NO: 1952-1954;

m) CDR H1-3 of SEQ ID NO: 1975 – 1977 and CDR L1-3 of SEQ ID NO: 1980 – 1982;

n) CDR H1-3 of SEQ ID NO: 1933 – 1935 and CDR L1-3 of SEQ ID NO: 1938 – 1940;

o) CDR H1-3 of SEQ ID NO: 1919 – 1921 and CDR L1-3 of SEQ ID NO: 1924 – 1926; and

p) CDR H1-3 of SEQ ID NO: 1905 – 1907 and CDR L1-3 of SEQ ID NO: 1910 – 1912.

In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH FAP alpha -VL FAP alpha -VH CD3-VL CD3 or VL FAP alpha -VH FAP alpha -VH CD3-VL CD3. More preferred, the binding domains are arranged in the order VL FAP alpha -VH FAP alpha -VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 1143, 1147, 1145, 1860, 1846, 1790, 1804, 1874, 1818, or 1832;

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 1144, 1148, 1146, 1861, 1847, 1791, 1805, 1875, 1818 or 1833; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 1143, 1147, 1145, 1860, 1846, 1790, 1804, 1874, 1818, or 1832, as well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 1143, 1147, 1145, 1860, 1846, 1790, 1804, 1874, 1818, or 1832. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 1144, 1148, 1146, 1861, 1847, 1791, 1805, 1875, 1818 or 1833, as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 1144, 1148, 1146, 1861, 1847, 1791, 1805, 1875, 1818 or 1833. It is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence having e.g. 85% (90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid sequences of the bispecific single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two

bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid residue. Said hypothesis is well known to the person skilled in the art (see e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the FAPalphaxCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen FAP alpha recognized by their second binding domain.

IGF-1RxCD3

According to a preferred embodiment of the invention an above characterized bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from the group consisting of:

a) CDR H1-3 of SEQ ID NO: 2016 - 2018and CDR L1-3 of SEQ ID NO: 2021 - 2023;

b) CDR H1-3 of SEQ ID NO: 2030 - 2032 and CDR L1-3 of SEQ ID NO: 2035 - 2037;

c) CDR H1-3 of SEQ ID NO: 2044 - 2046 and CDR L1-3 of SEQ ID NO: 2049 - 2051; and

d) CDR H1-3 of SEQ ID NO: 2058 - 2060 and CDR L1-3 of SEQ ID NO: 2063 – 2065;

e) CDR H1-3 of SEQ ID NO: 2072 – 2074 and CDR L1-3 of SEQ ID NO: 2077 – 2079;

f) CDR H1-3 of SEQ ID NO: 2086 – 2088 and CDR L1-3 of SEQ ID NO: 2091 – 2093;

g) CDR H1-3 of SEQ ID NO: 2100 – 2102 and CDR L1-3 of SEQ ID NO: 2105 – 2107;

h) CDR H1-3 of SEQ ID NO: 2114 – 2116 and CDR L1-3 of SEQ ID NO: 2119 – 2121;

i) CDR H1-3 of SEQ ID NO: 2128 – 2130 and CDR L1-3 of SEQ ID NO: 2133 – 2135;

j) CDR H1-3 of SEQ ID NO: 2142 – 2144 and CDR L1-3 of SEQ ID NO: 2147 – 2149:

k) CDR H1-3 of SEQ ID NO: 2156 – 2158 and CDR L1-3 of SEQ ID NO: 2161 – 2163;

l) CDR H1-3 of SEQ ID NO: 2170 – 2172 and CDR L1-3 of SEQ ID NO: 2175 – 2177;

m) CDR H1-3 of SEQ ID NO: 2184 – 2186 and CDR L1-3 of SEQ ID NO: 2189 – 2191;

n) CDR H1-3 of SEQ ID NO: 2198 – 2200 and CDR L1-3 of SEQ ID NO: 2203 – 2205; and

o) CDR H1-3 of SEQ ID NO: 2212 – 2214 and CDR L1-3 of SEQ ID NO: 2217 – 2219.

The sequences of the corresponding VL- and VH-regions of the second binding domain of the bispecific single chain antibody molecule of the invention as well as of the respective scFvs are shown in the sequence listing.

In the bispecific single chain antibody molecule of the invention the binding domains are arranged in the order VL-VH-VH-VL, VL-VH-VL-VH, VH-VL-VH-VL or VH-VL-VL-VH, as exemplified in the appended examples. Preferably, the binding domains are arranged in the order VH IGF-1R-VL IGF-1R-VH CD3-VL CD3 or VL IGF-1R-VH IGF-1R-VH CD3-VL CD3.

A particularly preferred embodiment of the invention concerns an above characterized polypeptide, wherein the bispecific single chain antibody molecule comprises a sequence selected from:

(a) an amino acid sequence as depicted in any of SEQ ID NOs: 2027, 2041, 2055, 2069, 2083, 2097, 2111, 2125, 2139, 2153, 2167, 2181, 2195, 2209, or 2223;

(b) an amino acid sequence encoded by a nucleic acid sequence as depicted in any of SEQ ID NOs: 2028, 2042, 2056, 2070, 2084, 2098, 2112, 2126, 2140, 2154, 2168, 2182, 2196, 2210, or 2224; and

(c) an amino acid sequence at least 90 % identical, more preferred at least 95 % identical, most preferred at least 96 % identical to the amino acid sequence of (a) or (b).

The invention relates to a bispecific single chain antibody molecule comprising an amino acid sequence as depicted in any of SEQ ID NOs: 2027, 2041, 2055, 2069, 2083, 2097, 2111, 2125, 2139, 2153, 2167, 2181, 2195, 2209, or 2223, as well as to an amino acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the amino acid sequence of SEQ ID NOs: 2027, 2041, 2055, 2069, 2083, 2097, 2111, 2125, 2139, 2153, 2167, 2181, 2195, 2209, or 2223. The invention relates also to the corresponding nucleic acid sequences as depicted in any of SEQ ID NOs: 2028, 2042, 2056, 2070, 2084, 2098, 2112, 2126, 2140, 2154, 2168, 2182, 2196, 2210, or 2224 as well as to nucleic acid sequences at least 85% identical, preferably 90 %, more preferred at least 95 % identical, most preferred at least 96, 97, 98, or 99 % identical to the nucleic acid sequences shown in SEQ ID NOs: 2028, 2042, 2056, 2070, 2084, 2098, 2112, 2126, 2140, 2154, 2168, 2182, 2196, 2210, or 2224. It is to be understood that the sequence identity is determined over the entire nucleotide or amino acid sequence. For sequence alignments, for example, the programs Gap or BestFit can be used (Needleman and Wunsch J. Mol. Biol. 48 (1970), 443-453; Smith and Waterman, Adv. Appl. Math 2 (1981), 482-489), which is contained in the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991). It is a routine method for those skilled in the art to determine and identify a nucleotide or amino acid sequence having e.g. 85% (90%, 95%, 96%, 97%, 98% or 99%) sequence identity to the nucleotide or amino acid sequences of the bispecific single single chain antibody of the invention. For example, according to Crick's Wobble hypothesis, the 5' base on the anti-codon is not as spatially confined as the other two bases, and could thus have non-standard base pairing. Put in other words: the third position in a codon triplet may vary so that two triplets which differ in this third position may encode the same amino acid

residue. Said hypothesis is well known to the person skilled in the art (see e.g. http://en.wikipedia.org/wiki/Wobble_Hypothesis; Crick, J Mol Biol 19 (1966): 548–55).

Preferred domain arrangements in the IGF-1RxCD3 bispecific single chain antibody constructs of the invention are shown in the following examples.

In a preferred embodiment of the invention, the bispecific single chain antibodies are cross-species specific for CD3 epsilon and for the human and non-chimpanzee primate cell surface antigen IGF-1R recognized by their second binding domain.

In an alternative embodiment the present invention provides a nucleic acid sequence encoding an above described bispecific single chain antibody molecule of the invention.

The present invention also relates to a vector comprising the nucleic acid molecule of the present invention.
Many suitable vectors are known to those skilled in molecular biology, the choice of which would depend on the function desired and include plasmids, cosmids, viruses, bacteriophages and other vectors used conventionally in genetic engineering. Methods which are well known to those skilled in the art can be used to construct various plasmids and vectors; see, for example, the techniques described in Sambrook et al. (loc cit.) and Ausubel, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. (1989), (1994). Alternatively, the polynucleotides and vectors of the invention can be reconstituted into liposomes for delivery to target cells. As discussed in further details below, a cloning vector was used to isolate individual sequences of DNA. Relevant sequences can be transferred into expression vectors where expression of a particular polypeptide is required. Typical cloning vectors include pBluescript SK, pGEM, pUC9, pBR322 and pGBT9. Typical expression vectors include pTRE, pCAL-n-EK, pESP-1, pOP13CAT.

Preferably said vector comprises a nucleic acid sequence which is a regulatory sequence operably linked to said nucleic acid sequence defined herein.
The term "regulatory sequence" refers to DNA sequences, which are necessary to effect the expression of coding sequences to which they are ligated. The nature of

such control sequences differs depending upon the host organism. In prokaryotes, control sequences generally include promoter, ribosomal binding site, and terminators. In eukaryotes generally control sequences include promoters, terminators and, in some instances, enhancers, transactivators or transcription factors. The term "control sequence" is intended to include, at a minimum, all components the presence of which are necessary for expression, and may also include additional advantageous components.

The term "operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences. In case the control sequence is a promoter, it is obvious for a skilled person that double-stranded nucleic acid is preferably used.

Thus, the recited vector is preferably an expression vector. An "expression vector" is a construct that can be used to transform a selected host and provides for expression of a coding sequence in the selected host. Expression vectors can for instance be cloning vectors, binary vectors or integrating vectors. Expression comprises transcription of the nucleic acid molecule preferably into a translatable mRNA. Regulatory elements ensuring expression in prokaryotes and/or eukaryotic cells are well known to those skilled in the art. In the case of eukaryotic cells they comprise normally promoters ensuring initiation of transcription and optionally poly-A signals ensuring termination of transcription and stabilization of the transcript. Possible regulatory elements permitting expression in prokaryotic host cells comprise, e.g., the P_L, *lac*, *trp* or *tac* promoter in *E. coli*, and examples of regulatory elements permitting expression in eukaryotic host cells are the *AOX1* or *GAL1* promoter in yeast or the CMV-, SV40-, RSV-promoter (Rous sarcoma virus), CMV-enhancer, SV40-enhancer or a globin intron in mammalian and other animal cells.

Beside elements, which are responsible for the initiation of transcription such regulatory elements may also comprise transcription termination signals, such as the SV40-poly-A site or the tk-poly-A site, downstream of the polynucleotide. Furthermore, depending on the expression system used leader sequences capable of directing the polypeptide to a cellular compartment or secreting it into the medium may be added to the coding sequence of the recited nucleic acid sequence and are well known in the art; see also the appended Examples. The leader sequence(s) is

(are) assembled in appropriate phase with translation, initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein, or a portion thereof, into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product; see supra. In this context, suitable expression vectors are known in the art such as Okayama-Berg cDNA expression vector pcDV1 (Pharmacia), pCDM8, pRc/CMV, pcDNA1, pcDNA3 (In-vitrogene), pEF-DHFR, pEF-ADA or pEF-neo (Mack et al. PNAS (1995) 92, 7021-7025 and Raum et al. Cancer Immunol Immunother (2001) 50(3), 141-150) or pSPORT1 (GIBCO BRL).

Preferably, the expression control sequences will be eukaryotic promoter systems in vectors capable of transforming of transfecting eukaryotic host cells, but control sequences for prokaryotic hosts may also be used. Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences, and as desired, the collection and purification of the bispecific single chain antibody molecule of the invention may follow; see, e.g., the appended examples.

An alternative expression system, which can be used to express a cell cycle interacting protein is an insect system. In one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The coding sequence of a recited nucleic acid molecule may be cloned into a nonessential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of said coding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein coat. The recombinant viruses are then used to infect *S. frugiperda* cells or *Trichoplusia* larvae in which the protein of the invention is expressed (Smith, J. Virol. 46 (1983), 584; Engelhard, Proc. Nat. Acad. Sci. USA 91 (1994), 3224-3227).

Additional regulatory elements may include transcriptional as well as translational enhancers. Advantageously, the above-described vectors of the invention comprise a selectable and/or scorable marker.

Selectable marker genes useful for the selection of transformed cells and, e.g., plant tissue and plants are well known to those skilled in the art and comprise, for example,

antimetabolite resistance as the basis of selection for dhfr, which confers resistance to methotrexate (Reiss, Plant Physiol. (Life Sci. Adv.) 13 (1994), 143-149); npt, which confers resistance to the aminoglycosides neomycin, kanamycin and paromycin (Herrera-Estrella, EMBO J. 2 (1983), 987-995) and hygro, which confers resistance to hygromycin (Marsh, Gene 32 (1984), 481-485). Additional selectable genes have been described, namely trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histinol in place of histidine (Hartman, Proc. Natl. Acad. Sci. USA 85 (1988), 8047); mannose-6-phosphate isomerase which allows cells to utilize mannose (WO 94/20627) and ODC (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue, 1987, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.) or deaminase from Aspergillus terreus which confers resistance to Blasticidin S (Tamura, Biosci. Biotechnol. Biochem. 59 (1995), 2336-2338).

Useful scorable markers are also known to those skilled in the art and are commercially available. Advantageously, said marker is a gene encoding luciferase (Giacomin, Pl. Sci. 116 (1996), 59-72; Scikantha, J. Bact. 178 (1996), 121), green fluorescent protein (Gerdes, FEBS Lett. 389 (1996), 44-47) or ß-glucuronidase (Jefferson, EMBO J. 6 (1987), 3901-3907). This embodiment is particularly useful for simple and rapid screening of cells, tissues and organisms containing a recited vector.

As described above, the recited nucleic acid molecule can be used alone or as part of a vector to express the bispecific single chain antibody molecule of the invention in cells, for, e.g., purification but also for gene therapy purposes. The nucleic acid molecules or vectors containing the DNA sequence(s) encoding any one of the above described bispecific single chain antibody molecule of the invention is introduced into the cells which in turn produce the polypeptide of interest. Gene therapy, which is based on introducing therapeutic genes into cells by ex-vivo or in-vivo techniques is one of the most important applications of gene transfer. Suitable vectors, methods or gene-delivery systems for in-vitro or in-vivo gene therapy are described in the literature and are known to the person skilled in the art; see, e.g., Giordano, Nature Medicine 2 (1996), 534-539; Schaper, Circ. Res. 79 (1996), 911-919; Anderson, Science 256 (1992), 808-813; Verma, Nature 389 (1994), 239; Isner, Lancet 348 (1996), 370-374; Muhlhauser, Circ. Res. 77 (1995), 1077-1086; Onodera,

Blood 91 (1998), 30-36; Verma, Gene Ther. 5 (1998), 692-699; Nabel, Ann. N.Y. Acad. Sci. 811 (1997), 289-292; Verzeletti, Hum. Gene Ther. 9 (1998), 2243-51; Wang, Nature Medicine 2 (1996), 714-716; WO 94/29469; WO 97/00957, US 5,580,859; US 5,589,466; or Schaper, Current Opinion in Biotechnology 7 (1996), 635-640; dos Santos Coura and Nardi Virol J. (2007), 4:99. The recited nucleic acid molecules and vectors may be designed for direct introduction or for introduction via liposomes, or viral vectors (e.g., adenoviral, retroviral) into the cell. Preferably, said cell is a germ line cell, embryonic cell, or egg cell or derived there from, most preferably said cell is a stem cell. An example for an embryonic stem cell can be, inter alia, a stem cell as described in Nagy, Proc. Natl. Acad. Sci. USA 90 (1993), 8424-8428.

The invention also provides for a host transformed or transfected with a vector of the invention. Said host may be produced by introducing the above described vector of the invention or the above described nucleic acid molecule of the invention into the host. The presence of at least one vector or at least one nucleic acid molecule in the host may mediate the expression of a gene encoding the above described single chain antibody constructs.

The described nucleic acid molecule or vector of the invention, which is introduced in the host may either integrate into the genome of the host or it may be maintained extrachromosomally.

The host can be any prokaryote or eukaryotic cell.

The term "prokaryote" is meant to include all bacteria, which can be transformed or transfected with DNA or RNA molecules for the expression of a protein of the invention. Prokaryotic hosts may include gram negative as well as gram positive bacteria such as, for example, E. coli, S. typhimurium, Serratia marcescens and Bacillus subtilis. The term "eukaryotic" is meant to include yeast, higher plant, insect and preferably mammalian cells. Depending upon the host employed in a recombinant production procedure, the protein encoded by the polynucleotide of the present invention may be glycosylated or may be non-glycosylated. Especially preferred is the use of a plasmid or a virus containing the coding sequence of the bispecific single chain antibody molecule of the invention and genetically fused thereto an N-terminal FLAG-tag and/or C-terminal His-tag. Preferably, the length of said FLAG-tag is about 4 to 8 amino acids, most preferably 8 amino acids. An above

described polynucleotide can be used to transform or transfect the host using any of the techniques commonly known to those of ordinary skill in the art. Furthermore, methods for preparing fused, operably linked genes and expressing them in, e.g., mammalian cells and bacteria are well-known in the art (Sambrook, loc cit.).
Preferably, said the host is a bacterium or an insect, fungal, plant or animal cell.
It is particularly envisaged that the recited host may be a mammalian cell. Particularly preferred host cells comprise CHO cells, COS cells, myeloma cell lines like SP2/0 or NS/0. As illustrated in the appended examples, particularly preferred are CHO-cells as hosts.
More preferably said host cell is a human cell or human cell line, e.g. per.c6 (Kroos, Biotechnol. Prog., 2003, 19:163-168).

In a further embodiment, the present invention thus relates to a process for the production of a bispecific single chain antibody molecule of the invention, said process comprising culturing a host of the invention under conditions allowing the expression of the bispecific single chain antibody molecule of the invention and recovering the produced polypeptide from the culture.
The transformed hosts can be grown in fermentors and cultured according to techniques known in the art to achieve optimal cell growth. The bispecific single chain antibody molecule of the invention can then be isolated from the growth medium, cellular lysates, or cellular membrane fractions. The isolation and purification of the, e.g., microbially expressed bispecific single chain antibody molecules may be by any conventional means such as, for example, preparative chromatographic separations and immunological separations such as those involving the use of monoclonal or polyclonal antibodies directed, e.g., against a tag of the bispecific single chain antibody molecule of the invention or as described in the appended examples.
The conditions for the culturing of a host, which allow the expression are known in the art to depend on the host system and the expression system/vector used in such process. The parameters to be modified in order to achieve conditions allowing the expression of a recombinant polypeptide are known in the art. Thus, suitable conditions can be determined by the person skilled in the art in the absence of further inventive input.
Once expressed, the bispecific single chain antibody molecule of the invention can be purified according to standard procedures of the art, including ammonium sulfate

precipitation, affinity columns, column chromatography, gel electrophoresis and the like; see, Scopes, "Protein Purification", Springer-Verlag, N.Y. (1982). Substantially pure polypeptides of at least about 90 to 95% homogeneity are preferred, and 98 to 99% or more homogeneity are most preferred, for pharmaceutical uses. Once purified, partially or to homogeneity as desired, the bispecific single chain antibody molecule of the invention may then be used therapeutically (including extracorporeally) or in developing and performing assay procedures. Furthermore, examples for methods for the recovery of the bispecific single chain antibody molecule of the invention from a culture are described in detail in the appended examples. The recovery can also be achieved by a method for the isolation of the bispecific single chain antibody molecule of the invention capable of binding to an epitope of human and non-chimpanzee primate CD3 epsilon (CD3ε, the method comprising the steps of:

(a) contacting the polypeptide(s) with an N-terminal fragment of the extracellular domain of CD3ε of maximal 27 amino acids comprising the amino acid sequence Gln-Asp-Gly-Asn-Glu-Glu-Met-Gly (SEQ ID NO. 341) or Gln-Asp-Gly-Asn-Glu-Glu-Ile-Gly (SEQ ID NO. 342), fixed via its C-terminus to a solid phase;

(b) eluting the bound polypeptide(s) from said fragment; and

(c) isolating the polypeptide(s) from the eluate of (b).

It is preferred that the polypeptide(s) isolated by the above method of the invention are human.

This method or the isolation of the bispecific single chain antibody molecule of the invention is understood as a method for the isolation of one or more different polypeptides with the same specificity for the fragment of the extracellular domain of CD3ε comprising at its N-terminus the amino acid sequence Gln-Asp-Gly-Asn-Glu-Glu-Met-Gly (SEQ ID NO. 341) or Gln-Asp-Gly-Asn-Glu-Glu-Ile-Gly (SEQ ID NO. 342) from a plurality of polypeptide candidates as well as a method for the purification of a polypeptide from a solution. A non-limiting example for the latter method for the purification of a bispecific single chain antibody molecule from a solution is e.g. the purification of a recombinantly expressed bispecific single chain antibody molecule from a culture supernatant or a preparation from such culture.

As stated above the fragment used in this method is an N-terminal fragment of the extracellular domain of the primate CD3ε molecule. The amino acid sequence of the extracellular domain of the CD3ε molecule of different species is depicted in SEQ ID

NOs: 1, 3, 5 and 7. The two forms of the N-terminal octamer are depicted in SEQ ID NOs: 341 and 342. It is preferred that this N-terminus is freely available for binding of the polypeptides to be identified by the method of the invention. The term "freely available" is understood in the context of the invention as free of additional motives such as a His-tag. The interference of such a His-tag with a binding molecule identified by the method of the invention is described in the appended Examples 6 and 20.

According to this method said fragment is fixed via its C-terminus to a solid phase. The person skilled in the art will easily and without any inventive ado elect a suitable solid phase support dependent from the used embodiment of the method of the invention. Examples for a solid support comprise but are not limited to matrices like beads (e.g. agarose beads, sepharose beads, polystyrol beads, dextran beads), plates (culture plates or MultiWell plates) as well as chips known e.g. from Biacore®. The selection of the means and methods for the fixation/immobilization of the fragment to said solid support depend on the election of the solid support. A commonly used method for the fixation/immobilization is a coupling via an N-hydroxysuccinimide (NHS) ester. The chemistry underlying this coupling as well as alternative methods for the fixation/immobilization are known to the person skilled in the art, e.g. from Hermanson "Bioconjugate Techniques", Academic Press, Inc. (1996). For the fixation to/immobilization on chromatographic supports the following means are commonly used: NHS-activated sepharose (e.g. HiTrap-NHS of GE Life Science-Amersham), CnBr-activated sepharose (e.g. GE Life Science-Amersham), NHS-activated dextran beads (Sigma) or activated polymethacrylate. These reagents may also be used in a batch approach. Moreover, dextran beads comprising iron oxide (e.g. available from Miltenyi) may be used in a batch approach. These beads may be used in combination with a magnet for the separation of the beads from a solution. Polypeptides can be immobilized on a Biacore chip (e.g. CM5 chips) by the use of NHS activated carboxymethyldextran. Further examples for an appropriate solid support are amine reactive MultiWell plates (e.g. Nunc Immobilizer™ plates).

According to this method said fragment of the extracellular domain of CD3 epsilon can be directly coupled to the solid support or via a stretch of amino acids, which might be a linker or another protein/polypeptide moiety. Alternatively, the extracellular domain of CD3 epsilon can be indirectly coupled via one or more adaptor molecule(s).

Means and methods for the eluation of a peptide or polypeptide bound to an immobilized epitope are well known in the art. The same holds true for methods for the isolation of the identified polypeptide(s) from the eluate.

A method for the isolation of one or more different bispecific single chain antibody molecule(s) with the same specificity for the fragment of the extracellular domain of CD3ε comprising at its N-terminus the amino acid sequence Gln-Asp-Gly-Asn-Glu-Glu-X-Gly (with X being Met or Ile) from a plurality of polypeptide candidates may comprise one or more steps of the following methods for the selection of antigen-specific entities:

CD3ε specific binding domains can be selected from antibody derived repertoires. A phage display library can be constructed based on standard procedures, as for example disclosed in "Phage Display: A Laboratory Manual"; Ed. Barbas, Burton, Scott & Silverman; Cold Spring Harbor Laboratory Press, 2001. The format of the antibody fragments in the antibody library can be scFv, but may generally also be a Fab fragment or even a single domain antibody fragment. For the isolation of antibody fragments naïve antibody fragment libraries may be used. For the selection of potentially low immunogenic binding entities in later therapeutic use, human antibody fragment libraries may be favourable for the direct selection of human antibody fragments. In some cases they may form the basis for synthetic antibody libraries (Knappik et al. J Mol. Biol. 2000, 296:57 ff). The corresponding format may be Fab, scFv (as described below) or domain antibodies (dAbs, as reviewed in Holt et al., Trends Biotechnol. 2003, 21:484 ff).

It is also known in the art that in many cases there is no immune human antibody source available against the target antigen. Therefore animals are immunized with the target antigen and the respective antibody libraries isolated from animal tissue as e.g. spleen or PBMCs. The N-terminal fragment may be biotinylated or covalently linked to proteins like KLH or bovine serum albumin (BSA). According to common approaches rodents are used for immunization. Some immune antibody repertoires of non-human origin may be especially favourable for other reasons, e.g. for the presence of single domain antibodies (VHH) derived from cameloid species (as described in Muyldermans, J Biotechnol. 74:277; De Genst et al. Dev Como Immunol. 2006, 30:187 ff). Therefore a corresponding format of the antibody library may be Fab, scFv (as described below) or single domain antibodies (VHH).

In one possible approach ten weeks old F1 mice from balb/c x C57black crossings

can be immunized with whole cells e.g. expressing transmembrane EpCAM N-terminally displaying as translational fusion the N-terminal amino acids 1 to 27 of the mature CD3ε chain. Alternatively, mice can be immunized with 1-27 CD3 epsilon-Fc fusion protein (a corresponding approach is described in the appended Example 2). After booster immunization(s), blood samples can be taken and antibody serum titer against the CD3-positive T cells can be tested e.g. in FACS analysis. Usually, serum titers are significantly higher in immunized than in non-immunized animals.

Immunized animals may form the basis for the construction of immune antibody libraries. Examples of such libraries comprise phage display libraries. Such libraries may be generally constructed based on standard procedures, as for example disclosed in "Phage Display: A Laboratory Manual"; Ed. Barbas, Burton, Scott & Silverman; Cold Spring Harbor Laboratory Press, 2001.

The non-human antibodies can also be humanized via phage display due to the generation of more variable antibody libraries that can be subsequently enriched for binders during selection.

In a phage display approach any one of the pools of phages that displays the antibody libraries forms a basis to select binding entities using the respective antigen as target molecule. The central step in which antigen specific, antigen bound phages are isolated is designated as panning. Due to the display of the antibody fragments on the surface of the phages, this general method is called phage display. One preferred method of selection is the use of small proteins such as the filamentous phage N2 domain translationally fused to the N-terminus of the scFv displayed by the phage. Another display method known in the art, which may be used to isolate binding entities is the ribosome display method (reviewed in Groves & Osbourn, Expert Opin Biol Ther. 2005, 5:125 ff; Lipovsek & Pluckthun, J Immunol Methods 2004, 290:52 ff). In order to demonstrate binding of scFv phage particles to a 1-27 CD3ε-Fc fusion protein a phage library carrying the cloned scFv-repertoire can be harvested from the respective culture supernatant by PEG (polyethyleneglycole). ScFv phage particles may be incubated with immobilized CD3ε Fc fusion protein. The immobilized CD3ε Fc fusion protein may be coated to a solid phase. Binding entities can be eluted and the eluate can be used for infection of fresh uninfected bacterial hosts. Bacterial hosts successfully transduced with a phagemid copy, encoding a human scFv-fragment, can be selected again for carbenicillin resistance and subsequently infected with e.g. VCMS 13 helper phage to start the second round of

antibody display and in vitro selection. A total of 4 to 5 rounds of selections is carried out, normally. The binding of isolated binding entities can be tested on CD3 epsilon positive Jurkat cells, HPBall cells, PBMCs or transfected eukaryotic cells that carry the N-terminal CD3ε sequence fused to surface displayed EpCAM using a flow cytometric assay (see appended Example 4).

Preferably, the above method may be a method, wherein the fragment of the extracellular domain of CD3ε consists of one or more fragments of a polypeptide having an amino acid sequence of any one depicted in SEQ ID NOs. 2, 4, 6 or 8. More preferably, said fragment is 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27 amino acid residues in length.

This method of identification of a bispecific single chain antibody molecule may be a method of screening a plurality of bispecific single chain antibody molecules comprising a cross-species specific binding domain binding to an epitope of human and non-chimpanzee primate CD3ε. Alternatively, the method of identification is a method of purification/isolation of a bispecific single chain antibody molecule comprising a cross-species specific binding domain binding to an epitope of human and non-chimpanzee primate CD3ε.

Furthermore, the invention provides for a composition comprising a bispecific single chain antibody molecule of the invention or a bispecific single chain antibody as produced by the process disclosed above. Preferably, said composition is a pharmaceutical composition.

The invention provides also for a bispecific single chain antibody molecule as defined herein, or produced according to the process as defined herein, wherein said bispecific single chain antibody molecule is for use in the prevention, treatment or amelioration of cancer or autoimmune diseases.

Preferably for a PSCAxCD3 bispecific single chain antibody molecule, said cancer is prostate cancer, bladder cancer or pancreatic cancer.

For a CD19xCD3 bispecific single chain antibody molecule it is preferred that said cancer is a B-cell malignancy, such as B-NHL (B cell non-Hodgkin Lymphoma), B-ALL (acute lymphoblastic B cell leukemia), B-CLL (chronic lymphocytic B cell leukemia), or Multiple Myeloma (wherein the bispecific single chain antibody molecule of the invention advantageously depletes CD19-positive cancer stem

cells/cancer initiating cells). However, the bispecific single chain antibody molecule is also for use in the prevention, treatment or amelioration of B-cell mediated autoimmune diseases or autoimmune diseases with a pathogenic B cell contribution such as rheumatoid arthritis or the depletion of B-cells.

For a c-METxCD3 bispecific single chain antibody molecule it is preferred that said cancer is a carcinoma, sarcoma, glioblastoma/astrocytoma, melanoma, mesothelioma, Wilms tumor or a hematopoietic malignancy such as leukemia, lymphoma or multiple myeloma. A comprehensive list of various cancer types which may be treated with the bispecific single chain antibody can be found e.g. in http://www.vai.org/met/.

For an EndosialinxCD3 bispecific single chain antibody molecule it is preferred that said cancer includes, but is not limited to, carcinomas (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), sarcomas, and neuroectodermal tumors (melanoma, glioma, neuroblastoma).

For an EpCAMxCD3 bispecific single chain antibody molecule it is preferred that said cancer is epithelial cancer or a minimal residual cancer.

For a FAPαxCD3 bispecific single chain antibody molecule it is preferred that said cancer is epithelial cancer.

For a IGF-1RxCD3 bispecific single chain antibody molecule it is preferred that said cancer is bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer. Alternatively, the IGF-1RxCD3 bispecific single chain antibody molecule of the invention is also used in the prevention, treatment or amelioration of autoimmune diseases, preferably psoriasis.

It is preferred that the bispecific single chain is further comprising suitable formulations of carriers, stabilizers and/or excipients. Moreover, it is preferred that said bispecific single chain antibody molecule is suitable to be administered in combination with an additional drug. Said drug may be a non-proteinaceous compound or a proteinaceous compound and may be administered simultaneously or non-simultaneously with the bispecific single chain antibody molecule as defined herein.

In accordance with the invention, the term "pharmaceutical composition" relates to a composition for administration to a patient, preferably a human patient. The particular

preferred pharmaceutical composition of this invention comprises bispecific single chain antibodies directed against and generated against context-independent CD3 epitopes. Preferably, the pharmaceutical composition comprises suitable formulations of carriers, stabilizers and/or excipients. In a preferred embodiment, the pharmaceutical composition comprises a composition for parenteral, transdermal, intraluminal, intraarterial, intrathecal and/or intranasal administration or by direct injection into tissue. It is in particular envisaged that said composition is administered to a patient via infusion or injection. Administration of the suitable compositions may be effected by different ways, e.g., by intravenous, intraperitoneal, subcutaneous, intramuscular, topical or intradermal administration. In particular, the present invention provides for an uninterrupted administration of the suitable composition. As a non-limiting example, uninterrupted, i.e. continuous administration may be realized by a small pump system worn by the patient for metering the influx of therapeutic agent into the body of the patient. The pharmaceutical composition comprising the bispecific single chain antibodies directed against and generated against context-independent CD3 epitopes of the invention can be administered by using said pump systems. Such pump systems are generally known in the art, and commonly rely on periodic exchange of cartridges containing the therapeutic agent to be infused. When exchanging the cartridge in such a pump system, a temporary interruption of the otherwise uninterrupted flow of therapeutic agent into the body of the patient may ensue. In such a case, the phase of administration prior to cartridge replacement and the phase of administration following cartridge replacement would still be considered within the meaning of the pharmaceutical means and methods of the invention together make up one "uninterrupted administration" of such therapeutic agent.

The continuous or uninterrupted administration of these bispecific single chain antibodies directed against and generated against context-independent CD3 epitopes of this invention may be intravenuous or subcutaneous by way of a fluid delivery device or small pump system including a fluid driving mechanism for driving fluid out of a reservoir and an actuating mechanism for actuating the driving mechanism. Pump systems for subcutaneous administration may include a needle or a cannula for penetrating the skin of a patient and delivering the suitable composition into the patient's body. Said pump systems may be directly fixed or attached to the skin of the patient independently of a vein, artery or blood vessel, thereby allowing a direct contact between the pump system and the skin of the patient. The pump

system can be attached to the skin of the patient for 24 hours up to several days. The pump system may be of small size with a reservoir for small volumes. As a non-limiting example, the volume of the reservoir for the suitable pharmaceutical composition to be administered can be between 0.1 and 50 ml.
The continuous administration may be transdermal by way of a patch worn on the skin and replaced at intervals. One of skill in the art is aware of patch systems for drug delivery suitable for this purpose. It is of note that transdermal administration is especially amenable to uninterrupted administration, as exchange of a first exhausted patch can advantageously be accomplished simultaneously with the placement of a new, second patch, for example on the surface of the skin immediately adjacent to the first exhausted patch and immediately prior to removal of the first exhausted patch. Issues of flow interruption or power cell failure do not arise.

The composition of the present invention, comprising in particular bispecific single chain antibodies directed against and generated against context-independent CD3 epitopes may further comprise a pharmaceutically acceptable carrier. Examples of suitable pharmaceutical carriers are well known in the art and include solutions, e.g. phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions, liposomes, etc. Compositions comprising such carriers can be formulated by well known conventional methods. Formulations can comprise carbohydrates, buffer solutions, amino acids and/or surfactants. Carbohydrates may be non-reducing sugars, preferably trehalose, sucrose, octasulfate, sorbitol or xylitol. Such formulations may be used for continuous administrations which may be intravenuous or subcutaneous with and/or without pump systems. Amino acids may be charged amino acids, preferably lysine, lysine acetate, arginine, glutamate and/or histidine. Surfactants may be detergents, preferably with a molecular weight of >1.2 KD and/or a polyether, preferably with a molecular weight of >3 KD. Non-limiting examples for preferred detergents are Tween 20, Tween 40, Tween 60, Tween 80 or Tween 85. Non-limiting examples for preferred polyethers are PEG 3000, PEG 3350, PEG 4000 or PEG 5000. Buffer systems used in the present invention can have a preferred pH of 5-9 and may comprise citrate, succinate, phosphate, histidine and acetate. The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. by dose escalating studies by administration of increasing doses

of the bispecific single chain antibody molecule of the invention exhibiting cross-species specificity described herein to non-chimpanzee primates, for instance macaques. As set forth above, the bispecific single chain antibody molecule of the invention exhibiting cross-species specificity described herein can be advantageously used in identical form in preclinical testing in non-chimpanzee primates and as drug in humans. These compositions can also be administered in combination with other proteinaceous and non-proteinaceous drugs. These drugs may be administered simultaneously with the composition comprising the bispecific single chain antibody molecule of the invention as defined herein or separately before or after administration of said polypeptide in timely defined intervals and doses. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases and the like. In addition, the composition of the present invention might comprise proteinaceous carriers, like, e.g., serum albumin or immunoglobulin, preferably of human origin. It is envisaged that the composition of the invention might comprise, in addition to the bispecific single chain antibody molecule of the invention defined herein, further biologically active agents, depending on the intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions (e.g. corticosteroids), drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art.

The biological activity of the pharmaceutical composition defined herein can be determined for instance by cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth et al. (Cancer Immunol. Immunother. 20 (2005), 1 – 12). "Efficacy" or "in vivo efficacy" as used herein refers to the response to therapy by the pharmaceutical composition of the invention, using e.g. standardized NCI response criteria. The success or *in vivo* efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, i.e. the ability of the composition to cause its desired effect, i.e. depletion of pathologic cells, e.g. tumor cells. The *in vivo* efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography (e.g. for National Cancer Institute-criteria based response assessment [Cheson BD, Horning SJ, Coiffier B, Shipp MA, Fisher RI, Connors JM, Lister TA, Vose J, Grillo-Lopez A, Hagenbeek A, Cabanillas F, Klippensten D, Hiddemann W, Castellino R, Harris NL, Armitage JO, Carter W, Hoppe R, Canellos GP. Report of an international workshop to standardize response criteria for non-Hodgkin's lymphomas. NCI Sponsored International Working Group. J Clin Oncol. 1999 Apr;17(4):1244]), positron-emission tomography scanning, white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration, lymph node biopsies/histologies, and various cancer specific clinical chemistry parameters (e.g. lactate dehydrogenase) and other established standard methods may be used.

Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that effect the ability of a particular drug to treat a given condition, is established. Pharmacokinetic parameters of the drug influencing the ability of a drug for treating a certain disease entity include, but are not limited to: half-life, volume of distribution, hepatic first-pass metabolism and the degree of blood

serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

"Half-life" means the time where 50% of an administered drug are eliminated through biological processes, e.g. metabolism, excretion, etc.

By "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver.

"Volume of distribution" means the degree of retention of a drug throughout the various compartments of the body, like e.g. intracellular and extracellular spaces, tissues and organs, etc. and the distribution of the drug within these compartments.

"Degree of blood serum binding" means the propensity of a drug to interact with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

Pharmacokinetic parameters also include bioavailability, lag time (Tlag), Tmax, absorption rates, more onset and/or Cmax for a given amount of drug administered.

"Bioavailability" means the amount of a drug in the blood compartment.

"Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma.

"Tmax" is the time after which maximal blood concentration of the drug is reached, and "Cmax" is the blood concentration maximally obtained with a given drug. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is influenced by all parameters. Pharmacokinetik parameters of bispecific single chain antibodies exhibiting cross-species specificity, which may be determined in preclinical animal testing in non-chimpanzee primates as outlined above are also set forth e.g. in the publication by Schlereth et al. (Cancer Immunol. Immunother. 20 (2005), 1 – 12).

The term "toxicity" as used herein refers to the toxic effects of a drug manifested in adverse events or severe adverse events. These side events might refer to a lack of tolerability of the drug in general and/or a lack of local tolerance after administration. Toxicity could also include teratogenic or carcinogenic effects caused by the drug.

The term "safety", "in vivo safety" or "tolerability" as used herein defines the administration of a drug without inducing severe adverse events directly after administration (local tolerance) and during a longer period of application of the drug.

"Safety", "in vivo safety" or "tolerability" can be evaluated e.g. at regular intervals during the treatment and follow-up period. Measurements include clinical evaluation, e.g. organ manifestations, and screening of laboratory abnormalities. Clinical evaluation may be carried out and deviating to normal findings recorded/coded according to NCI-CTC and/or MedDRA standards. Organ manifestations may include criteria such as allergy/immunology, blood/bone marrow, cardiac arrhythmia, coagulation and the like, as set forth e.g. in the Common Terminology Criteria for adverse events v3.0 (CTCAE). Laboratory parameters which may be tested include for instance haematology, clinical chemistry, coagulation profile and urine analysis and examination of other body fluids such as serum, plasma, lymphoid or spinal fluid, liquor and the like. Safety can thus be assessed e.g. by physical examination, imaging techniques (i.e. ultrasound, x-ray, CT scans, Magnetic Resonance Imaging (MRI), other measures with technical devices (i.e. electrocardiogram), vital signs, by measuring laboratory parameters and recording adverse events. For example, adverse events in non-chimpanzee primates in the uses and methods according to the invention may be examined by histopathological and/or histochemical methods.

The term "effective and non-toxic dose" as used herein refers to a tolerable dose of the bispecific single chain antibody as defined herein which is high enough to cause depletion of pathologic cells, tumor elimination, tumor shrinkage or stabilization of disease without or essentially without major toxic effects. Such effective and non-toxic doses may be determined e.g. by dose escalation studies described in the art and should be below the dose inducing severe adverse side events (dose limiting toxicity, DLT).

The above terms are also referred to e.g. in the Preclinical safety evaluation of biotechnology-derived pharmaceuticals S6; ICH Harmonised Tripartite Guideline; ICH Steering Committee meeting on July 16, 1997.

Moreover, the invention relates to a pharmaceutical composition comprising a bispecific single chain antibody molecule of this invention or produced according to the process according to the invention for the prevention, treatment or amelioration of cancer or autoimmune diseases.

Preferably, said cancer is for a PSCAxCD3 bispecific single chain antibody molecule prostate cancer, bladder cancer or pancreatic cancer.
Preferably, said cancer is for a CD19xCD3 bispecific single chain antibody molecule a B-cell malignancy such as non-Hodgkin Lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells.
Preferably, said cancer is for a c-METxCD3 bispecific single chain antibody molecule is a carcinoma, sarcoma, glioblastoma/astrocytoma, melanoma, mesothelioma, Wilms tumor or a hematopoietic malignancy such as leukemia, lymphoma or multiple myeloma.
Preferably, said cancer is for an EndosialinxCD3 bispecific single chain antibody molecule a carcinoma (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), a sarcoma, or a neuroectodermal tumor (melanoma, glioma, neuroblastoma).
Preferably, said cancer is for an EpCAMxCD3 bispecific single chain antibody molecule epithelial cancer or a minimal residual cancer.
Preferably, said cancer is for a FAPαxCD3 bispecific single chain antibody molecule epithelial cancer.
Preferably, said cancer is for a an IGF-1RxCD3 bispecific single chain antibody molecule bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer. Alternatively, the IGF-1RxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above is also used in the prevention, treatment or amelioration of autoimmune diseases, preferably psoriasis.

Preferably, said pharmaceutical composition further comprises suitable formulations of carriers, stabilizers and/or excipients.

A further aspect of the invention relates to a use of a bispecific single chain antibody molecule/polypeptide as defined herein above or produced according to a process defined herein above, for the preparation of a pharmaceutical composition for the prevention, treatment or amelioration of a disease. Preferably, said disease is cancer or autoimmune diseases.

More preferably for a PSCAxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is prostate cancer, bladder cancer or pancreatic cancer.

More preferably for a CD19xCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is a B-cell malignancy such as non-Hodgkin Lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells.

More preferably for a c-METxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is a carcinoma, sarcoma, glioblastoma/astrocytoma, melanoma, mesothelioma, Wilms tumor or a hematopoietic malignancy such as leukemia, lymphoma or multiple myeloma.

More preferably for an EndosialinxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is a carcinoma (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), a sarcoma, or a neuroectodermal tumor (melanoma, glioma, neuroblastoma).

More preferably for an EpCAMxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is epithelial cancer or a minimal residual cancer.

More preferably for a FAPαxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is epithelial cancer.

More preferably for an IGF-1RxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer. Alternatively, the IGF-1RxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above is also used in the prevention, treatment or amelioration of autoimmune diseases, preferably psoriasis.

In another preferred embodiment of use of the bispecific single chain antibody molecule of the invention said pharmaceutical composition is suitable to be administered in combination with an additional drug, i.e. as part of a co-therapy. In said co-therapy, an active agent may be optionally included in the same pharmaceutical composition as the bispecific single chain antibody molecule of the invention, or may be included in a separate pharmaceutical composition. In this latter

case, said separate pharmaceutical composition is suitable for administration prior to, simultaneously as or following administration of said pharmaceutical composition comprising the bispecific single chain antibody molecule of the invention. The additional drug or pharmaceutical composition may be a non-proteinaceous compound or a proteinaceous compound. In the case that the additional drug is a proteinaceous compound, it is advantageous that the proteinaceous compound be capable of providing an activation signal for immune effector cells.
Preferably, said proteinaceous compound or non-proteinaceous compound may be administered simultaneously or non-simultaneously with the bispecific single chain antibody molecule of the invention, a nucleic acid molecule as defined hereinabove, a vector as defined as defined hereinabove, or a host as defined as defined hereinabove.

Another aspect of the invention relates to a method for the prevention, treatment or amelioration of a disease in a subject in the need thereof, said method comprising the step of administration of an effective amount of a pharmaceutical composition of the invention. Preferably, said disease is cancer or autoimmune diseases.
More preferably for a PSCAxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above,, said cancer is prostate cancer, bladder cancer or pancreatic cancer.
More preferably for a CD19xCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is a B-cell malignancy such as non-Hodgkin Lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells.
More preferably for a c-METxCD3 bispecific bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is a carcinoma, sarcoma, glioblastoma/astrocytoma, melanoma, mesothelioma, Wilms tumor or a hematopoietic malignancy such as leukemia, lymphoma or multiple myeloma.
More preferably for an EndosialinxCD3 bispecific bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is a carcinoma (breast, kidney, lung, colorectal, colon, pancreas mesothelioma), a sarcoma, or a neuroectodermal tumor (melanoma, glioma, neuroblastoma).

More preferably for an EpCAMxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is epithelial cancer or a minimal residual cancer.

More preferably for a FAPαxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is epithelial cancer

More preferably for an IGF-1RxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above, said cancer is bone or soft tissue cancer (e.g. Ewing sarcoma), breast, liver, lung, head and neck, colorectal, prostate, leiomyosarcoma, cervical and endometrial cancer, ovarian, prostate, and pancreatic cancer. Alternatively, the IGF-1RxCD3 bispecific single chain antibody molecule/polypeptide as defined herein above is also used in the prevention, treatment or amelioration of autoimmune diseases, preferably psoriasis.

In another preferred embodiment of the method of the invention said pharmaceutical composition is suitable to be administered in combination with an additional drug, i.e. as part of a co-therapy. In said co-therapy, an active agent may be optionally included in the same pharmaceutical composition as the bispecific single chain antibody molecule of the invention, or may be included in a separate pharmaceutical composition. In this latter case, said separate pharmaceutical composition is suitable for administration prior to, simultaneously as or following administration of said pharmaceutical composition comprising the bispecific single chain antibody molecule of the invention. The additional drug or pharmaceutical composition may be a non-proteinaceous compound or a proteinaceous compound. In the case that the additional drug is a proteinaceous compound, it is advantageous that the proteinaceous compound be capable of providing an activation signal for immune effector cells.

Preferably, said proteinaceous compound or non-proteinaceous compound may be administered simultaneously or non-simultaneously with the bispecific single chain antibody molecule of the invention, a nucleic acid molecule as defined hereinabove, a vector as defined as defined hereinabove, or a host as defined as defined hereinabove.

It is preferred for the above described method of the invention that said subject is a human.

In a further aspect, the invention relates to a kit comprising a bispecific single chain antibody molecule of the invention, a nucleic acid molecule of the invention, a vector of the invention, or a host of the invention.

These and other embodiments are disclosed and encompassed by the description and Examples of the present invention. Recombinant techniques and methods in immunology are described e.g. in Sambrook et al. Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press, 3rd edition 2001; Lefkovits; Immunology Methods Manual; The Comprehensive Sourcebook of Techniques; Academic Press, 1997; Golemis; Protein-Protein Interactions: A Molecular Cloning Manual; Cold Spring Laboratory Press, 2002. Further literature concerning any one of the antibodies, methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries and databases, using for example electronic devices. For example, the public database "Medline", available on the Internet, may be utilized, for example under http://www.ncbi.nlm.nih.gov/PubMed/medline.html. Further databases and addresses such as http://www.ncbi.nlm.nih.gov/ or listed at the EMBL-services homepage under http://www.embl.de/services/index.html are known to the person skilled in the art and can also be obtained using, e. g., http://www. google.com.

The figures show:

Figure 1

Fusion of the N-terminal amino acids 1-27 of primate CD3 epsilon to a heterologous soluble protein.

Figure 2

The figure shows the average absorption values of quadruplicate samples measured in an ELISA assay detecting the presence of a construct consisting of the N-terminal amino acids 1-27 of the mature human CD3 epsilon chain fused to the hinge and Fc gamma portion of human IgG1 and a C-terminal 6 Histidine tag in a supernatant of transiently transfected 293 cells. The first column labeled “27 aa huCD3E” shows the average absorption value for the construct, the second column labeled “irrel. SN” shows the average value for a supernatant of 293 cells transfected with an irrelevant construct as negative control. The comparison of the values obtained for the

construct with the values obtained for the negative control clearly demonstrates the presence of the recombinant construct.

Figure 3

The figure shows the average absorption values of quadruplicate samples measured in an ELISA assay detecting the binding of the cross species specific anti-CD3 binding molecules in form of crude preparations of periplasmatically expressed single-chain antibodies to a construct comprising the N-terminal 1-27 amino acids of the mature human CD3 epsilon chain fused to the hinge and Fc gamma portion of human IgG1 and a C-terminal His6 tag. The columns show from left to right the average absorption values for the specificities designated as A2J HLP, I2C HLP E2M HLP, F7O HLP, G4H HLP, H2C HLP, E1L HLP, F12Q HLP, F6A HLP and H1E HLP. The rightmost column labelled "neg. contr." shows the average absorption value for the single-chain preparation of a murine anti-human CD3 antibody as negative control. The comparison of the values obtained for the anti-CD3 specificities with the values obtained for the negative control clearly demonstrates the strong binding of the anti-CD3 specificities to the N-terminal 1-27 amino acids of the mature human CD3 epsilon chain.

Figure 4

Fusion of the N-terminal amino acids 1-27 of primate CD3 epsilon to a heterologous membrane bound protein.

Figure 5

Histogram overlays of different transfectants tested in a FACS assay detecting the presence of recombinant transmembrane fusion proteins consisting of cynomolgus EpCAM and the N-terminal 1-27 amino acids of the human, marmoset, tamarin, squirrel monkey and domestic swine CD3 epsilon chain respectively. The histogram overlays from left to right and top to bottom show the results for the transfectants expressing the constructs comprising the human 27 mer, marmoset 27 mer, tamarin 27 mer, squirrel monkey 27 mer and swine 27 mer respectively. In the individual overlays the thin line represents a sample incubated with PBS with 2% FCS instead of anti-Flag M2 antibody as negative control and the bold line shows a sample incubated with the anti-Flag M2 antibody. For each construct the overlay of the histograms shows binding of the anti-Flag M2 antibody to the transfectants, which clearly demonstrates the expression of the recombinant constructs on the transfectants.

Figure 6

Histogram overlays of different transfectants tested in a FACS assay detecting the binding of the cross-species specific anti-CD3 binding molecules in form of crude preparations of periplasmatically expressed single-chain antibodies to the N-terminal amino acids 1-27 of the human, marmoset, tamarin and squirrel monkey CD3 epsilon chain respectively fused to cynomolgus EpCAM.

Figure 6A:

The histogram overlays from left to right and top to bottom show the results for the transfectants expressing the 1-27 CD3-EpCAM comprising the human 27 mer tested with the CD3 specific binding molecules designated H2C HLP, F12Q HLP, E2M HLP and G4H HLP respectively.

Figure 6B:

The histogram overlays from left to right and top to bottom show the results for the transfectants expressing the 1-27 CD3-EpCAM comprising the marmoset 27 mer tested with the CD3 specific binding molecules designated H2C HLP, F12Q HLP, E2M HLP and G4H HLP respectively.

Figure 6C:

The histogram overlays from left to right and top to bottom show the results for the transfectants expressing the 1-27 CD3-EpCAM comprising the tamarin 27 mer tested with the CD3 specific binding molecules designated H2C HLP, F12Q HLP, E2M HLP and G4H HLP respectively.

Figure 6D:

The histogram overlays from left to right and top to bottom show the results for the transfectants expressing the 1-27 CD3-EpCAM comprising the squirrel monkey 27 mer tested with the CD3 specific binding molecules designated H2C HLP, F12Q HLP, E2M HLP and G4H HLP respectively.

Figure 6E:

The histogram overlays from left to right and top to bottom show the results for the transfectants expressing the 1-27 CD3-EpCAM comprising the swine 27 mer tested with the CD3 specific binding molecules designated H2C HLP, F12Q HLP, E2M HLP and G4H HLP respectively.

In the individual overlays the thin line represents a sample incubated with a single-chain preparation of a murine anti-human CD3-antibody as negative control and the bold line shows a sample incubated with the respective anti-CD3 binding molecules

indicated. Considering the lack of binding to the swine 27 mer transfectants and the expression levels of the constructs shown in Figure 5 the overlays of the histograms show specific and strong binding of the tested anti-CD3 specificities of the fully cross-species specific human bispecific single chain antibodies to cells expressing the recombinant transmembrane fusion proteins comprising the N-terminal amino acids 1-27 of the human, marmoset, tamarin and squirrel monkey CD3 epsilon chain respectively fused to cynomolgus EpCAM and show therefore multi primate cross-species specificity of the anti-CD3 binding molecules.

Figure 7

FACS assay for detection of human CD3 epsilon on transfected murine EL4 T cells. Graphical analysis shows an overlay of histograms. The bold line shows transfected cells incubated with the anti-human CD3 antibody UCHT-1. The thin line represents cells incubated with a mouse IgG1 isotype control. Binding of the anti CD3 antibody UCHT1 clearly shows expression of the human CD3 epsilon chain on the cell surface of transfected murine EL4 T cells.

Figure 8

Binding of cross-species specific anti CD3 antibodies to alanine-mutants in an alanine scanning experiment. In the individual Figures the columns show from left to right the calculated binding values in arbitrary units in logarithmic scale for the wild-type transfectant (WT) and for all alanine-mutants from the position 1 to 27. The binding values are calculated using the following formula:

$$value_Sample(x,y) = \frac{Sample(x,y) - neg_Contr.(x)}{(UCHT-1(x) - neg_Contr.(x)) * \frac{WT(y) - neg_Contr.(wt)}{UCHT-1(wt) - neg_Contr.(wt)}}$$

In this equation *value_Sample* means the value in arbitrary units of binding depicting the degree of binding of a specific anti-CD3 antibody to a specific alanine-mutant as shown in the Figure, *Sample* means the geometric mean fluorescence value obtained for a specific anti-CD3 antibody assayed on a specific alanine-scanning transfectant, *neg_Contr.* means the geometric mean fluorescence value obtained for the negative control assayed on a specific alanine-mutant, *UCHT-1* means the geometric mean fluorescence value obtained for the UCHT-1 antibody assayed on a specific alanine-mutant, *WT* means the geometric mean fluorescence value obtained for a specific anti-CD3 antibody assayed on the wild-type transfectant, *x* specifies the respective transfectant, *y* specifies the respective anti-CD3 antibody and *wt* specifies that the respective transfectant is the wild-type. Individual alanine-mutant positions are

labelled with the single letter code of the wild-type amino acid and the number of the position.

Figure 8A:

The figure shows the results for cross-species specific anti CD3 antibody A2J HLP expressed as chimeric IgG molecule. Reduced binding activity is observed for mutations to alanine at position 4 (asparagine), at position 23 (threonine) and at position 25 (isoleucine). Complete loss of binding is observed for mutations to alanine at position 1 (glutamine), at position 2 (aspartate), at position 3 (glycine) and at position 5 (glutamate).

Figure 8B:

The figure shows the results for cross-species specific anti CD3 antibody E2M HLP, expressed as chimeric IgG molecule. Reduced binding activity is observed for mutations to alanine at position 4 (asparagine), at position 23 (threonine) and at position 25 (isoleucine). Complete loss of binding is observed for mutations to alanine at position 1 (glutamine), at position 2 (aspartate), at position 3 (glycine) and at position 5 (glutamate).

Figure 8C:

The figure shows the results for cross-species specific anti CD3 antibody H2C HLP, expressed as chimeric IgG molecule. Reduced binding activity is observed for mutations to alanine at position 4 (asparagine). Complete loss of binding is observed for mutations to alanine glutamine at position 1 (glutamine), at position 2 (aspartate), at position 3 (glycine) and at position 5 (glutamate).

Figure 8D:

shows the results for cross-species specific anti CD3 antibody F12Q HLP, tested as periplasmatically expressed single-chain antibody. Complete loss of binding is observed for mutations to alanine at position 1 (glutamine), at position 2 (aspartate), at position 3 (glycine) and at position 5 (glutamate).

Figure 9

FACS assay detecting the binding of the cross-species specific anti-CD3 binding molecule H2C HLP to human CD3 with and without N-terminal His6 tag.

Histogram overlays are performed of the EL4 cell line transfected with wild-type human CD3 epsilon chain (left histogram) or the human CD3 epsilon chain with N-terminal His6 tag (right histogram) tested in a FACS assay detecting the binding of cross-species specific binding molecule H2C HLP. Samples are incubated with an

appropriate isotype control as negative control (thin line), anti-human CD3 antibody UCHT-1 as positive control (dotted line) and cross-species specific anti-CD3 antibody H2C HLP in form of a chimeric IgG molecule (bold line).

Histogram overlays show comparable binding of the UCHT-1 antibody to both transfectants as compared to the isotype control demonstrating expression of both recombinant constructs. Histogram overlays also show binding of the anti-CD3 binding molecule H2C HLP only to the wild-type human CD3 epsilon chain but not to the His6-human CD3 epsilon chain. These results demonstrate that a free N-terminus is essential for binding of the cross-species specific anti-CD3 binding molecule H2C HLP.

Figure 10

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with the human MCSP D3, human CD3+ T cell line HPB-ALL, CHO cells transfected with cynomolgus MCSP D3 and a macaque T cell line 4119 LnPx. The FACS staining is performed as described in Example 10. The thick line represents cells incubated with 2 µg/ml purified protein that are subsequently incubated with the anti-his antibody and the PE labeled detection antibody. The thin histogram line reflects the negative control: cells only incubated with the anti-his antibody and the detection antibody.

Figure 11

FACS binding analysis of designated cross-species specific bispecific single chain constructs CHO cells transfected with the human MCSP D3, human CD3+ T cell line HPB-ALL, CHO cells transfected with cynomolgus MCSP D3 and a macaque T cell line 4119 LnPx. The FACS staining is performed as described in Example 10. The thick line represents cells incubated with 2 µg/ml purified protein that are subsequently incubated with the anti-his antibody and the PE labeled detection antibody. The thin histogram line reflects the negative control: cells only incubated with the anti-his antibody and the detection antibody.

Figure 12

FACS binding analysis of designated cross-species specific bispecific single chain constructs CHO cells transfected with the human MCSP D3, human CD3+ T cell line HPB-ALL, CHO cells transfected with cynomolgus MCSP D3 and a macaque T cell line 4119 LnPx. The FACS staining is performed as described in Example 10. The thick line represents cells incubated with 2 µg/ml purified monomeric protein that are

subsequently incubated with the anti-his antibody and the PE labeled detection antibody. The thin histogram line reflects the negative control: cells only incubated with the anti-his antibody and the detection antibody.

Figure 13

Cytotoxicity activity induced by designated cross-species specific MCSP specific single chain constructs redirected to indicated target cell lines. A) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human MCSP D3 as target cells. B) The macaque T cell line 4119 LnPx are used as effector cells, CHO cells transfected with cynomolgus MCSP D3 as target cells. The assay is performed as described in Example 11.

Figure 14

Cytotoxicity activity induced by designated cross-species specific MCSP specific single chain constructs redirected to indicated target cell lines. A) and B) The macaque T cell line 4119 LnPx are used as effector cells, CHO cells transfected with cynomolgus MCSP D3 as target cells. The assay is performed as described in Example 11.

Figure 15

Cytotoxicity activity induced by designated cross-species specific MCSP specific single chain constructs redirected to indicated target cell lines. A) and B) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human MCSP D3 as target cells. The assay is performed as described in Example 11.

Figure 16

Cytotoxicity activity induced by designated cross-species specific MCSP specific single chain constructs redirected to indicated target cell lines. A) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human MCSP D3 as target cells. B) The macaque T cell line 4119 LnPx are used as effector cells, CHO cells transfected with cynomolgus MCSP D3 as target cells. The assay is performed as described in Example 11.

Figure 17

Cytotoxicity activity induced by designated cross-species specific MCSP specific single chain constructs redirected to indicated target cell lines. A) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human MCSP D3 as target cells. B) The macaque T cell line 4119 LnPx are used as effector

cells, CHO cells transfected with cynomolgus MCSP D3 as target cells. The assay is performed as described in Example 11.

Figure 18

Plasma stability of MCSP and CD3 cross-species specific bispecific single chain antibodies tested by the measurement of cytotoxicity activity induced by samples of the designated single chain constructs incubated with 50% human plasma at 37°C and 4°C for 24 hours respectively or with addition of 50% human plasma immediately prior to cytotoxicity testing or without addition of plasma. CHO cells transfected with human MCSP are used as target cell line and stimulated CD4-/CD56- human PBMCs are used as effector cells. The assay is performed as described in Example 12.

Figure 19

Initial drop and recovery (i.e. redistribution) of absolute T cell counts (open squares), in peripheral blood of B-NHL patients (patent numbers 1, 7, 23, 30, 31, and 33 of Table 4), who had essentially no circulating CD19-positive target B cells (filled triangles), during the starting phase of intravenous infusion with the CD3 binding molecule CD19xCD3 recognizing a conventional context dependent CD3 epitope. Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. The CD19xCD3 dose is given in parentheses beside the patient number.

Figure 20

(A) Repeated T cell redistribution (open squares) in B-NHL patient #19 (Table 4) who had no circulating CD19-positive target B cells (filled triangles) and developed CNS symptoms under continuous intravenous infusion with CD19xCD3 at a starting dose of 5µg/m^2/24h for one day followed by a sudden dose increase to 15µg/m^2/24h. Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. After recovery of circulating T cells from the first episode of redistribution triggered by the treatment start at 5µg/m^2/24h the stepwise dose increase from 5 to 15µg/m^2/24h triggered a second episode of T cell redistribution that was associated with the development of CNS symptoms dominated by confusion and disorientation.

(B) Repeated T cell redistribution in a B-NHL patient, who developed CNS symptoms under repeated intravenous bolus infusion with CD19xCD3 at 1.5µg/m^2. Absolute cell counts are given in 1000 cells per microliter blood. The infusion time for each bolus administration was 2 to 4 hours. Vertical arrows indicate the start of bolus infusions.

Data points at the beginning of each bolus administration show the T cell counts immediately prior to start of bolus infusion. Each bolus infusion triggered an episode of T cell redistribution followed by recovery of the T cell counts prior to the next bolus infusion. Finally the third episode of T cell redistribution was associated with the development of CNS symptoms in this patient.

Figure 21

Complex T cell redistribution pattern (open squares) in B-NHL patient #20 (Table 4) without circulating CD19-positive target B cells (filled triangles), during ramp initiation of the CD19xCD3 infusion i.e. even gradual increase of flow-rate from almost zero to 15µg/m^2/24h during the first 24 hours of treatment. Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. The CD19xCD3 dose is given in parentheses beside the patient number. T cells reappearing in the circulating blood after the initial redistribution triggered by the first exposure to CD19xCD3 are partially induced to redisappear from circulating blood again by still increasing levels of CD19xCD3 during the ramp phase.

Figure 22

T and B cell counts during treatment with CD19xCD3 of B-NHL patient #13 (Table 4) who had a significant number of circulating CD19-positive target B (lymphoma) cells (filled triangles). Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. The CD19xCD3 dose is given in parentheses beside the patient number. T cells (open squares) disappear completely from the circulation upon start of CD19xCD3 infusion and do not reappear until the circulating CD19-positive B (lymphoma) cells (filled triangles) are depleted from the peripheral blood.

Figure 23

Repeated T cell redistribution (open squares) in B-NHL patient #24 (Table 4), who had essentially no circulating CD19-positive target B cells (filled triangles) and developed CNS symptoms upon initiation of CD19xCD3 infusion without additional HSA as required for stabilisation of the drug (upper panel). After first recovery of circulating T cells from initial redistribution the uneven drug flow due to the lack of stabilizing HSA triggered a second episode of T cell redistribution that was associated with the development of CNS symptoms dominated by confusion and disorientation. When the same patient was restarted correctly with CD19xCD3

solution containing additional HSA for drug stabilisation, no repeated T cell redistribution was observed (lower panel) and the patient did not again develop any CNS symptoms. Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. The CD19xCD3 dose is given in parentheses beside the patient number.

Figure 24

Model of T cell adhesion to endothelial cells induced by monovalent binding to context dependent CD3 epitopes. Monovalent interaction of a conventional CD3 binding molecule to its context dependent epitope on CD3 epsilon can lead to an allosteric change in the conformation of CD3 followed by the recruitment of Nck2 to the cytoplasmic domain of CD3 epsilon (Gil et al. (2002) Cell 109: 901). As Nck2 is directly linked to integrins via PINCH and ILK (Legate et al. (2006) Nat Rev Mol Cell Biol 7: 20), recruitment of Nck2 to the cytoplasmic domain of CD3 epsilon following an allosteric change in the conformation of CD3 through binding of a conventional CD3 binding molecule (like the CD19xCD3 of example 13) to its context dependent epitope on CD3 epsilon, can increase the adhesiveness of T cells to endothelial cells by transiently switching integrins on the T cell surface into their more adhesive isoform via inside-out-signalling.

Figure 25

Cytotoxic activity of CD33-AF5 VH-VL x I2C VH-VL test material used for the in vivo study in cynomolgus monkeys as described in Example 14. Specific lysis of CD33-positive target cells was determined in a standard ^{51}Chromium release assay at increasing concentrations of CD33-AF5 VH-VL x I2C VH-VL. Assay duration was 18 hours. The macaque T cell line 4119 LnPx was used as source of effector cells. CHO cells transfected with cynomolgus CD33 served as target cells. Effector- to target cell ratio (E:T-ratio) was 10:1. The concentration of CD33-AF5 VH-VL x I2C VH-VL required for half-maximal target cell lysis (EC50) was calculated from the dose response curve with a value of 2.7 ng/ml.

Figure 26

(A) Dose- and time-dependent depletion of CD33-positive monocytes from the peripheral blood of cynomolgus monkeys through intravenous continuous infusion of CD33-AF5 VH-VL x I2C VH-VL as described in Example 14. The percentage relative to baseline (i.e. 100%) of absolute circulating CD33-positive monocyte counts after the duration of treatment as indicated above the columns is shown for each of two

cynomolgus monkeys per dose level. The dose level (i.e. infusion flow-rate) is indicated below the columns. No depletion of circulating CD33-positive monocytes was observed in animals 1 and 2 treated for 7 days at a dose of 30 µg/m^2/24h. In animals 3 and 4 treated for 7 days at a dose of 60 µg/m^2/24h circulating CD33-positive monocyte counts were reduced to 68% and 40% of baseline, respectively. At 240 µg/m^2/24h circulating CD33-positive monocytes were almost completely depleted from the peripheral blood after 3 days of treatment (animals 5 and 6). At 1000 µg/m^2/24h depletion of circulating CD33-positive monocytes from the peripheral blood was completed already after 1 day of treatment (animals 7 and 8).

(B) Course of T cell and CD33-monocyte counts in peripheral blood of two cynomolgus monkeys during continuous infusion of CD33-AF5 VH-VL x I2C VH-VL for 14 days at 120 µg/m^2/24h. Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. After initial mobilisation of CD33-monocytes during the first 12 hours upon start of infusion CD33-monocytes in peripheral blood (filled triangles) are depleted by two thirds (animal 10) and 50% (animal 9) relative to the respective baseline counts during the further course of infusion. Circulating T cell counts (open squares) show a limited initial drop followed by recovery still during the presence of circulating CD33-positive monocytic target cells.

Figure 27

Cytotoxic activity of MCSP-G4 VH-VL x I2C VH-VL test material used for the in vivo study in cynomolgus monkeys as described in Example 15. Specific lysis of MCSP-positive target cells was determined in a standard ^{51}Chromium release assay at increasing concentrations of MCSP-G4 VH-VL x I2C VH-VL. Assay duration was 18 hours. The macaque T cell line 4119 LnPx was used as source of effector cells. CHO cells transfected with cynomolgus MCSP served as target cells. Effector- to target cell ratio (E:T-ratio) was 10:1. The concentration of MCSP-G4 VH-VL x I2C VH-VL required for half-maximal target cell lysis (EC50) was calculated from the dose response curve with a value of 1.9 ng/ml.

Figure 28

Absence of initial episodes of drop and subsequent recovery of absolute T cell counts (i.e. redistribution) in peripheral blood of cynomolgus monkeys during the starting phase of intravenous infusion with the CD3 binding molecule MCSP-G4 VH-VL x I2C VH-VL recognizing an essentially context independent CD3 epitope.

Absolute cell counts are given in 1000 cells per microliter blood. The first data point shows baseline counts immediately prior to the start of infusion. The MCSP-G4 VH-VL x I2C VH-VL dose is given in parentheses beside the animal number. In the known absence of MCSP-positive target cells from the circulating blood of cynomolgus monkeys there is no induction of T cell redistribution (i.e. an initial episode of drop and subsequent recovery of absolute T cell counts) through target cell mediated crosslinking of CD3. Moreover, induction of T cell redistribution (i.e. an initial episode of drop and subsequent recovery of absolute T cell counts) through a signal, which the T cells may receive through exclusive interaction with a CD3 binding site only, can be avoided by the use of CD3 binding molecules like MCSP-G4 VH-VL x I2C VH-VL recognizing an essentially context independent CD3 epitope.

Figure 29

FACS binding analysis of designated cross-species specific bispecific constructs to CHO cells transfected with human CD33, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque CD33 and macaque PBMC respectively. The FACS staining is performed as described in Example 16.4. The bold lines represent cells incubated with 5 µg/ml purified bispecific single chain construct or cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms reflect the negative controls. Supernatant of untransfected CHO cells was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque CD33 and human and macaque CD3.

Figure 30

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific CD33 specific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays are performed as described in Example 16.5. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector cells against human and macaque CD33 transfected CHO cells, respectively.

Figure 31

SDS PAGE gel and Western blot monitoring the purification of the cross-species specific bispecific single chain molecule designated E292F3 HL x I2C HL. Samples

from the eluate, the cell culture supernatant (SN) and the flow through of the column (FT) were analyzed as indicated. A protein marker (M) was applied as size reference. A strong protein band with a molecular weight between 50 and 60 kDa in the SDS PAGE gel demonstrates the efficient purification of the cross-species specific bispecific single chain molecule to a very high degree of purity with the one-step purification method described in Example 17.2. The Western blot detecting the histidine$_6$ tag confirms the identity of the protein band in the eluate as the cross-species specific bispecific single chain molecule. The faint signal for the flow through sample in this sensitive detection method further shows the nearly complete capture of bispecific single chain molecules by the purification method.

Figure 32

SDS PAGE gel and Western blot monitoring the purification of the cross-species specific bispecific single chain molecule designated V207C12 HL x H2C HL. Samples from the eluate, the cell culture supernatant (SN) and the flow through of the column (FT) were analyzed as indicated. A protein marker (M) was applied as size reference. A strong protein band with a molecular weight between 50 and 60 kDa in the SDS PAGE gel demonstrates the efficient purification of the cross-species specific bispecific single chain molecule to a very high degree of purity with the one-step purification method described in Example 17.2. The Western blot detecting the histidine$_6$ tag confirms the identity of the protein band in the eluate as the cross-species specific bispecific single chain molecule. The faint signal for the flow through sample in this sensitive detection method further shows the nearly complete capture of bispecific single chain molecules by the purification method.

Figure 33

SDS PAGE gel and Western blot monitoring the purification of the cross-species specific bispecific single chain molecule designated AF5HLxF12QHL. Samples from the eluate, the cell culture supernatant (SN) and the flow through of the column (FT) were analyzed as indicated. A protein marker (M) was applied as size reference. A strong protein band with a molecular weight between 50 and 60 kDa in the SDS PAGE gel demonstrates the efficient purification of the cross-species specific bispecific single chain molecule to a very high degree of purity with the one-step purification method described in Example 17.2. The Western blot detecting the histidine$_6$ tag confirms the identity of the protein band in the eluate as the cross-species specific bispecific single chain molecule. The signal in the flow through

sample in this sensitive detection method is explained by saturation of the affinity column due to the high concentration of bispecific single chain molecules in the supernatant.

Figure 34

Standard curve of AF5HLxI2CHL in 50% macaque monkey serum. The upper diagram shows the standard curve generated for the assay as described in Example 18.2.

The lower diagram shows results for quality control samples of AF5HLxI2CHL in 50% macaque monkey serum. The recovery rates are above 90% for the high and mid QC sample and above 80% for the low QC sample.

Thus the assay allows for detection of AF5HLxI2CHL in serum samples in the range from 10 ng/ml to 200 ng/ml (before dilution).

Figure 35

Standard curve of MCSP-G4 HL x I2C HL in 50% macaque monkey serum. The upper diagram shows the standard curve generated for the assay as described in Example 18.2.

The lower diagram shows results for quality control samples of MCSP-G4 HL x I2C HL in 50% macaque monkey serum. The recovery rates are above 98% for the high and mid QC sample and above 85% for the low QC sample.

Thus the assay allows for detection of MCSP-G4 HL x I2C HL in serum samples in the range from 10 ng/ml to 200 ng/ml (before dilution).

Figure 36

FACS binding analysis of an anti-Flag antibody to CHO cells transfected with the 1-27 N-terminal amino acids of CD3 epsilon of the designated species fused to cynomolgus EpCAM. The FACS staining was performed as described in Example 19.1. The bold lines represent cells incubated with the anti-Flag antibody. The filled histograms reflect the negative controls. PBS with 2 % FCS was used as negative control. The histograms show strong and comparable binding of the anti-Flag antibody to all transfectants indicating strong and equal expression of the transfected constructs.

Figure 37

FACS binding analysis of the I2C IgG1 construct to CHO cells expressing the 1-27 N-terminal amino acids of CD3 epsilon of the designated species fused to cynomolgus EpCAM. The FACS staining is performed as described in Example 19.3. The bold

lines represent cells incubated with 50 µl cell culture supernatant of cells expressing the I2C IgG1 construct. The filled histograms reflect the negative control. Cells expressing the 1-27 N-terminal amino acids of CD3 epsilon of swine fused to cynomolgus EpCAM were used as negative control. In comparison with the negative control the histograms clearly demonstrate binding of the I2C IgG1 construct to 1-27 N-terminal amino acids of CD3 epsilon of human, marmoset, tamarin and squirrel monkey.

Figure 38

FACS binding analysis of the I2C IgG1 construct as described in Example 19.2 to human CD3 with and without N-terminal His6 tag as described in Examples 6.1 and 5.1 respectively. The bold lines represent cells incubated with the anti-human CD3 antibody UCHT-1, the penta-His antibody (Qiagen) and cell culture supernatant of cells expressing the I2C IgG1 construct respectively as indicated. The filled histograms reflect cells incubated with an irrelevant murine IgG1 antibody as negative control.

The upper two histogram overlays show comparable binding of the UCHT-1 antibody to both transfectants as compared to the isotype control demonstrating expression of both recombinant constructs. The centre histogram overlays show binding of the penta his antibody to the cells expressing the His6-human CD3 epsilon chain (His6-CD3) but not to the cells expressing the wild-type CD3 epsilon chain (WT-CD3). The lower Histogram overlays show binding of the I2C IgG1 construct to the wild-type human CD3 epsilon chain but not to the His6-human CD3 epsilon chain. These results demonstrate that a free N-terminus is essential for binding of the cross-species specific anti-CD3 binding molecule I2C to the CD3 epsilon chain.

Figure 39

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human MCSP D3, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque MCSP D3 and the macaque T cell line 4119 LnPx respectively. The FACS staining was performed as described in Example 10. The bold lines represents cells incubated with 2 µg/ml purified bispecific single chain construct or cell supernatant containing the bispecific single chain construct respectively. The filled histograms reflect the negative controls. Supernatant of untransfected CHO cells was used as negative control for binding to the T cell lines. A single chain construct with irrelevant target specificity was used as

negative control for binding to the MCSP D3 transfected CHO cells. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque MCSP D3 and human and macaque CD3.

Figure 40

Cytotoxic activity induced by designated cross-species specific MCSP D3 specific single chain constructs redirected to the indicated target cell lines. Effector cells and effector to target ratio were also used as indicated. The assay is performed as described in Example 11. The diagrams clearly demonstrate potent cross-species specific recruitment of cytotoxic activity by each construct.

Figure 41

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human CD33, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque CD33 and macaque PBMC respectively. The FACS staining was performed as described in Example 21.2. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms reflect the negative controls. Supernatant of untransfected CHO cells was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque CD33 and human and macaque CD3.

Figure 42

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific CD33 specific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays are performed as described in Example 21.3. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector cells against human and macaque CD33 transfected CHO cells, respectively.

Figure 43

T cell redistribution in a chimpanzee under weekly intravenous bolus infusion with PBS/5% HSA and PBS/5% HSA plus single-chain EpCAM/CD3-bispecific antibody construct at doses of 1.6, 2.0, 3.0 and 4.5 µg/kg. The infusion time for each bolus administration was 2 hours. Vertical arrows indicate the start of bolus infusions. Data

points at the beginning of each bolus administration show the T cell counts immediately prior to start of bolus infusion. Each bolus infusion of the single-chain EpCAM/CD3-bispecific antibody construct, which recognizes a conventional context dependent CD3 epitope, triggered an episode of T cell redistribution followed by recovery of T cells to baseline values prior to the next bolus infusion.

Figure 44

CD3 specific ELISA analysis of periplasmic preparations containing Flag tagged scFv protein fragments from selected clones. Periplasmic preparations of soluble scFv protein fragments were added to wells of an ELISA plate, which had been coated with soluble human CD3 epsilon (aa 1-27)- Fc fusion protein and had been additionally blocked with PBS 3% BSA. Detection was performed by a monoclonal anti Flag-Biotin-labeled antibody followed by peroxidase-conjugated Streptavidin. The ELISA was developed by an ABTS substrate solution. The OD values (y axis) were measured at 405 nm by an ELISA reader. Clone names are presented on the x axis.

Figure 45

ELISA analysis of periplasmic preparations containing Flag tagged scFv protein fragments from selected clones. The same periplasmic preparations of soluble scFv protein fragments as in Figure 44 were added to wells of an ELISA plate which had not been coated with human CD3 epsilon (aa 1-27)- Fc fusion protein but with hulgG1 (Sigma) and blocked with 3% BSA in PBS.

Detection was performed by a monoclonal anti Flag-Biotin-labeled antibody followed by peroxidase-conjugated Streptavidin. The ELISA was developed by an ABTS substrate solution. The OD values (y axis) were measured at 405 nm by an ELISA reader. Clone names are presented on the x axis.

Figure 46

Figures 46A-G: FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human PSCA, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque PSCA and to the macaque T cell line 4119LnPx, respectively. The FACS staining was performed as described in Example 24.5. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms reflect the negative controls. Supernatant of untransfected cells was used as a negative control. For each cross-species specific

bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque PSCA and human and macaque CD3.

Figure 47

Figure 47A-C: The diagrams show results of chromium release assays measuring cytotoxic activity induced by the designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays were performed as described in Example 24.6. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector cells against cells positive for human and macaque PSCA, respectively.

Figure 48

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human PSCA, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque PSCA and to the macaque T cell line 4119LnPx, respectively. The FACS staining was performed as described in Example 45.5. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms show the negative controls. Supernatant of untransfected cells was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque PSCA and human and macaque CD3.

Figure 49

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays were performed as described in Example 24.6. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector T cells against target cells positive for human and macaque PSCA, respectively.

Figure 50

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human CD19, the human CD3-positive T cell line HPB-ALL, and the CD3-positive macaque T cell line 4119 LnPx. The FACS staining is performed as described in Example 25.4. The thick-line histograms

represent cells incubated with cell culture supernatant and subsequently with a murine anti-His-tag antibody followed by a PE-labeled anti-murine Ig detection antibody. The thin-lined histograms represent the negative control i.e. cells only incubated with the anti-His-tag antibody and the anti-murine Ig detection antibody.

Figure 51

Cytotoxic T cell activity redirected by designated cross-species specific bispecific single chain constructs against the indicated target cell line. A) Stimulated CD4/CD56-depleted human PBMCs are used as effector T cells and CHO cells transfected with human CD19 as target cells. B) The macaque T cell line 4119 LnPx is used as source of effector cells and CHO cells transfected with human CD19 are used as target cells. The assay is performed as described in Example 25.5.

Figure 52

FACS binding analysis of the designated cross-species specific bispecific single chain constructs to the C-MET positive human breast cancer cell line MDA-MB-231, the human CD3+ T cell line HPB-ALL and to the macaque CD3+ T cell line 4119LnPx respectively. The FACS staining was performed as described in Example 26.5. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms represent the negative controls. Supernatant of untransfected cells was used as a negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to C-MET and human and macaque CD3.

Figure 53

The diagrams show results of chromium release assays measuring cytotoxic activity induced by the designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays were performed as described in Example 26.6. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human effector cells against cells positive for C-MET.

Figure 54

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells expressing human cMET as described in Example 27.1, the human CD3+ T cell line HPB-ALL, CHO cells expressing macaque cMET as described in Example 27.1 and the macaque T cell line 4119LnPx, respectively. The

FACS staining was performed as described in Example 27.2. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms show the negative controls. Supernatant of untransfected CHO cells was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque cMET and human and macaque CD3.

Figure 55

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific cMET specific single chain constructs redirected to the indicated target cell line generated as described in Example 27.1. Effector cells were also used as indicated. The assays were performed as described in Example 27.4. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of macaque effector T cells against target cells positive for macaque cMET.

Figure 56

FACS binding analysis of designated cross-species specific scFv antibodies to CHO cells expressing human cMET as described in Example 27.1 and CHO cells expressing macaque cMET as described in Example 27.1, respectively. The FACS staining was performed as described in Example 27.3. The bold lines represent cells incubated with periplasmic preparations containing the cross-species specific scFv antibodies. The filled histograms show the negative controls. The Buffer used for periplasmic preparations was used as negative control. For each cross-species specific scFv antibody the overlay of the histograms shows specific binding of the construct to human and macaque cMET.

Figure 57

FACS binding analysis of a cross-species specific scFv-antibody fragment to CHO cells transfected with human Endosialin and to CHO cells transfected with macaque Endosialin. The FACS staining was performed as described in Example 28.3. The bold lines represent cells incubated with a periplasmic preparation containing the scFv-antibody fragment. The thin lines represent the negative controls. Untransfected CHO cells were used as a negative control. The overlays of the histograms show specific binding of the scFv-antibody fragment to human and macaque Endosialin.

Figure 58

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human CD248, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque CD248 and the macaque T cell line 4119LnPx, respectively. The FACS staining was performed as described in Example 29.1. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The thin lines show the negative controls. Supernatant of untransfected CHO cells was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque CD248 and human and macaque CD3.

Figure 59

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific CD248 specific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays were performed as described in Example 29.1. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector T cells against target cells positive for human and macaque CD248, respectively.

Figure 60

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human EpCAM, human CD3+ T cell line HPB-ALL, and the macaque T cell line 4119 LnPx. The FACS staining was performed as described in Example 30.4. The thick line represents cells incubated with cell culture supernatant that were subsequently incubated with the anti-his antibody and the PE labeled detection antibody. The thin histogram line shows the negative control: cells only incubated with the anti-his antibody and the detection antibody.

Figure 61

Cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. A) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human EpCAM as target cells. B) The macaque T cell line 4119 LnPx were used as effector cells, CHO cells transfected with human EpCAM as target cells. The assay was performed as described in Example 30.5.

Figure 62

Cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. A) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human EpCAM as target cells. B) The macaque T cell line 4119 LnPx were used as effector cells, CHO cells transfected with human EpCAM as target cells. The assay was performed as described in Example 30.5.

Figure 63

Cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. A) and B) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human EpCAM as target cells. The assay was performed as described in Example 30.5.

Figure 64 and 65

Cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. A) and B) The macaque T cell line 4119 LnPx were used as effector cells, CHO cells transfected with human EpCAM as target cells. The assay was performed as described in Example 30.5

Figure 66

Cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. A) Stimulated CD4-/CD56- human PBMCs are used as effector cells, CHO cells transfected with human EpCAM as target cells. B) The macaque T cell line 4119 LnPx were used as effector cells, CHO cells transfected with human EpCAM as target cells. The assay was performed as described in Example 30.5

Figure 67

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human, mouse or human-mouse hybrid EpCAM. The FACS staining was performed as described in Example 30.7. The bars represent the median fluorescence intensity of the designated constructs to the stated EpCAM antigens.

Figure 68

In the FACS analysis, the indicated constructs showed binding to CD3 and FAPalpha compared to the negative control. Cross-species specificity of the bispecific

antibodies to human and macaque CD3 and FAP alpha antigens, respectively, was demonstrated. The assay was performed as described in Example 31

Figure 69

All of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against human FAPalpha positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and macaque FAPalpha positive target cells elicited by the macaque T cell line 4119LnPx. The assay was performed as described in Example 31

Figure 70

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human FAPalpha, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque FAPalpha and the macaque T cell line 4119LnPx, respectively. The FACS staining was performed as described in Example 32.1. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The thin lines show the negative controls. Supernatant of untransfected CHO cells was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque FAPalpha and human and macaque CD3.

Figure 71

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific FAPalpha specific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays were performed as described in Example 32.1. The diagrams clearly demonstrate for each construct the potent recruitment of cytotoxic activity of human and macaque effector T cells against target cells positive for human and macaque FAPalpha, respectively.

Figure 72

FACS binding analysis of designated cross-species specific scFv antibodies to CHO cells transfected with human FAPalpha and CHO cells transfected with macaque FAPalpha, respectively. The FACS staining was performed as described in Example 32.2. The bold lines represent cells incubated with periplasmic preparations containing the cross-species specific scFv antibodies. The filled histograms show the negative controls. The Buffer used for periplasmic preparations was used as negative

control. For each cross-species specific scFv antibody the overlay of the histograms shows specific binding of the construct to human and macaque FAPalpha.

Figure 73

FACS binding analysis of designated cross-species specific bispecific single chain constructs to CHO cells transfected with human IGF-1R, the human CD3+ T cell line HPB-ALL, CHO cells transfected with macaque IGF-1R and to the macaque T cell line 4119LnPx, respectively. The FACS staining was performed as described in Example 33.3. The bold lines represent cells incubated with cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The filled histograms show the negative controls. Cell culture medium was used as negative control. For each cross-species specific bispecific single chain construct the overlay of the histograms shows specific binding of the construct to human and macaque IGF-1R and human and macaque CD3.

Figure 74

The diagrams show results of chromium release assays measuring cytotoxic activity induced by designated cross-species specific bispecific single chain constructs redirected to the indicated target cell lines. Effector cells were also used as indicated. The assays were performed as described in Example 33.3. The diagrams clearly demonstrate for each construct the recruitment of cytotoxic activity of human and macaque effector T cells against target cells positive for human and macaque IGF-1R, respectively.

The present invention is additionally described by way of the following illustrative non-limiting examples that provide a better understanding of the present invention and of its many advantages.

EXAMPLES

1. Identification of CD3epsilon sequences from blood samples of non-human primates

Blood samples of the following non-human primates were used for CD3epsilon-identification: *Callithrix jacchus*, *Saguinus oedipus* and *Saimiris ciureus*. Fresh heparin-treated whole blood samples were prepared for isolating total cellular RNA according to manufacturer's protocol (QIAamp RNA Blood Mini Kit, Qiagen). The extracted mRNA was transcribed into cDNA according to published protocols. In

brief, 10 µl of precipitated RNA was incubated with 1.2 µl of 10x hexanucleotide mix (Roche) at 70 °C for 10 minutes and stored on ice. A reaction mix consisting of 4 µl of 5x superscript II buffer, 0.2 µl of 0.1M dithiothreitole, 0.8 µl of superscript II (Invitrogen), 1.2 µl of desoxyribonucleoside triphosphates (25 µM), 0.8 µl of RNase Inhibitor (Roche) and 1.8 µl of DNase and RNase free water (Roth) was added. The reaction mix was incubated at room temperature for 10 minutes followed by incubation at 42 °C for 50 minutes and at 90 °C for 5 minutes. The reaction was cooled on ice before adding 0.8 µl of RNaseH (1 U/µl, Roche) and incubated for 20 minutes at 37 °C.

The first-strand cDNAs from each species were subjected to separate 35-cycle polymerase chain reactions using Taq DNA polymerase (Sigma) and the following primer combination designed on database research: forward primer 5'-AGAGTTCTGGGCCTCTGC-3' (SEQ ID NO: 253); reverse primer 5'-CGGATGGGCTCATAGTCTG-3' (SEQ ID NO: 254);. The amplified 550 bp-bands were gel purified (Gel Extraction Kit, Qiagen) and sequenced (Sequiserve, Vaterstetten/Germany, see sequence listing).

CD3epsilon *Callithrix jacchus*

Nucleotides

CAGGACGGTAATGAAGAAATGGGTGATACTACACAGAACCCATATAAAGTTTCCATCTCAGG
AACCACAGTAACACTGACATGCCCTCGGTATGATGGACATGAAATAAAATGGCTCGTAAATA
GTCAAAACAAAGAAGGTCATGAGGACCACCTGTTACTGGAGGACTTTTCGGAAATGGAGCAA
AGTGGTTATTATGCCTGCCTCTCCAAAGAGACTCCCGCAGAAGAGGCGAGCCATTATCTCTA
CCTGAAGGCAAGAGTGTGTGAGAACTGCGTGGAGGTGGAT

Amino acids (SEQ ID NO: 3)

QDGNEEMGDTTQNPYKVSISGTTVTLTCPRYDGHEIKWLVNSQNKEGHEDHLLLEDFSEMEQ
SGYYACLSKETPAEEASHYLYLKARVCENCVEVD

CD3epsilon *Saguinus oedipus*

Nucleotides

CAGGACGGTAATGAAGAAATGGGTGATACTACACAGAACCCATATAAAGTTTCCATCTCAGG
AACCACAGTAACACTGACATGCCCTCGGTATGATGGACATGAAATAAAATGGCTTGTAAATA
GTCAAAACAAAGAAGGTCATGAGGACCACCTGTTACTGGAGGATTTTTCGGAAATGGAGCAA
AGTGGTTATTATGCCTGCCTCTCCAAAGAGACTCCCGCAGAAGAGGCGAGCCATTATCTCTA
CCTGAAGGCAAGAGTGTGTGAGAACTGCGTGGAGGTGGAT

Amino acids (SEQ ID NO: 5)

QDGNEEMGDTTQNPYKVSISGTTVTLTCPRYDGHEIKWLVNSQNKEGHEDHLLLEDFSEMEQ
SGYYACLSKETPAEEASHYLYLKARVCENCVEVD

CD3epsilon *Saimiris ciureus*

Nucleotides

CAGGACGGTAATGAAGAGATTGGTGATACTACCCAGAACCCATATAAAGTTTCCATCTCAGG
AACCACAGTAACACTGACATGCCCTCGGTATGATGGACAGGAAATAAAATGGCTCGTAAATG
ATCAAAACAAAGAAGGTCATGAGGACCACCTGTTACTGGAAGATTTTTCAGAAATGGAACAA
AGTGGTTATTATGCCTGCCTCTCCAAAGAGACCCCCACAGAAGAGGCGAGCCATTATCTCTA
CCTGAAGGCAAGAGTGTGTGAGAACTGCGTGGAGGTGGAT

Amino acids (SEQ ID NO: 7)

QDGNEEIGDTTQNPYKVSISGTTVTLTCPRYDGQEIKWLVNDQNKEGHEDHLLLEDFSEMEQ
SGYYACLSKETPTEEASHYLYLKARVCENCVEVD

2. Generation of cross-species specific single chain antibody fragments (scFv) binding to the N-terminal amino acids 1-27 of CD3epsilon of man and different non-chimpanzee primates

2.1. Immunization of mice using the N-terminus of CD3epsilon separated from its native CD3-context by fusion to a heterologous soluble protein

Ten weeks old F1 mice from balb/c x C57black crossings were immunized with the CD3epsilon-Fc fusion protein carrying themost N-terminal amino acids 1-27 of the mature CD3epsilon chain (1-27 CD3-Fc) of man and/or saimiris ciureus. To this end 40 µg of the 1-27 CD3-Fc fusion protein with 10 nmol of a thioate-modified CpG-Oligonucleotide (5'-tccatgacgttcctgatgct-3') (SEQ ID No. 343) in 300 ul PBS were injected per mouse intra-peritoneally. Mice receive booster immunizations after 21, 42 and optionally 63 days in the same way. Ten days after the first booster immunization, blood samples were taken and antibody serum titer against 1-27 CD3-Fc fusion protein iwa tested by ELISA. Additionally, the titer against the CD3-positive human T cell line HPBall was tested in flow cytometry according to standard protocols. Serum titers were significantly higher in immunized than in non-immunized animals.

2.2. Generation of an immune murine antibody scFv library: Construction of a combinatorial antibody library and phage display

Three days after the last injection the murine spleen cells were harvested for the preparation of total RNA according to standard protocols.

A library of murine immunoglobuline (Ig) light chain (kappa) variable region (VK) and Ig heavy chain variable region (VH) DNA-fragments was constructed by RT-PCR on murine spleen RNA using VK-and VH specific primer. cDNA was synthesized according to standard protocols.

The primers were designed in a way to give rise to a 5'-XhoI and a 3'-BstEII recognition site for the amplified heavy chain V-fragments and to a 5'-SacI and a 3'-SpeI recognition site for amplified VK DNA fragments.

For the PCR-amplification of the VH DNA-fragments eight different 5'-VH-family specific primers (MVH1(GC)AG GTG CAG CTC GAG GAG TCA GGA CCT (SEQ ID No. 344); MVH2 GAG GTC CAG CTC GAG CAG TCT GGA CCT (SEQ ID No. 345); MVH3 CAG GTC CAA CTC GAG CAG CCT GGG GCT (SEQ ID No. 346); MVH4 GAG GTT CAG CTC GAG CAG TCT GGG GCA (SEQ ID No. 347); MVH5 GA(AG) GTG AAG CTC GAG GAG TCT GGA GGA (SEQ ID No. 348); MVH6 GAG GTG AAG CTT CTC GAG TCT GGA GGT (SEQ ID No. 349); MVH7 GAA GTG AAG CTC GAG GAG TCT GGG GGA (SEQ ID No. 350); MVH8 GAG GTT CAG CTC GAG CAG TCT GGA GCT (SEQ ID No. 351)) were each combined with one 3'-VH primer (3'MuVHBstEII tga gga gac ggt gac cgt ggt ccc ttg gcc cca g (SEQ ID No. 352)); for the PCR amplification of the VK-chain fragments seven different 5'-VK-family specific primers (MUVK1 CCA GTT CCG AGC TCG TTG TGA CTC AGG AAT CT (SEQ ID No. 353); MUVK2 CCA GTT CCG AGC TCG TGT TGA CGC AGC CGC CC (SEQ ID No. 354); MUVK3 CCA GTT CCG AGC TCG TGC TCA CCC AGT CTC CA (SEQ ID No. 355); MUVK4 CCA GTT CCG AGC TCC AGA TGA CCC AGT CTC CA (SEQ ID No. 356); MUVK5 CCA GAT GTG AGC TCG TGA TGA CCC AGA CTC CA (SEQ ID No. 357); MUVK6 CCA GAT GTG AGC TCG TCA TGA CCC AGT CTC CA (SEQ ID No. 358); MUVK7 CCA GTT CCG AGC TCG TGA TGA CAC AGT CTC CA (SEQ ID No. 359)) were each combined with one 3'-VK primer (3'MuVkHindIII/BsiW1 tgg tgc act agt cgt acg ttt gat ctc aag ctt ggt ccc (SEQ ID No. 360)).

The following PCR program was used for amplification: denaturation at 94°C for 20 sec; primer annealing at 52°C for 50 sec and primer extension at 72°C for 60 sec and 40 cycles, followed by a 10 min final extension at 72°C.

450 ng of the kappa light chain fragments (SacI-SpeI digested) were ligated with 1400 ng of the phagemid pComb3H5Bhis (SacI-SpeI digested; large fragment). The resulting combinatorial antibody library was then transformed into 300 ul of

electrocompetent Escherichia coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 uFD, 200 Ohm, Biorad gene-pulser) resulting in a library size of more than 10^7 independent clones. After one hour of phenotype expression, positive transformants were selected for carbenicilline resistance encoded by the pComb3H5BHis vector in 100 ml of liquid super broth (SB)-culture over night. Cells were then harvested by centrifugation and plasmid preparation was carried out using a commercially available plasmid preparation kit (Qiagen).

2800 ng of this plasmid-DNA containing the VK-library (XhoI-BstEII digested; large fragment) were ligated with 900 ng of the heavy chain V-fragments (XhoI-BstEII digested) and again transformed into two 300 ul aliquots of electrocompetent E. coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 uFD, 200 Ohm) resulting in a total VH-VK scFv (single chain variable fragment) library size of more than 10^7 independent clones.

After phenotype expression and slow adaptation to carbenicillin, the E. coli cells containing the antibody library were transferred into SB-Carbenicillin (50 ug/mL) selection medium. The E. coli cells containing the antibody library wass then infected with an infectious dose of 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein phage particle contains single stranded pComb3H5BHis-DNA encoding a murine scFv-fragment and displayed the corresponding scFv-protein as a translational fusion to phage coat protein III. This pool of phages displaying the antibody library was later used for the selection of antigen binding entities.

2.3. Phage display based selection of CD3-specific binders

The phage library carrying the cloned scFv-repertoire was harvested from the respective culture supernatant by PEG8000/NaCl precipitation and centrifugation. Approximately $10^{11}$to 10^{12} scFv phage particles were resuspended in 0.4 ml of PBS/0.1% BSA and incubated with 10^5 to 10^7 Jurkat cells (a CD3-positive human T-cell line) for 1 hour on ice under slow agitation. These Jurkat cells were grown beforehand in RPMI medium enriched with fetal calf serum (10 %), glutamine and penicillin/streptomycin, harvested by centrifugation, washed in PBS and resuspended in PBS/1 % FCS (containing Na Azide). scFv phage which do not specifically bind to the Jurkat cells were eliminated by up to five washing steps with PBS/1 % FCS (containing Na Azide). After washing, binding entities were eluted from the cells by resuspending the cells in HCl-glycine pH 2.2 (10 min incubation with subsequent

vortexing) and after neutralization with 2 M Tris pH 12, the eluate was used for infection of a fresh uninfected E. coli XL1 Blue culture (OD600 > 0.5). The E. coli culture containing E. coli cells successfully transduced with a phagemid copy, encoding a human scFv-fragment, were again selected for carbenicillin resistance and subsequently infected with VCMS 13 helper phage to start the second round of antibody display and in vitro selection. A total of 4 to 5 rounds of selections were carried out, normally.

2.4. Screening for CD3-specific binders

Plasmid DNA corresponding to 4 and 5 rounds of panning was isolated from E. coli cultures after selection. For the production of soluble scFv-protein, VH-VL-DNA fragments were excised from the plasmids (XhoI-SpeI). These fragments were cloned via the same restriction sites in the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis in that the expression construct (e.g. scFv) includes a Flag-tag (TGD YKDDDDK) between the scFv and the His6-tag and the additional phage proteins were deleted. After ligation, each pool (different rounds of panning) of plasmid DNA was transformed into 100 µl heat shock competent E. coli TG1 or XLI blue and plated onto carbenicillin LB-agar. Single colonies were picked into 100 ul of LB carb (50 ug/ml).

E. coli transformed with pComb3H5BHis containing a VL-and VH-segment produce soluble scFv in sufficient amounts after excision of the gene III fragment and induction with 1 mM IPTG. Due to a suitable signal sequence, the scFv-chain was exported into the periplasma where it folds into a functional conformation.

Single E. coli TG1 bacterial colonies from the transformation plates were picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM MgCl2 and carbenicillin 50µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. By four rounds of freezing at –70°C and thawing at 37°C, the outer membrane of the bacteria was destroyed by temperature shock and the soluble periplasmic proteins including the scFvs were released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the human anti-human CD3-scFvs was collected and used for further examination.

2.5. Identification of CD3-specific binders

Binding of the isolated scFvs was tested by flow cytometry on eukaryotic cells, which on their surface express a heterologous protein displaying at its N-terminus the first 27 N-terminal amino acids of CD3epsilon.

As described in Example 4, the first amino acids 1-27 of the N-terminal sequence of the mature CD3 epsilon chain of the human T cell receptor complex (amino acid sequence: QDGNEEMGGITQTPYKVSISGTTVILT SEQ ID NO: 2) were fused to the N-terminus of the transmembrane protein EpCAM so that the N-terminus was located at the outer cell surface. Additionally, a FLAG epitope was inserted between the N-terminal 1-27 CD3epsilon sequence and the EpCAM sequence. This fusion product was expressed in human embryonic kidney (HEK) and chinese hamster ovary (CHO) cells.

Eukaryotic cells displaying the 27 most N-terminal amino acids of mature CD3epsilon of other primate species were prepared in the same way for Saimiri ciureus (Squirrel monkey) (CD3epsilon N-terminal amino acid sequence: QDGNEEIGDTTQNPYKVSISGTTVTLT SEQ ID NO: 8), for Callithrix jacchus (CD3epsilon N-terminal amino acid sequence: QDGNEEMGDTTQNPYKVSISGTTVTLT SEQ ID NO: 4) and for Saguinus oedipus (CD3epsilon N-terminal amino acid sequence: QDGNEEMGDTTQNPYKVSISGTTVTLT SEQ ID NO: 6).

For flow cytometry $2,5x10^5$ cells are incubated with 50 ul supernatant or with 5 µg/ml of the purified constructs in 50 µl PBS with 2% FCS. The binding of the constructs was detected with an anti-His antibody (Penta-His Antibody, BSA free, Qiagen GmbH, Hilden, FRG) at 2 µg/ml in 50 µl PBS with 2% FCS. As a second step reagent a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG (Fc-gamma fragment specific), diluted 1:100 in 50 µl PBS with 2% FCS (Dianova, Hamburg, FRG) was used. The samples were measured on a FACSscan (BD biosciences, Heidelberg, FRG).

Binding was always confirmed by flowcytometry as described in the foregoing paragraph on primary T cells of man and different primates (e.g. saimiris ciureus, callithrix jacchus, saguinus oedipus).

2.6. Generation of human/humanized equivalents of non-human CD3epsilon specific scFvs

The VH region of the murine anti-CD3 scFv was aligned against human antibody germline amino acid sequences. The human antibody germline VH sequence was

chosen which has the closest homology to the non-human VH and a direct alignment of the two amino acid sequences was performed. There were a number of framework residues of the non-human VH that differ from the human VH framework regions ("different framework positions"). Some of these residues may contribute to the binding and activity of the antibody to its target.

To construct a library that contain the murine CDRs and at every framework position that differs from the chosen human VH sequence both possibilities (the human and the maternal murine amino acid residue), degenerated oligonucleotides were synthesized. These oligonucleotides incorporate at the differing positions the human residue with a probability of 75 % and the murine residue with a probability of 25 %. For one human VH e.g. six of these oligonucleotides had to be synthesized that overlap in a terminal stretch of approximately 20 nucleotides. To this end every second primer was an antisense primer. Restriction sites needed for later cloning within the oligonucleotides were deleted.

These primers may have a length of 60 to 90 nucleotides, depending on the number of primers that were needed to span over the whole V sequence.

These e.g. six primers were mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix was incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product was run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

This PCR product was then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VH approximately 350 nucleotides) was isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VH DNA fragment was amplified. This VH fragment was now a pool of VH fragments that have each one a different amount of human and murine residues at the respective differing framework positions (pool of humanized VH). The same procedure was performed for the VL region of the murine anti-CD3 scFv (pool of humanized VL).

The pool of humanized VH was then combined with the pool of humanized VL in the phage display vector pComb3H5Bhis to form a library of functional scFvs from which – after display on filamentous phage - anti-CD3 binders were selected, screened, identified and confirmed as described above for the parental non-human (murine) anti-CD3 scFv. Single clones were then analyzed for favorable properties and amino acid sequence. Those scFvs which were closest in amino acid sequence homology to human germline V-segments are preferred particularly those wherein at least one CDR among CDR I and II of VH and CDR I and II of VLkappa or CDR I and II of VLlambda shows more than 80% amino acid sequence identity to the closest respective CDR of all human germline V-segments. Anti-CD3 scFvs were converted into recombinant bispecific single chain antibodies as described in the following Examples 9, 16, and 24.

3. Generation of a recombinant fusion protein of the N-terminal amino acids 1-27 of the human CD3 epsilon chain fused to the Fc-part of an IgG1 (1-27 CD3-Fc).

3.1. Cloning and expression of 1-27 CD3-Fc

The coding sequence of the 1-27 N-terminal amino acids of the human CD3 epsilon chain fused to the hinge and Fc gamma region of human immunoglobulin IgG1 as well as an 6 Histidine Tag were obtained by gene synthesis according to standard protocols (cDNA sequence and amino acid sequence of the recombinant fusion protein are listed under SEQ ID NOs 230 and 229). The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by an 19 amino acid immunoglobulin leader peptide, followed in frame by the coding sequence of the first 27 amino acids of the extracellular portion of the mature human CD3 epsilon chain, followed in frame by the coding sequence of the hinge region and Fc gamma portion of human IgG1, followed in frame by the coding sequence of a 6 Histidine tag and a stop codon (Figure 1). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the cDNA coding for the fusion protein. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, are utilized in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025 and Raum et al. Cancer Immunol Immunother

50 (2001) 141-150) following standard protocols. A sequence verified plasmid was used for transfection in the FreeStyle 293 Expression System (Invitrogen GmbH, Karlsruhe, Germany) according to the manufacturers protocol. After 3 days cell culture supernatants of the transfectants were harvested and tested for the presence of the recombinant construct in an ELISA assay. Goat anti-human IgG, Fc-gamma fragment specific antibody (obtained from Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK) was diluted in PBS to 5 µg/ml and coated with 100 µl per well onto a MaxiSorp 96-well ELISA plate (Nunc GmbH & Co. KG, Wiesbaden, Germany) over night at 4 °C. Wells were washed with PBS with 0,05 % Tween 20 (PBS/Tween and blocked with 3 % BSA in PBS (bovine Albumin, fraction V, Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) for 60 minutes at room temperature (RT). Subsequently, wells were washed again PBS/Tween and then incubated with cell culture supernatants for 60 minutes at RT. After washing wells were incubated with a peroxidase conjugated anti-His6 antibody (Roche Diagnostics GmbH, Roche Applied Science, Mannheim, Germany) diluted 1:500 in PBS with 1 % BSA for 60 minutes at RT. Subsequently, wells were washed with 200 µl PBS/Tween and 100 µl of the SIGMAFAST OPD (SIGMAFAST OPD [o-Phenylenediamine dihydrochloride] substrate solution (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) was added according to the manufacturers protocol. The reaction was stopped by adding 100 µl 1 M H_2SO_4. Color reaction was measured on a PowerWaveX microplate spectrophotometer (BioTek Instruments, Inc., Winooski, Vermont, USA) at 490 nm and subtraction of background absorption at 620 nm. As shown in Figure 2 presence of the construct as compared to irrelevant supernatant of mock-transfected HEK 293 cells used as negative control was clearly detectable.

3.2. Binding assay of cross-species specific single chain antibodies to 1-27 CD3-Fc.

Binding of crude preparations of periplasmatically expressed cross-species specific single chain antibodies specific for CD3 epsilon to 1-27 CD3-Fc was tested in an ELISA assay. Goat anti-human IgG, Fc-gamma fragment specific antibody (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK) was diluted in PBS to 5 µg/ml and coated with 100 µl per well onto a MaxiSorp 96-well ELISA plate (Nunc GmbH & Co. KG, Wiesbaden, Germany) over night at 4 °C. Wells were washed with PBS with 0,05 % Tween 20 (PBS/Tween and blocked with PBS with 3 % BSA (bovine Albumin, fraction V, Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany)

for 60 minutes at RT. Subsequently, wells were washed with PBS/Tween and incubated with supernatants of cells expressing the 1-27 CD3-Fc construct for 60 minutes at RT. Wells were washed with PBS/Tween and incubated with crude preparations of periplasmatically expressed cross-species specific single-chain antibodies as described above for 60 minutes at room temperature. After washing with PBS/Tween wells were incubated with peroxidase conjugated anti-Flag M2 antibody (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) diluted 1:10000 in PBS with 1 % BSA for 60 minutes at RT. Wells were washed with PBS/Tween and incubated with 100 µl of the SIGMAFAST OPD (OPD [o-Phenylenediamine dihydrochloride] substrate solution (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) according to the manufacturers protocol. Color reaction was stopped with 100 µl 1 M H_2SO_4 and measured on a PowerWaveX microplate spectrophotometer (BioTek Instruments, Inc., Winooski, Vermont, USA) at 490 nm and subtraction of background absorption at 620 nm. Strong binding of cross-species specific human single chain antibodies specific for CD3 epsilon to the 1-27 CD3-Fc construct compared to a murine anti CD3 single-chain antibody was observed (Figure 3).

4. Generation of recombinant transmembrane fusion proteins of the N-terminal amino acids 1-27 of CD3 epsilon from different non-chimpanzee primates fused to EpCAM from cynomolgus monkey (1-27 CD3-EpCAM).

4.1. Cloning and expression of 1-27 CD3-EpCAM

CD3 epsilon was isolated from different non-chimpanzee primates (marmoset, tamarin, squirrel monkey) and swine. The coding sequences of the 1-27 N-terminal amino acids of CD3 epsilon chain of the mature human, common marmoset (*Callithrix jacchus*), cottontop tamarin (*Saguinus oedipus),* common squirrel monkey (*Saimiri sciureus*) and domestic swine (*Sus scrofa*; used as negative control) fused to the N-terminus of Flag tagged cynomolgus EpCAM were obtained by gene synthesis according to standard protocols. cDNA sequence and amino acid sequence of the recombinant fusion proteins are listed under SEQ ID NOs 231 to 240). The gene synthesis fragments were designed as to contain first a BsrGI site to allow fusion in correct reading frame with the coding sequence of a 19 amino acid immunoglobulin leader peptide already present in the target expression vector, which is followed in frame by the coding sequence of the N-terminal 1-27 amino acids of the extracellular portion of the mature CD3 epsilon chains, which is followed in frame by the coding

sequence of a Flag tag and followed in frame by the coding sequence of the mature cynomolgus EpCAM transmembrane protein (Figure 4). The gene synthesis fragments were also designed to introduce a restriction site at the end of the cDNA coding for the fusion protein. The introduced restriction sites BsrGI at the 5' end and SalI at the 3' end, were utilized in the following cloning procedures. The gene synthesis fragments were then cloned via BsrGI and SalI into a derivative of the plasmid designated pEF DHFR (pEF-DHFR is described in Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025), which already contained the coding sequence of the 19 amino acid immunoglobulin leader peptide following standard protocols. Sequence verified plasmids were used to transiently transfect 293-HEK cells using the MATra-A Reagent (IBA GmbH, Göttingen, Germany) and 12 µg of plasmid DNA for adherent 293-HEK cells in 175 ml cell culture flasks according to the manufacturers protocol. After 3 days of cell culture the transfectants were tested for cell surface expression of the recombinant transmembrane protein via an FACS assay according to standard protocols. For that purpose a number of $2{,}5x10^5$ cells were incubated with the anti-Flag M2 antibody (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) at 5 µg/ml in PBS with 2% FCS. Bound antibody was detected with an R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). The samples were measured on a FACScalibur (BD biosciences, Heidelberg, Germany). Expression of the Flag tagged recombinant transmembrane fusion proteins consisting of cynomolgus EpCAM and the 1-27 N-terminal amino acids of the human, marmoset, tamarin, squirrel monkey and swine CD3 epsilon chain respectively on transfected cells was clearly detectable (Figure 5).

4.2. Binding of cross-species specific anti-CD3 single chain antibodies to the 1-27 CD3-EpCAM

Binding of crude preparations of periplasmatically expressed cross-species specific anti CD3 single-chain antibodies to the 1-27 N-terminal amino acids of the human, marmoset, tamarin and squirrel monkey CD3 epsilon chains respectively fused to cynomolgus Ep-CAM was tested in an FACS assay according to standard protocols. For that purpose a number of $2{,}5x10^5$ cells were incubated with crude preparations of periplasmatically expressed cross-species specific anti CD3 single-chain antibodies (preparation was performed as described above and according to standard protocols)

and a single-chain murine anti-human CD3 antibody as negative control. As secondary antibody the Penta-His antibody (Qiagen GmbH, Hildesheim, Germany) was used at 5 µg/ml in 50 µl PBS with 2% FCS. The binding of the antibody was detected with an R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). The samples were measured on a FACScalibur (BD biosciences, Heidelberg, Germany). As shown in Figures 6 (A to E) binding of single chain antibodies to the transfectants expressing the recombinant transmembrane fusion proteins consisting of the 1-27 N-terminal amino acids of CD3 epsilon of the human, marmoset, tamarin or squirrel monkey fused to cynomolgus EpCAM was observed. No binding of cross-species specific single chain antibodies was observed to a fusion protein consisting of the 1-27 N-terminal CD3 epsilon of swine fused to cynomolgus EpCAM used as negative control. Multi-primate cross-species specificity of the anti-CD3 single chain antibodies was shown. Signals obtained with the anti Flag M2 antibody and the cross-species specific single chain antibodies were comparable, indicating a strong binding activity of the cross-species specific single chain antibodies to the N-terminal amino acids 1-27 of CD3 epsilon.

5. Binding analysis of cross-species specific anti-CD3 single chain antibodies by alanine-scanning of mouse cells transfected with the human CD3 epsilon chain and its alanine mutants

5.1. Cloning and expression of human wild-type CD3 epsilon

The coding sequence of the human CD3 epsilon chain was obtained by gene synthesis according to standard protocols (cDNA sequence and amino acid sequence of the human CD3 epsilon chain are listed under SEQ ID NOs 242 and 241). The gene synthesis fragment was designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the cDNA coding for human CD3 epsilon. The introduced restriction sites EcoRI at the 5' end and SalI at the 3' end, were utilized in the following cloning procedures. The gene synthesis fragment was then cloned via EcoRI and SalI into a plasmid designated pEF NEO following standard protocols. pEF NEO was derived of pEF DHFR (Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025) by replacing the cDNA of the DHFR with the cDNA of the neomycin resistance by

conventional molecular cloning. A sequence verified plasmid was used to transfect the murine T cell line EL4 (ATCC No. TIB-39) cultivated in RPMI with stabilized L-glutamine supplemented with 10 % FCS, 1% penicillin/streptomycin, 1% HEPES, 1% pyruvate, 1% non-essential amino acids (all Biochrom AG Berlin, Germany) at 37 °C, 95 % humidity and 7 % CO_2. Transfection was performed with the SuperFect Transfection Reagent (Qiagen GmbH, Hilden, Germany) and 2 µg of plasmid DNA according to the manufacturer's protocol. After 24 hours the cells were washed with PBS and cultivated again in the aforementioned cell culture medium with600 µg/ml G418 for selection (PAA Laboratories GmbH, Pasching, Austria). 16 to 20 days after transfection the outgrowth of resistant cells was observed. After additional 7 to 14 days cells were tested for expression of human CD3 epsilon by FACS analysis according to standard protocols. $2{,}5x10^5$ cells were incubated with anti-human CD3 antibody UCHT-1 (BD biosciences, Heidelberg, Germany) at 5 µg/ml in PBS with 2% FCS. The binding of the antibody was detected with an R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). The samples were measured on a FACSCalibur (BD biosciences, Heidelberg, Germany). Expression of human wild-type CD3 on transfected EL4 cells is shown in Figure 7.

5.2. Cloning and expression of the cross-species specific anti-CD3 single chain antibodies as IgG1 antibodies

In order to provide improved means of detection of binding of the cross-species specific single chain anti-CD3 antibodies H2C HLP, A2J HLP and E2M HLP were converted into IgG1 antibodies with murine IgG1 and human lambda constant regions. cDNA sequences coding for the heavy and light chains of respective IgG antibodies were obtained by gene synthesis according to standard protocols. The gene synthesis fragments for each specificity were designed as to contain first a Kozak site to allow eukaryotic expression of the construct, which is followed by an 19 amino acid immunoglobulin leader peptide (SEQ ID NOs 244 and 243), which is followed in frame by the coding sequence of the respective heavy chain variable region or respective light chain variable region, followed in frame by the coding sequence of the heavy chain constant region of murine IgG1 (SEQ ID NOs 246 and 245) or the coding sequence of the human lambda light chain constant region (SEQ ID NO 248 and 247), respectively. Restriction sites were introduced at the beginning

and the end of the cDNA coding for the fusion protein. Restriction sites EcoRI at the 5' end and SalI at the 3' end were used for the following cloning procedures. The gene synthesis fragments were cloned via EcoRI and SalI into a plasmid designated pEF DHFR (Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025) for the heavy chain constructs and pEF ADA (pEF ADA is described in Raum et al., Cancer Immunol Immunother., 50(3), (2001), 141-50) for the light chain constructs) according to standard protocols. Sequence verified plasmids were used for co-transfection of respective light and heavy chain constructs in the FreeStyle 293 Expression System (Invitrogen GmbH, Karlsruhe, Germany) according to the manufacturers protocol. After 3 days cell culture supernatants of the transfectants were harvested and used for the alanine-scanning experiment.

5.3. Cloning and expression of alanine mutants of human CD3 epsilon for alanine-scanning

27 cDNA fragments coding for the human CD3 epsilon chain with an exchange of one codon of the wild-type sequence of human CD3 epsilon into a codon coding for alanine (GCC) for each amino acid of amino acids 1-27 of the extracellular domain of the mature human CD3 epsilon chain respectively were obtained by gene synthesis. Except for the exchanged codon the cDNA fragments were identical to the aforementioned human wild-type CD3 cDNA fragment. Only one codon was replaced in each construct compared to the human wild-type CD3 cDNA fragment described above. Restriction sites EcoRI and SalI were introduced into the cDNA fragments at identical positions compared to the wild-type construct. All alanine-scanning constructs were cloned into pEF NEO and sequence verified plasmids were transfected into EL4 cells. Transfection and selection of transfectants was performed as described above. As result a panel of expressed constructs was obtained wherein the first amino acid of the human CD3 epsilon chain, glutamine (Q, Gln) at position 1 was replaced by alanine. The last amino acid replaced by alanine was the threonine (T, Thr) at position 27 of mature human wild-type CD3 epsilon. For each amino acid between glutamine 1 and threonine 27 respective transfectants with an exchange of the wild-type amino acid into alanine were generated.

5.4. Alanine-scanning experiment

Chimeric IgG antibodies as described in 5.2 and cross-species specific single chain antibodies specific for CD3 epsilon were tested in alanine-scanning experiment. Binding of the antibodies to the EL4 cell lines transfected with the alanine-mutant

constructs of human CD3 epsilon as described in 5.3 was tested by FACS assay according to standard protocols. $2,5x10^5$ cells of the respective transfectants were incubated with 50 µl of cell culture supernatant containing the chimeric IgG antibodies or with 50 µl of crude preparations of periplasmatically expressed single-chain antibodies. For samples incubated with crude preparations of periplasmatically expressed single-chain antibodies the anti-Flag M2 antibody (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) was used as secondary antibody at 5 µg/ml in 50 µl PBS with 2% FCS. For samples incubated with the chimeric IgG antibodies a secondary antibody was not necessary. For all samples the binding of the antibody molecules was detected with an R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). Samples were measured on a FACSCalibur (BD biosciences, Heidelberg, Germany). Differential binding of chimeric IgG molecules or cross-species specific single-chain antibodies to the EL4 cell lines transfected with the alanine-mutants of human CD3 epsilon was detected. As negative control either an isotype control or a crude preparation of a periplasmatically expressed single-chain antibody of irrelevant specificity was used respectively. UCHT-1 antibody was used as positive control for the expression level of the alanine-mutants of human CD3 epsilon. The EL4 cell lines transfected with the alanine-mutants for the amino acids tyrosine at position 15, valine at position 17, isoleucine at position 19, valine at position 24 or leucine at position 26 of the mature CD3 epsilon chain were not evaluated due to very low expression levels (data not shown). Binding of the cross-species specific single chain antibodies and the single chain antibodies in chimeric IgG format to the EL4 cell lines transfected with the alanine-mutants of human CD3 epsilon is shown in Figure 8 (A-D) as relative binding in arbitrary units with the geometric mean fluorescence values of the respective negative controls subtracted from all respective geometric mean fluorescence sample values. To compensate for different expression levels all sample values for a certain transfectant were then divided through the geometric mean fluorescence value of the UCHT-1 antibody for the respective transfectant. For comparison with the wild-type sample value of a specificity all sample values of the respective specificity were finally divided through the wild-type sample value, thereby setting the wild-type sample value to 1 arbitrary unit of binding.

The calculations used are shown in detail in the following formula:

$$value_Sample(x,y) = \frac{Sample(x,y) - neg_Contr.(x)}{(UCHT-1(x) - neg_Contr.(x)) * \frac{WT(y) - neg_Contr.(wt)}{UCHT-1(wt) - neg_Contr.(wt)}}$$

In this equation *value_Sample* means the value in arbitrary units of binding depicting the degree of binding of a specific anti-CD3 antibody to a specific alanine-mutant as shown in Figure 8 (A-D), *Sample* means the geometric mean fluorescence value obtained for a specific anti-CD3 antibody assayed on a specific alanine-scanning transfectant, *neg_Contr.* means the geometric mean fluorescence value obtained for the negative control assayed on a specific alanine-mutant, *UCHT-1* means the geometric mean fluorescence value obtained for the UCHT-1 antibody assayed on a specific alanine-mutant, *WT* means the geometric mean fluorescence value obtained for a specific anti-CD3 antibody assayed on the wild-type transfectant, *x* specifies the respective transfectant, *y* specifies the respective anti-CD3 antibody and *wt* specifies that the respective transfectant is the wild-type.

As can be seen in Figure 8 (A-D) the IgG antibody A2J HLP showed a pronounced loss of binding for the amino acids asparagine at position 4, threonine at position 23 and isoleucine at position 25 of the mature CD3 epsilon chain. A complete loss of binding of IgG antibody A2J HLP was observed for the amino acids glutamine at position 1, aspartate at position 2, glycine at position 3 and glutamate at position 5 of the mature CD3 epsilon chain. IgG antibody E2M HLP showed a pronounced loss of binding for the amino acids asparagine at position 4, threonine at position 23 and isoleucine at position 25 of the mature CD3 epsilon chain. IgG antibody E2M HLP showed a complete loss of binding for the amino acids glutamine at position 1, aspartate at position 2, glycine at position 3 and glutamate at position 5 of the mature CD3 epsilon chain. IgG antibody H2C HLP showed an intermediate loss of binding for the amino acid asparagine at position 4 of the mature CD3 epsilon chain and it showed a complete loss of binding for the amino acids glutamine at position 1, aspartate at position 2, glycine at position 3 and glutamate at position 5 of the mature CD3 epsilon chain. Single chain antibody F12Q HLP showed an essentially complete loss of binding for the amino acids glutamine at position 1, aspartate at position 2, glycine at position 3 of the mature CD3 epsilon chain and glutamate at position 5 of the mature CD3 epsilon chain.

6. Binding analysis of the cross-species specific anti-CD3 binding molecule H2C HLP to the human CD3 epsilon chain with and without N-terminal His6 tag transfected into the murine T cell line EL4

6.1. Cloning and expression of the human CD3 epsilon chain with N-terminal six histidine tag (His6 tag)

A cDNA fragment coding for the human CD3 epsilon chain with a N-terminal His6 tag was obtained by gene synthesis. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, which is followed in frame by the coding sequence of a 19 amino acid immunoglobulin leader peptide, which is followed in frame by the coding sequence of a His6 tag which is followed in frame by the coding sequence of the mature human CD3 epsilon chain (the cDNA and amino acid sequences of the construct are listed as SEQ ID NOs 256 and 255). The gene synthesis fragment was also designed as to contain restriction sites at the beginning and the end of the cDNA. The introduced restriction sites EcoRI at the 5' end and SalI at the 3' end, were used in the following cloning procedures. The gene synthesis fragment was then cloned via EcoRI and SalI into a plasmid designated pEF-NEO (as described above) following standard protocols. A sequence verified plasmid was used to transfect the murine T cell line EL4. Transfection and selection of the transfectants were performed as described above. After 34 days of cell culture the transfectants were used for the assay described below.

6.2. Binding of the cross-species specific anti-CD3 binding molecule H2C HLP to the human CD3 epsilon chain with and without N-terminal His6 tag

A chimeric IgG antibody with the binding specificity H2C HLP specific for CD3 epsilon was tested for binding to human CD3 epsilon with and without N-terminal His6 tag. Binding of the antibody to the EL4 cell lines transfected the His6-human CD3 epsilon and wild-type human CD3 epsilon respectively was tested by an FACS assay according to standard protocols. $2{,}5 \times 10^5$ cells of the transfectants were incubated with 50 µl of cell culture supernatant containing the chimeric IgG antibody or 50 µl of the respective control antibodies at 5µg/ml in PBS with 2% FCS. As negative control an appropriate isotype control and as positive control for expression of the constructs the CD3 specific antibody UCHT-1 were used respectively. The binding of the antibodies was detected with a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK).

Samples were measured on a FACSCalibur (BD biosciences, Heidelberg, Germany). Compared to the EL4 cell line transfected with wild-type human CD3 epsilon a clear loss of binding of the chimeric IgG with binding specificity H2C HLP to human-CD3 epsilon with an N-terminal His6 tag was detected. These results showed that a free N-terminus of CD3 epsilon is essential for binding of the cross-species specific anti-CD3 binding specificity H2C HLP to the human CD3 epsilon chain (Figure 9).

7. Cloning and expression of the C-terminal, transmembrane and truncated extracellular domains of human MCSP

The coding sequence of the C-terminal, transmembrane and truncated extracellular domain of human MCSP (amino acids 1538 – 2322) was obtained by gene synthesis according to standard protocols (cDNA sequence and amino acid sequence of the recombinant construct for expression of the C-terminal, transmembrane and truncated extracellular domain of human MCSP (designated as human D3) are listed under SEQ ID NOs 250 and 249). The gene synthesis fragment was designed as to contain first a Kozak site to allow eukaryotic expression of the construct followed by the coding sequence of an 19 amino acid immunoglobulin leader peptide followed in frame by a FLAG tag, followed in frame by a sequence containing several restriction sites for cloning purposes and coding for a 9 amino acid artificial linker (SRTRSGSQL), followed in frame by the coding sequence of the C-terminal, transmembrane and truncated extracellular domain of human MCSP and a stop codon. Restriction sites were introduced at the beginning and at the end of the DNA fragment. The restriction sites EcoRI at the 5' end and SalI at the 3' end were used in the following cloning procedures. The fragment was digested with EcoRI and SalI and cloned into pEF-DHFR (pEF-DHFR is described in Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025) following standard protocols. A sequence verified plasmid was used to transfect CHO/dhfr- cells (ATCC No. CRL 9096). Cells were cultivated in RPMI 1640 with stabilized glutamine, supplemented with 10% FCS, 1% penicillin/streptomycin (all obtained from Biochrom AG Berlin, Germany) and nucleosides from a stock solution of cell culture grade reagents (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) to a final concentration of 10 µg/ml Adenosine, 10 µg/ml Deoxyadenosine and 10 µg/ml Thymidine, in an incubator at 37 °C, 95% humidity and 7% CO_2. Transfection was performed using the PolyFect Transfection Reagent (Qiagen GmbH, Hilden, Germany) and 5 µg of plasmid DNA

according to the manufacturer's protocol. After cultivation for 24 hours cells were washed once with PBS and cultivated again in RPMI 1640 with stabilized glutamine and 1% penicillin/streptomycin. Thus the cell culture medium did not contain nucleosides and thereby selection was applied on the transfected cells. Approximately 14 days after transfection the outgrowth of resistant cells was observed. After an additional 7 to 14 days the transfectants were tested for expression of the construct by FACS analysis. $2,5x10^5$ cells were incubated with 50 µl of an anti-Flag-M2 antibody (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) diluted to 5 µg/ml in PBS with 2% FCS. The binding of the antibody was detected with a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific diluted 1:100 in PBS with 2% FCS (ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). The samples were measured on a FACScalibur (BD biosciences, Heidelberg, Germany).

8. Cloning and expression of the C-terminal, transmembrane and truncated extracellular domains of macaque MCSP

The cDNA sequence of the C-terminal, transmembrane and truncated extracellular domains of macaque MCSP (designated as macaque D3) was obtained by a set of three PCRs on macaque skin cDNA (Cat No. C1534218-Cy-BC; BioCat GmbH, Heidelberg, Germany) using the following reaction conditions: 1 cycle at 94°C,3 min., 40 cycles with 94°C for 0,5 min., 52°C for 0,5 min. and 72°C for 1,75 min., terminal cycle of 72°C for 3 min.. The following primers were used:

forward primer: 5'-GATCTGGTCTACACCATCGAGC-3' (SEQ ID No. 361)
reverse primer: 5'-GGAGCTGCTGCTGGCTCAGTGAGG-3' (SEQ ID No. 362)
forward primer: 5'- TTCCAGCTGAGCATGTCTGATGG-3' (SEQ ID No. 363)
reverse primer: 5'- CGATCAGCATCTGGGCCCAGG-3' (SEQ ID No. 364)
forward primer: 5'- GTGGAGCAGTTCACTCAGCAGGACC-3' (SEQ ID No. 365)
reverse primer: 5'- GCCTTCACACCCAGTACTGGCC-3' (SEQ ID No. 366)

Those PCRs generated three overlapping fragments (A: 1-1329, B: 1229-2428, C: 1782-2547) which were isolated and sequenced according to standard protocols using the PCR primers and thereby provided a 2547 bp portion of the cDNA sequence of macaque MCSP (the cDNA sequence and amino acid sequence of this portion of macaque MCSP are listed under SEQ ID NOs 252 and 251) from 74 bp upstream of the coding sequence of the C-terminal domain to 121 bp downstream of

the stop codon. Another PCR using the following reaction conditions: 1 cycle at 94°C for 3 min, 10 cycles with 94°C for 1 min, 52°C for 1 min and 72°C for 2,5 min, terminal cycle of 72°C for 3 min was used to fuse the PCR products of the aforementioned reactions A and B. The following primers are used:

forward primer: 5'-tcccgtacgagatctggatcccaattggatggcggactcgtgctgttctcacacagagg-3' (SEQ ID No. 367)

reverse primer: 5'-agtgggtcgactcacacccagtactggccattcttaagggcaggg-3' (SEQ ID No. 368)

The primers for this PCR were designed to introduce restriction sites at the beginning and at the end of the cDNA fragment coding for the C-terminal, transmembrane and truncated extracellular domains of macaque MCSP. The introduced restriction sites MfeI at the 5' end and SalI at the 3' end, were used in the following cloning procedures. The PCR fragment was then cloned via MfeI and SalI into a Bluescript plasmid containing the EcoRI/MfeI fragment of the aforementioned plasmid pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) by replacing the C-terminal, transmembrane and truncated extracellular domains of human MCSP. The gene synthesis fragment contained the coding sequences of the immunoglobulin leader peptide and the Flag tag as well as the artificial linker (SRTRSGSQL) in frame to the 5' end of the cDNA fragment coding for the C-terminal, transmembrane and truncated extracellular domains of macaque MCSP. This vector was used to transfect CHO/dhfr- cells (ATCC No. CRL 9096). Cells were cultivated in RPMI 1640 with stabilized glutamine supplemented with 10% FCS, 1% penicillin/streptomycin (all from Biochrom AG Berlin, Germany) and nucleosides from a stock solution of cell culture grade reagents (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) to a final concentration of 10 µg/ml Adenosine, 10 µg/ml Deoxyadenosine and 10 µg/ml Thymidine, in an incubator at 37 °C, 95% humidity and 7% CO2. Transfection was performed with PolyFect Transfection Reagent (Qiagen GmbH, Hilden, Germany) and 5 µg of plasmid DNA according to the manufacturer's protocol. After cultivation for 24 hours cells were washed once with PBS and cultivated again in RPMI 1640 with stabilized glutamine and 1% penicillin/streptomycin. Thus the cell culture medium did not contain nucleosides and thereby selection was applied on the transfected cells. Approximately 14 days after transfection the outgrowth of resistant cells is observed. After an additional 7 to 14 days the transfectants were tested for expression of the

recombinant construct via FACS. $2,5x10^5$ cells were incubated with 50 µl of an anti-Flag-M2 antibody (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) diluted to 5 µg/ml in PBS with 2% FCS. Bound antibody was detected with a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). Samples were measured on a FACScalibur (BD biosciences, Heidelberg, Germany).

9. Generation and characterisation of MCSP and CD3 cross-species specific bispecific single chain molecules

Bispecific single chain antibody molecules each comprising a binding domain cross-species specific for human and non-chimpanzee primate CD3 epsilon as well as a binding domain cross-species-specific for human and non-chimpanzee primate MCSP, are designed as set out in the following Table 1:

Table 1: Formats of MCSP and CD3 cross-species specific bispecific single chain antibodies

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
190/189	MCSP-G4 HL x H2C HL
192/191	MCSP-G4 HL x F12Q HL
194/193	MCSP-G4 HL x I2C HL
196/195	MCSP-G4 HLP x F6A HLP
198/197	MCSP-G4 HLP x H2C HLP
202/201	MCSP-G4 HLP x G4H HLP
206/205	MCSP-G4 HLP x E1L HLP
208/207	MCSP-G4 HLP x E2M HLP
212/211	MCSP-G4 HLP x F12Q HL
214/213	MCSP-G4 HLP x I2C HL
216/215	MCSP-D2 HL x H2C HL
218/217	MCSP-D2 HL x F12Q HL
220/219	MCSP-D2 HL x I2C HL
222/221	MCSP-D2 HLP x H2C HLP
224/223	MCSP-F9 HL x H2C HL
226/225	MCSP-F9 HLP x H2C HLP
228/227	MCSP-F9 HLP x G4H HLP
318/317	MCSP-A9 HL x H2C HL
320/319	MCSP-A9 HL x F12Q HL
322/321	MCSP-A9 HL x I2C HL
324/323	MCSP-C8 HL x I2C HL

328/327	MCSP-B7 HL x I2C HL
326/325	MCSP-B8 HL x I2C HL
330/329	MCSP-G8 HL x I2C HL
332/331	MCSP-D5 HL x I2C HL
334/333	MCSP-F7 HL x I2C HL
336/335	MCSP-G5 HL x I2C HL
338/337	MCSP-F8 HL x I2C HL
340/339	MCSP-G10 HL x I2C HL

The aforementioned constructs containing the variable heavy-chain (VH) and variable light-chain (VL) domains cross-species specific for human and macaque MCSP D3 and the VH and VL domains cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by a 19 amino acid immunoglobulin leader peptide, followed in frame by the coding sequence of the respective bispecific single chain antibody molecule, followed in frame by the coding sequence of a histidine$_6$-tag and a stop codon. The gene synthesis fragment was also designed as to introduce suitable N- and C-terminal restriction sites. The gene synthesis fragment was cloned via these restriction sites into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). The constructs were transfected stably or transiently into DHFR-deficient CHO-cells (ATCC No. CRL 9096) by electroporation or alternatively into HEK 293 (human embryonal kidney cells, ATCC Number: CRL-1573) in a transient manner according to standard protocols.

Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the constructs was induced by addition of increasing concentrations of methothrexate (MTX) up to final concentrations of 20 nM MTX. After two passages of stationary culture the cells were grown in roller bottles with nucleoside-free HyQ PF CHO liquid soy medium (with 4.0 mM L-Glutamine with 0.1% Pluronic F – 68; HyClone) for 7 days before harvest. The cells were removed by centrifugation and the supernatant containing the expressed protein is stored at –20°C.

Äkta® Explorer System (GE Health Systems) and Unicorn® Software were used for chromatography. Immobilized metal affinity chromatography ("IMAC") was performed using a Fractogel EMD chelate® (Merck) which was loaded with $ZnCl_2$ according to

the protocol provided by the manufacturer. The column was equilibrated with buffer A (20 mM sodium phosphate buffer pH 7.2, 0.1 M NaCl) and the cell culture supernatant (500 ml) was applied to the column (10 ml) at a flow rate of 3 ml/min. The column was washed with buffer A to remove unbound sample. Bound protein was eluted using a two step gradient of buffer B (20 mM sodium phosphate buffer pH 7.2, 0.1 M NaCl, 0.5 M Imidazole) according to the following:

Step 1: 20% buffer B in 6 column volumes

Step 2: 100% buffer B in 6 column volumes

Eluted protein fractions from step 2 were pooled for further purification. All chemicals are of research grade and purchased from Sigma (Deisenhofen) or Merck (Darmstadt).

Gel filtration chromatography was performed on a HiLoad 16/60 Superdex 200 prep grade column (GE/Amersham) equilibrated with Equi-buffer (25 mM Citrate, 200 mM Lysine, 5% Glycerol, pH 7.2). Eluted protein samples (flow rate 1 ml/min) were subjected to standard SDS-PAGE and Western Blot for detection. Prior to purification, the column was calibrated for molecular weight determination (molecular weight marker kit, Sigma MW GF-200). Protein concentrations were determined using OD280 nm.

Purified bispecific single chain antibody protein was analyzed in SDS PAGE under reducing conditions performed with pre-cast 4-12% Bis Tris gels (Invitrogen). Sample preparation and application were performed according to the protocol provided by the manufacturer. The molecular weight was determined with MultiMark protein standard (Invitrogen). The gel was stained with colloidal Coomassie (Invitrogen protocol). The purity of the isolated protein is >95% as determined by SDS-PAGE.

The bispecific single chain antibody has a molecular weight of about 52 kDa under native conditions as determined by gel filtration in phosphate buffered saline (PBS). All constructs were purified according to this method.

Western Blot was performed using an Optitran® BA-S83 membrane and the Invitrogen Blot Module according to the protocol provided by the manufacturer. For detection of the bispecific single chain antibody protein antibodies an anti-His Tag antibody was used (Penta His, Qiagen). A Goat-anti-mouse Ig antibody labeled with alkaline phosphatase (AP) (Sigma) was used as secondary antibody and BCIP/NBT (Sigma) as substrate. A single band was detected at 52 kD corresponding to the purified bispecific single chain antibody.

Alternatively, constructs were transiently expressed in DHFR deficient CHO cells. In brief, 4 x 105 cells per construct were cultivated in 3 ml RPMI 1640 all medium with stabilized glutamine supplemented with 10% fetal calf serum, 1% penicillin/streptomycin and nucleosides from a stock solution of cell culture grade reagents (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) to a final concentration of 10 µg/ml Adenosine, 10 µg/ml Deoxyadenosine and 10 µg/ml Thymidine, in an incubator at 37 °C, 95% humidity and 7% CO2 one day before transfection. Transfection was performed with Fugene 6 Transfection Reagent (Roche, # 11815091001) according to the manufacturer's protocol. 94 µl OptiMEM medium (Invitrogen) and 6 µl Fugene 6 are mixed and incubated for 5 minutes at room temperature. Subsequently, 1.5 µg DNA per construct were added, mixed and incubated for 15 minutes at room temperature. Meanwhile, the DHFR deficient CHO cells were washed with 1x PBS and resuspended in 1.5 ml RPMI 1640 all medium. The transfection mix was diluted with 600 µl RPMI 1640 all medium, added to the cells and incubated overnight at 37 °C, 95% humidity and 7% CO2. The day after transfection the incubation volume of each approach was extended to 5 ml RPMI 1640 all medium. Supernatant was harvested after 3 days of incubation.

10. Flow cytometric binding analysis of the MCSP and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs regarding the capability to bind to human and macaque MCSP D3 and CD3, respectively, a FACS analysis was performed. For this purpose CHO cells transfected with human MCSP D3 (as described in Example 7) and the human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used to test the binding to human antigens. The binding reactivity to macaque antigens was tested by using the generated macaque MCSP D3 transfectant (described in Example 8) and a macaque T cell line 4119LnPx (kindly provided by Prof. Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; published in Knappe A, et al., and Fickenscher H., Blood 2000, 95, 3256-61). 200.000 cells of the respective cell lines were incubated for 30 min on ice with 50 µl of the purified protein of the cross-species specific bispecific antibody constructs (2 µg/ml) or cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The cells were washed twice in PBS with 2% FCS and binding

of the construct was detected with a murine anti-His antibody (Penta His antibody; Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti-His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Supernatant of untransfected CHO cells was used as negative control for binding to the T cell lines. A single chain construct with irrelevant target specificity was used as negative control for binding to the MCSP-D3 transfected CHO cells.

Flow cytometry was performed on a FACS-Calibur apparatus; the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

The bispecific binding of the single chain molecules listed above, which are cross-species specific for MCSP D3 and cross-species specific for human and macaque CD3 was clearly detectable as shown in Figures 10, 11, 12 and 39. In the FACS analysis all constructs showed binding to CD3 and MCSP D3 as compared to the respective negative controls. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and MCSP D3 antigens was demonstrated.

11. Bioactivity of MCSP and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the MCSP D3 positive cell lines described in Examples 7 and 8. As effector cells stimulated human CD4/CD56 depleted PBMC, stimulated human PBMC or the macaque T cell line 4119LnPx are used as specified in the respective figures.

Generation of the stimulated CD4/CD56 depleted PBMC was performed as follows:

Coating of a Petri dish (145 mm diameter, Greiner bio-one GmbH, Kremsmünster) was carried out with a commercially available anti-CD3 specific antibody (e.g. OKT3, Othoclone) in a final concentration of 1 µg/ml for 1 hour at 37°C. Unbound protein was removed by one washing step with PBS. The fresh PBMC were isolated from peripheral blood (30 – 50 ml human blood) by Ficoll gradient centrifugation according to standard protocols. 3 – 5 x 10^7 PBMC were added to the precoated petri dish in 120 ml of RPMI 1640 with stabilized glutamine / 10% FCS / IL-2 20 U/ml (Proleukin,

Chiron) and stimulated for 2 days. On the third day the cells were collected and washed once with RPMI 1640. IL-2 was added to a final concentration of 20 U/ml and the cells were cultivated again for one day in the same cell culture medium as above. By depletion of CD4+ T cells and CD56+ NK cells according to standard protocols CD8+ cytotoxic T lymphocytes (CTLs) were enriched.

Target cells were washed twice with PBS and labelled with 11.1 MBq ^{51}Cr in a final volume of 100 µl RPMI with 50% FCS for 45 minutes at 37°C. Subsequently the labelled target cells were washed 3 times with 5 ml RPMI and then used in the cytotoxicity assay. The assay was performed in a 96 well plate in a total volume of 250µl supplemented RPMI (as above) with an E:T ratio 10:1. 1 µg/ml of the cross-species specific bispecific single chain antibody molecules and 20 threefold dilutions thereof were applied. If using supernatant containing the cross-species specific bispecific single chain antibody molecules, 21 two- and 20 threefold dilutions thereof were applied for the macaque and the human cytotoxicity assay, respectively. The assay time was 18 hours and cytotoxicity was measured as relative values of released chromium in the supernatant related to the difference of maximum lysis (addition of Triton-X) and spontaneous lysis (without effector cells). All measurements were done in quadruplicates. Measurement of chromium activity in the supernatants was performed with a Wizard 3" gamma counter (Perkin Elmer Life Sciences GmbH, Köln, Germany). Analysis of the experimental data was performed with Prism 4 for Windows (version 4.02, GraphPad Software Inc., San Diego, California, USA). Sigmoidal dose response curves typically have R^2 values >0.90 as determined by the software. EC_{50} values calculated by the analysis program were used for comparison of bioactivity.

As shown in Figures 13 to 17 and 40, all of the generated cross-species specific bispecific single chain antibody constructs demonstrate cytotoxic activity against human MCSP D3 positive target cells elicited by stimulated human CD4/CD56 depleted PBMC or stimulated PBMC and against macaque MCSP D3 positive target cells elicited by the macaque T cell line 4119LnPx.

12. Plasma stability of MCSP and CD3 cross-species specific bispecific single chain antibodies

Stability of the generated bispecific single chain antibodies in human plasma was analyzed by incubation of the bispecific single chain antibodies in 50% human

Plasma at 37°C and 4°C for 24 hours and subsequent testing of bioactivity. Bioactivity was studied in a chromium 51 (^{51}Cr) release in vitro cytotoxicity assay using a MCSP positive CHO cell line (expressing MCSP as cloned according to example 14 or 15) as target and stimulated human CD8 positive T cells as effector cells.

EC_{50} values calculated by the analysis program as described above were used for comparison of bioactivity of bispecific single chain antibodies incubated with 50% human plasma for 24 hours at 37°C and 4°C respectively with bispecific single chain antibodies without addition of plasma or mixed with the same amount of plasma immediately prior to the assay.

As shown in Figure 18 and Table 2 the bioactivity of the G4 H-L x I2C H-L, G4 H-L x H2C H-L and G4 H-L x F12Q H-L bispecific antibodies was not significantly reduced as compared with the controls without the addition of plasma or with addition of plasma immediately before testing of bioactivity.

Table 2: bioactivity of the bispecific antibodies without or with the addition of Plasma

Construct	Without plasma	With plasma	Plasma 37°C	Plasma 4°C
G4 H-L x I2C H-L	300	796	902	867
G4 H-L x H2C H-L	496	575	2363	1449
G4 H-L x F12Q H-L	493	358	1521	1040

13. Redistribution of circulating T cells in the absence of circulating target cells by first exposure to CD3 binding molecules directed at conventional i.e. context dependent CD3 epitopes is a major risk factor for adverse events related to the initiation of treatment

T cell redistribution in patients with B-cell Non-Hodgkin-Lymphoma (B-NHL) following initiation of treatment with the conventional CD3 binding molecule

A conventional CD19xCD3 binding molecules is a CD3 binding molecule of the bispecific tandem scFv format (Loffler (2000, Blood, Volume 95, Number 6) or WO 99/54440). It consists of two different binding portions directed at (i) CD19 on the surface of normal and malignant human B cells and (ii) CD3 on human T cells. By crosslinking CD3 on T cells with CD19 on B cells, this construct triggers the redirected lysis of normal and malignant B cells by the cytotoxic activity of T cells.

The CD3 epitope recognized by such a conventional CD3 binding molecule is localized on the CD3 epsilon chain, where it only takes the correct conformation if it is embedded within the rest of the epsilon chain and held in the right position by heterodimerization of the epsilon chain with either the CD3 gamma or delta chain. Interaction of this highly context dependent epitope with a conventional CD3 binding molecule (see e.g. Loffler (2000, Blood, Volume 95, Number 6) or WO 99/54440) – even when it occurs in a purely monovalent fashion and without any crosslinking - can induce an allosteric change in the conformation of CD3 leading to the exposure of an otherwise hidden proline-rich region within the cytoplasmic domain of CD3 epsilon. Once exposed, the proline-rich region can recruit the signal transduction molecule Nck2, which is capable of triggering further intracellular signals. Although this is not sufficient for full T cell activation, which definitely requires crosslinking of several CD3 molecules on the T cell surface, e.g. by crosslinking of several anti-CD3 molecules bound to several CD3 molecules on a T cell by several CD19 molecules on the surface of a B cell, pure monovalent interaction of conventional CD3 binding molecules to their context dependent epitope on CD3 epsilon is still not inert for T cells in terms of signalling. Without being bound by theory, monovalent conventional CD3 binding molecules (known in the art) may induce some T cell reactions when infused into humans even in those cases where no circulating target cells are available for CD3 crosslinking. An important T cell reaction to the intravenous infusion of monovalent conventional CD19xCD3 binding molecule into B-NHL patients who have essentially no circulating CD19-positive B cells is the redistribution of T cells after start of treatment. It has been found in a phase I clinical trial that this T cell reaction occurs during the starting phase of intravenous CD19xCD3 binding molecule infusion in all individuals without circulating CD19-positive target B cells essentially independent of the CD19xCD3 binding molecule dose (Fig. 19). However, sudden increases in CD19xCD3 binding molecule exposure have been found to trigger virtually the same redistributional T cell reaction in these patients as the initial exposure of T cells to CD19xCD3 binding molecule at treatment start (Fig. 20 A) and even gradual increases in CD19xCD3 binding molecule exposure still can have redistributional effects on circulating T cells (Fig. 21). Moreover, it has been found that this essentially dose-independent redistributional T cell reaction in the absence of circulating target cells as triggered by conventional CD3 binding molecules like the CD19xCD3 binding molecule (e.g. disclosed in WO 99/54440) in 100% of all treated

individuals is a major risk factor for adverse events related to the initiation of treatment.

According to the study protocol, patients with relapsed histologically confirmed indolent B-cell Non-Hodgkin-Lymphoma (B-NHL) including mantle cell lymphoma were recruited in an open-label, multi-center phase I interpatient dose-escalation trial. The study protocol was approved by the independent ethics committees of all participating centers and sent for notification to the responsible regulatory authority.

Measurable disease (at least one lesion ≥ 1.5 cm) as documented by CT scan was required for inclusion into the study. Patients received conventional CD19xCD3 binding molecule by continuous intravenous infusion with a portable minipump system over four weeks at constant flow rate (i.e. dose level). Patients were hospitalized during the first two weeks of treatment before they were released from the hospital and continued treatment at home. Patients without evidence of disease progression after four weeks were offered to continue treatment for further four weeks. So far six different dose levels were tested without reaching a maximum tolerated dose (MTD): 0.5, 1.5, 5, 15, 30 and 60 µg/m^2/24h. Cohorts consisted of three patients each if no adverse events defined by the study protocol as DLT (dose limiting toxicity) were observed. In case of one DLT among the first three patients the cohort was expanded to six patients, which – in the absence of a second DLT – allowed further dose escalation. Accordingly, dose levels without DLT in cohorts with 3 patients or with one DLT in cohorts with 6 patients were regarded as safe. Study treatment was stopped in all patients who developed a DLT. At 15 and 30 µg/m^2/24h different modes of treatment initiation during the first 24h were tested in several additional cohorts: (i) Stepwise increase after 5 µg/m^2/24h for the first 24h to 15 µg/m^2/24h maintenance dose (patient cohort 15-step), (ii) even continuous increase of flow-rate from almost zero to 15 or 30 µg/m^2/24h (patient cohorts 15-ramp and 30-ramp) and (iii) start with the maintenance dose from the very beginning (patient cohorts 15-flat, 30-flat and 60-flat). Patient cohorts at dose levels 0.5, 1.5 and 5 µg/m^2/24h were all started with the maintenance dose from the very beginning (i.e. flat initiation).

Time courses of absolute B- and T-cell counts in peripheral blood were determined by four color FACS analysis as follows:

Collection of blood samples and routine analysis

In patient cohorts 15-ramp, 15-flat, 30-ramp, 30-flat and 60-flat blood samples (6 ml) were obtained before and 0.75, 2, 6, 12, 24, 30, 48 hours after start of CD19xCD3 binding molecule (as disclosed in WO 99/54440) infusion as well as on treatment days 8, 15, 17, 22, 24, 29, 36, 43, 50, 57 and 4 weeks after end of conventional CD19xCD3 binding molecule infusion using EDTA-containing Vacutainer™ tubes (Becton Dickinson) which were shipped for analysis at 4°C. In patient cohorts 15-step blood samples (6 ml) were obtained before and 6, 24, 30, 48 hours after start of CD19xCD3 binding molecule infusion as well as on treatment days 8, 15, 22, 29, 36, 43, 50, 57 and 4 weeks after end of CD19xCD3 binding molecule infusion. At dose levels 0.5, 1.5 and 5 µg/m^2/24h blood samples (6 ml) were obtained before and 6, 24, 48 hours after start of CD19xCD3 binding molecule infusion as well as on treatment days 8, 15, 22, 29, 36, 43, 50, 57 and 4 weeks after end of CD19xCD3 binding molecule infusion. In some cases slight variations of these time points occurred for operational reasons. FACS analysis of lymphocyte subpopulations was performed within 24 – 48 h after blood sample collection. Absolute numbers of leukocyte subpopulations in the blood samples were determined through differential blood analysis on a CoulterCounter™ (Coulter).

Isolation of PBMC from blood samples

PBMC (peripheral blood mononuclear cells) isolation was performed by an adapted Ficoll™ gradient separation protocol. Blood was transferred at room temperature into 10 ml Leucosep™ tubes (Greiner) pre-loaded with 3 ml Biocoll™ solution (Biochrom). Centrifugation was carried out in a swing-out rotor for 15 min at 1700xg and 22°C without deceleration. The PBMC above the Biocoll™ layer were isolated, washed once with FACS buffer (PBS / 2% FBS [Foetal Bovine Serum; Biochrom]), centrifuged and resuspended in FACS buffer. Centrifugation during all wash steps was carried out in a swing-out rotor for 4 min at 800xg and 4°C. If necessary, lysis of erythrocytes was performed by incubating the isolated PBMC in 3 ml erythrocyte lysis buffer (8.29 g NH_4Cl, 1.00 g $KHCO_3$, 0.037 g EDTA, ad 1.0 l H_2O_{bidest}, pH 7.5) for 5 min at room temperature followed by a washing step with FACS buffer.

Staining of PBMC with fluorescence-labeled antibodies against cell surface molecules

Monoclonal antibodies were obtained from Invitrogen ([1]Cat. No. MHCD1301, [2]Cat. No. MHCD1401), Dako ([5]Cat. No. C7224) or Becton Dickinson ([3]Cat. No. 555516, [4]Cat. No. 345766) used according to the manufacturers` recommendations. 5x10^5 –

$1x10^6$ cells were stained with the following antibody combination: anti-CD13[1] / anti-CD14[2] (FITC) x anti-CD56[3] (PE) x anti-CD3[4] (PerCP) x anti-CD19[5] (APC). Cells were pelleted in V-shaped 96 well multititer plates (Greiner) and the supernatant was removed. Cell pellets were resuspended in a total volume of 100 µl containing the specific antibodies diluted in FACS buffer. Incubation was carried out in the dark for 30 min at 4°C. Subsequently, samples were washed twice with FACS buffer and cell pellets were resuspended in FACS buffer for flowcytometric analysis.

Flowcytometric detection of stained lymphocytes by FACS

Data collection was performed with a 4 color BD FACSCalibur™ (Becton Dickinson). For each measurement $1x10^4$ cells of defined lymphocyte subpopulations were acquired. Statistical analysis was performed with the program CellQuest Pro™ (Becton Dickinson) to obtain lymphocyte subpopulation percentages and to classify cell surface molecule expression intensity. Subsequently, percentages of single lymphocyte subsets related to total lymphocytes (i.e. B plus T plus NK cells excluding any myeloid cells via CD13/14-staining) as determined by FACS were correlated with the lymphocyte count from the differential blood analysis to calculate absolute cell numbers of T cells ($CD3^+$, $CD56^-$, $CD13/14^-$) and B cells ($CD19^+$, $CD13/14^-$).

T cell redistribution during the starting phase of conventional CD19xCD3 binding molecule (e.g. disclosed in WO 99/54440) treatment in all those patients who had essentially no circulating CD19-positive B cells at treatment start is shown in (Fig. 19). For comparison, a representative example of T cell redistribution during the starting phase of CD19xCD3 binding molecule treatment in a patient with a significant number of circulating CD19-positive B cells is shown in Fig. 22.

In both cases (i.e. essentially no or many circulating B cells) circulating T cell counts rapidly decrease upon treatment start. However, in the absence of circulating B cells T cells tend to return into the circulating blood very early, while the return of T cells into the circulating blood of those patients who have a significant number of circulating B cells at treatment start is usually delayed until these circulating B cells are depleted. Thus, the T cell redistribution patterns mainly differ in the kinetics of T cell reappearance in the circulating blood.

Assessment of efficacy based on CT scan was carried out by central reference radiology after 4 weeks of treatment and in patients receiving additional 4 weeks also after 8 weeks of treatment plus in all cases four weeks after end of treatment.

Disappearance and/or normalization in size of all known lesions (including an enlarged spleen) plus clearance of bone marrow from lymphoma cells in cases of bone marrow infiltration was counted as complete response (CR). Reduction by at least 50% from baseline of the sum of products of the two biggest diameters (SPD) of each predefined target lesion was defined as partial response (PR); a reduction by at least 25% was regarded a minimal response (MR). Progressive disease (PD) was defined as ≥ 50% increase of SPD from baseline. SPD deviations from baseline between +50% and –25% were regarded as stable disease (SD).

Patient demographics, doses received and clinical outcome in 34 patients are summarized in Table 3. Clinical anti-tumor activity of the CD19xCD3 binding molecule was clearly dose dependent: Consistent depletion of circulating CD19-positive B (lymphoma) cell from peripheral blood was observed from 5 µg/m^2/24h onwards. At 15 µg/m^2/24h and 30 µg/m^2/24h first objective clinical responses (PRs and CRs) were recorded as well as cases of partial and complete elimination of B lymphoma cells from infiltrated bone marrow. Finally, at 60 µg/m^2/24h the response rate increased to 100% (PRs and CRs) and bone marrow clearance from B lymphoma cells was complete in all evaluable cases.

The CD19xCD3 binding molecule was well tolerated by the majority of patients. Most frequent adverse events of grades 1-4 in 34 patients, regardless of causality are summarized in Table 4. CD19xCD3 binding molecule-related adverse events usually were transient and fully reversible. In particular, there were 2 patients (patients # 19 and # 24 in Table 3) essentially without circulating CD19-positive B cells whose treatment was stopped early because of CNS adverse events (lead symptoms: confusion and disorientation) related to repeated T cell redistribution during the starting phase of CD19xCD3 binding molecule infusion.

One of these patients (#19) was in cohort 15-step. He received 5 µg/m^2/24h CD19xCD3 binding molecule for the first 24h followed by sudden increase to 15 µg/m^2/24h maintenance dose. The corresponding T cell redistribution pattern shows that circulating T cell counts rapidly decreased upon start of infusion at 5 µg/m^2/24h followed by early reappearance of T cells in the circulating blood essentially without circulating CD19-positive B cells. As a consequence, the peripheral T cell counts had fully recovered when the CD19xCD3 binding molecule dose was increased after 24h from 5 to 15 µg/m^2/24h. Therefore the dose step could trigger a second episode of T cell redistribution as shown in Fig. 20 A. This repeated T cell redistribution was

related with CNS side effects (lead symptoms: confusion and disorientation) in this patient, which led to the stop of infusion. The relationship between repeated T cell redistribution and such CNS adverse events was also observed in previous phase I clinical trials in B-NHL patients who received CD19xCD3 binding molecule (e.g. disclosed in WO 99/54440) as repeated bolus infusion for 2 to 4 hours each usually followed by 2 days of treatment free interval (Fig. 20 B). Every single bolus infusion triggered one episode of T cell redistribution consisting of a fast decrease in circulating T cell counts and T cell recovery prior to the next bolus infusion. In total, CNS adverse events related to repeated T cell redistribution were observed in 5 out of 21 patients. Fig. 20 B shows the representative example of one patient from the bolus infusion trials, who developed CNS symptoms after the third episode of T cell redistribution. Typically, patients with CNS adverse events in the bolus infusion trials also had low circulating B cell counts.

The second patient (#24) from the continuous infusion trial, whose treatment was stopped early because of CNS adverse events (lead symptoms: confusion and disorientation) related to repeated T cell redistribution during the starting phase of CD19xCD3 binding molecule infusion, was in cohort 15-flat. By mistake, this patient received an CD19xCD3 binding molecule infusion without additional HSA as required for stabilization of the drug. The resulting uneven drug flow triggered repeated episodes of T cell redistribution instead of only one (Fig. 23 A) with the consequence that the infusion had to be stopped because of developing CNS symptoms. Yet, when the same patient was restarted correctly with CD19xCD3 binding molecule solution containing additional HSA for drug stabilization (e.g. disclosed in WO 99/54440), no repeated T cell redistribution was observed and the patient did not again develop any CNS symptoms (Fig. 23 B). Because this patient also had essentially no circulating B cells, the circulating T cells could react with fast redistribution kinetics even to subtle changes in drug exposure as observed. The CNS adverse events related to T cell redistribution in patients who have essentially no circulating target cells can be explained by a transient increase of T cell adhesiveness to the endothelial cells followed by massive simultaneous adhesion of circulating T cells to the blood vessel walls with a consecutive drop of T cell numbers in the circulating blood as observed. The massive simultaneous attachment of T cells to the blood vessel walls can cause an increase in endothelial permeability and endothelial cell activation. The consequences of increased endothelial permeability

are fluid shifts from the intravascular compartment into interstitial tissue compartments including the CNS interstitium. Endothelial cell activation by attached T cells can have procoagulatory effects (Monaco et al. J Leukoc Biol 71 (2002) 659-668) with possible disturbances in blood flow (including cerebral blood flow) particularly with regard to capillary microcirculation. Thus, CNS adverse events related to T cell redistribution in patients essentially without circulating target cells can be the consequence of capillary leak and/or disturbances in capillary microcirculation through adherence of T cells to endothelial cells. The endothelial stress caused by one episode of T cell redistribution is tolerated by the majority of patients, while the enhanced endothelial stress caused by repeated T cell redistribution frequently causes CNS adverse events. More than one episode of T cell redistribution may be less risky only in patients who have low baseline counts of circulating T cells. However, also the limited endothelial stress caused by one episode of T cell redistribution can cause CNS adverse events in rare cases of increased susceptibility for such events as observed in 1 out of 21 patients in the bolus infusion trials with the CD19xCD3 binding molecule.

Without being bound by theory, the transient increase of T cell adhesiveness to the endothelial cells in patients who have essentially no circulating target cells can be explained as T cell reaction to the monovalent interaction of a conventional CD3 binding molecule, like the CD19xCD3 binding molecule (e.g. WO 99/54440), to its context dependent epitope on CD3 epsilon resulting in an allosteric change in the conformation of CD3 followed by the recruitment of Nck2 to the cytoplasmic domain of CD3 epsilon as described above. As Nck2 is directly linked to integrins via PINCH and ILK (Fig 28), recruitment of Nck2 to the cytoplasmic domain of CD3 epsilon following an allosteric change in the conformation of CD3 through binding of a conventional CD3 binding molecule, like the CD19xCD3 binding molecule, to its context dependent epitope on CD3 epsilon, can increase the adhesiveness of T cells to endothelial cells by transiently switching integrins on the T cell surface into their more adhesive isoform via inside-out-signalling.

Table 3. Patient demographics and clinical outcome

Cohort	Patient	Age/ Sex	Disease (Ann Arbor Classification)	Dose Level [mg/m^2/Day]	Clearance of Bone Marrow	Best Response* (CR Duration in Months or

						Weeks)
1	1	71/m	IC, Binet C	0.0005	None	SD
	2	67/f	MCL, Stage IV/A/E	0.0005	n.d.	PD
	3	67/m	CLL, Stage IV/B/E	0.0005	n.d.	MR
2	4	69/m	MCL, Stage IV/B	0.0015	n.i.	SD
	5	49/m	MCL, Stage IV/A/S	0.0015	n.d.	SD
	6	71/m	MCL, Stage IV/B/E	0.0015	n.i.	PD
	7	77/m	MCL, Stage IV/B/E/S	0.0015	n.i.	SD
	8	65/m	CLL, Stage IV/B/E/S	0.0015	n.d.	PD
	9	75/m	FL, Stage II/B	0.0015	n.i.	SD
3	10	58/m	MCL, Stage III/B/S	0.005	n.i.	PD
	11	68/f	FL, Stage IV/B	0.005	n.d.	SD
	12	65/m	MCL, Stage III/A/E	0.005	n.i.	SD
4[a]	13	60/m	SLL, Stage IV/B/S	0.015	Complete	**PR**
	14	73/m	MCL, Stage II/A/E	0.015	n.i.	SD
	15	44/m	FL, Stage IV/B/E/S	0.015	Partial	**PR**
	16	61/m	FL, Stage IV/A/S	0.015	Complete	**CR** (7mo)
	17	67/m	MZL, Stage IV/B/S	0.015	n.i.	n.e.
	18	64/m	FL, Stage IV/A/E	0.015	n.i.	PD
	19	75/m	MCL, Stage III/A	0.015	n.i.	n.e.
	20	65/f	FL; Stage III/A	0.015	n.i.	SD
	21	60/m	MCL, Stage IV/A/E	0.015	None	SD
	22	67/f	FL, Stage IV/B	0.015	Complete	MR
	23	67/m	DLBCL, Stage III/B	0.015	n.i.	n.e.
	24	65/f	FL, Stage III/A	0.015	n.d.	SD
	25	74/f	WD, Stage IV/B	0.015	Partial	SD
5	26	67/m	MCL, Stage IV/A	0.03	Complete	SD
	27	48/m	FL, Stage III/A	0.03	n.i.	PD
	28	58/m	MCL, Stage III/A	0.03	n.i.	**CR** (10mo+)
	29	45/f	MCL, Stage	0.03	Partial	PD

			IV/B			
	30	59/m	MZL, Stage III/A	0.03	n.i.	n.e.
	31	43/m	FL, Stage III/A	0.03	n.i.	MR
6	32	72/m	MCL, Stage IV/A	0.06	Complete	**PR**
	33	55/m	MCL, Stage IV/B	0.06	Complete	**CR** (4mo+)
	34	52/m	FL, Stage IV/A	0.06	n.i.	**CR**[b] (1w+)

*Centrally confirmed complete (CR) and partial (PR) responses by Cheson criteria in bold; MR, minimal response (≥25 to <50%); SD, stable disease; PD, progressive disease; duration from first documentation of response in parentheses; + denotes an ongoing response

[a]Cohort 4 was expanded to study three different schedules of treatment initiation

[b]PR after 8 weeks of treatment that turned into a CR after an additional treatment cycle of 4 weeks at the same dose following 7 weeks of treatment free interval

n.e.: not evaluable, because of treatment period <7 d

n.d.: not determined (infiltrated, but no second biopsy performed at end of treatment)

n.i.: not infiltrated at start of treatment

Table 4. Incidence of adverse events observed during treatment

Adverse events regardless of relationship, occuring in ≥ 3 patients (N=34)	**Grade 1-4 N (%)**	**Grade 3-4 N (%)**
Pyrexia	22 (64.7)	2 (5.9)
Leukopenia	21 (61.8)	11 (32.4)
Lymphopenia	21 (61.8)	21 (61.8)
Coagulopathy (increase in D-dimers)	16 (47.1)	6 (17.6)
Enzyme abnormality (AP, LDH, CRP)	16 (47.1)	10 (29.4)
Hepatic function abnormality (ALT, AST, GGT)	16 (47.1)	1 (2.9)
Anaemia	13 (38.2)	5 (14.7)
Chills	13 (38.2)	0 (0.0)
Headache	12 (35.3)	1 (2.9)
Hypokalaemia	12 (35.3)	2 (5.9)
Thrombocytopenia	12 (35.3)	6 (17.6)
Weight increased	12 (35.3)	0 (0.0)
Hyperglycaemia	11 (32.4)	2 (5.9)
Neutropenia	11 (32.4)	8 (23.5)
Haematuria	10 (29.4)	0 (0.0)
Oedema peripheral	10 (29.4)	2 (5.9)
Anorexia	9 (26.5)	1 (2.9)
Diarrhoea	9 (26.5)	0 (0.0)

Weight decreased	9 (26.5)	0 (0.0)
Fatigue	8 (23.5)	1 (2.9)
Proteinuria	8 (23.5)	0 (0.0)
Hypocalcaemia	7 (20.6)	2 (5.9)
Pancreatic enzyme abnormality	7 (20.6)	0 (0.0)
Cough	6 (17.6)	0 (0.0)
Dyspnoea	6 (17.6)	0 (0.0)
Back pain	5 (14.7)	0 (0.0)
Catheter site pain	5 (14.7)	0 (0.0)
Hyperbilirubinaemia	5 (14.7)	2 (5.9)
Hypoalbuminaemia	5 (14.7)	0 (0.0)
Hypogammaglobulinaemia	5 (14.7)	1 (2.9)
Hypoproteinaemia	5 (14.7)	0 (0.0)
Pleural effusion	5 (14.7)	1 (2.9)
Vomiting	5 (14.7)	0 (0.0)
Asthenia	4 (11.8)	1 (2.9)
Confusional state	4 (11.8)	0 (0.0)
Constipation	4 (11.8)	0 (0.0)
Dizziness	4 (11.8)	0 (0.0)
Hypertension	4 (11.8)	0 (0.0)
Hyponatraemia	4 (11.8)	2 (5.9)
Mucosal dryness	4 (11.8)	0 (0.0)
Muscle spasms	4 (11.8)	0 (0.0)
Nausea	4 (11.8)	0 (0.0)
Night sweats	4 (11.8)	0 (0.0)
Abdominal pain	3 (8.8)	1 (2.9)
Ascites	3 (8.8)	0 (0.0)
Hypercoagulation	3 (8.8)	0 (0.0)
Hyperhidrosis	3 (8.8)	0 (0.0)
Hypoglobulinaemia	3 (8.8)	0 (0.0)
Insomnia	3 (8.8)	0 (0.0)
Liver disorder	3 (8.8)	1 (2.9)
Nasopharyngitis	3 (8.8)	0 (0.0)
Pruritus	3 (8.8)	0 (0.0)

Abbreviations used are: AE, adverse event; AP, alkaline phosphatase; LDH, lactate dehydrogenase; CRP, C-reactive protein; ALT, alanine transaminase; AST, aspartate transaminase; GGT, gamma-glutamyl transferase; AE data from the additional treatment cycle of patient 34 not yet included.

As explained above, conventional CD3 binding molecules (e.g. disclosed in WO 99/54440) capable of binding to a context-dependent epitope, though functional, lead to the undesired effect of T cell redistribution in patients causing CNS adverse events. In contrast, binding molecules of the present invention, by binding to the context-independent N-terminal 1-27 amino acids of the CD3 epsilon chain, do not lead to such T cell redistribution effects. As a consequence, the CD3 binding

molecules of the invention are associated with a better safety profile compared to conventional CD3 binding molecules.

14. Bispecific CD3 binding molecules of the invention inducing T cell mediated target cell lysis by recognizing a surface target antigen deplete target antigen positive cells in vivo

A bispecific CD3 binding molecule of the invention recognizing CD33 as target antigen depletes CD33-positive circulating monocytes from the peripheral blood of cynomolgus monkeys

CD33-AF5 VH-VL x I2C VH-VL (amino acid sequence: SEQ ID NO.267) was produced by expression in CHO cells using the coding nucleotide sequence SEQ ID NO. 268. The coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His_6-tag followed by a stop codon were both attached in frame to the nucleotide sequence SEQ ID NO 268 prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). Stable transfection of DHFR-deficient CHO cells, selection for DHFR-positive transfectants secreting the CD3 binding molecule CD33-AF5 VH-VL x I2C VH-VL into the culture supernatant and gene amplification with methotrexat for increasing expression levels were carried out as described (Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025). The analytical SEC-profile of CD33-AF5 VH-VL x I2C VH-VL for use in cynomolgus monkeys revealed that the test material almost exclusively consisted of monomer. The potency of the test material was measured in a cytotoxicity assay as described in example 16.5 using CHO cells transfected with cynomolgus CD33 as target cells and the macaque T cell line 4119LnPx as source of effector cells (FIG. 25). The concentration of CD33-AF5 VH-VL x I2C VH-VL required for half-maximal target cell lysis by the effector T cells (EC50) was determined to be 2.7 ng/ml.

Young (approx. 3 years old) adult cynomolgus monkeys (Macaca fascicularis) were treated by continuous intravenous infusion of CD3 binding molecule CD33-AF5 VH-VL x I2C VH-VL at different flow-rates (i.e. dose levels) to study depletion of circulating CD33-positive monocytes from the peripheral blood. This situation is equivalent to the treatment with the conventional CD3 binding molecule CD19xCD3 (specific for CD19 on B cells and CD3 on T cells) of those B-NHL patients, who have

circulating CD19-positive target B cells (see e.g. WO99/54440). Depletion of circulating CD19-positive target B cells from the peripheral blood had turned out as a valid surrogate for the general clinical efficacy of the conventional CD3 binding molecule (CD19xCD3 as provided in WO99/54440) in patients with CD19-positive B-cell malignomas like B-NHL. Likewise, depletion of circulating CD33-positive monocytes from the peripheral blood is regarded as a valid surrogate of the general clinical efficacy of CD33-directed bispecific CD3 binding molecules of the invention like CD33-AF5 VH-VL x I2C VH-VL in patients with CD33-positive myeloid malignomas like AML (acute myeloid leukemia).

Continuous infusion was carried out according to the Swivel method as follows: The monkeys are catheterized via the vena femoralis into the vena cava caudalis using a vein catheter. The catheter is tunneled subcutaneously to the dorsal shoulder region and exteriorized at the caudal scapula. Then a tube is passed through a jacket and a protection spring. The jacket is fastened around the animal and the catheter, via the tube, is connected to an infusion pump.

Administration solution (1.25 M lysine, 0.1% tween 80, pH 7) without test material was infused continuously at 48 ml/24h for 7 days prior to treatment start to allow acclimatization of the animals to the infusion conditions. Treatment was started by adding CD33-AF5 VH-VL x I2C VH-VL test material to the administration solution at the amount required for each individual dose level to be tested (i.e. flow rate of CD33-AF5 VH-VL x I2C VH-VL). The infusion reservoir was changed every day throughout the whole acclimatization and treatment phase. Planned treatment duration was 7 days except for the 120µg/m^2/24h dose level, where animals received 14 days of treatment.

Time courses of absolute counts in circulating T cells and CD33-positive monocytes were determined by 4- or 3-colour FACS analysis, respectively:

Collection of blood samples and routine analysis

Blood samples (1 ml) were obtained before and 0.75, 2, 6, 12, 24, 30, 48, 72 hours after start of continuous infusion with MCSP-G4 VH-VL x I2C VH-VL as well as after 7 and 14 days (and after 9 days at the 120 µg/m^2/24h dose level) of treatment using EDTA-containing Vacutainer™ tubes (Becton Dickinson) which were shipped for analysis at 4°C. In some cases slight variations of these time points occurred for operational reasons. FACS analysis of lymphocyte subpopulations was performed within 24 – 48 h after blood sample collection. Absolute numbers of leukocyte

subpopulations in the blood samples were determined through differential blood analysis in a routine veterinary lab.

Isolation of PBMC from blood samples

PBMC (peripheral blood mononuclear cells) were isolated in analogy to the protocol described in example 13, above, with adaptations of the used volumes.

Staining of PBMC with fluorescence-labeled antibodies against cell surface molecules

Monoclonal antibodies reactive with cynomolgus antigens were obtained from Becton Dickinson ([1]Cat. No. 345784, [2]Cat. No. 556647, [3]Cat. No. 552851, [6]Cat. No. 557710), Beckman Coulter ([4]Cat. No. IM2470) and Miltenyi ([5]Cat. No. 130-091-732) and used according to the manufacturers' recommendations. $5x10^5$ – $1x10^6$ cells were stained with the following antibody combinations: anti-CD14[1] (FITC) x anti-CD56[2] (PE) x anti-CD3[3] (PerCP) x anti-CD19[4] (APC) and anti-CD14[1] (FITC) x anti-CD33[5] (PE) x anti-CD16[6] (Alexa Fluor 647™). Additional steps were performed as described in example 13, above.

Flowcytometric detection of stained lymphocytes by FACS

Data collection was performed with a 4 color BD FACSCalibur™ (Becton Dickinson). For each measurement $1x10^4$ cells of defined lymphocyte subpopulations were acquired. Statistical analysis was performed with the program CellQuest Pro™ (Becton Dickinson) to obtain lymphocyte subpopulation percentages and to classify cell surface molecule expression intensity. Subsequently, percentages of single lymphocyte subsets related to total lymphocytes (i.e. B plus T plus NK cells excluding myeloid cells via CD14-staining) as determined by FACS were correlated with the lymphocyte count from the differential blood analysis to calculate absolute cell numbers of T cells ($CD3^+$, $CD56^-$, $CD14^-$). Absolute numbers of CD33-positive monocytes were calculated by multiplying the monocyte counts from the differential blood analysis with the corresponding ratios of CD33-positive monocytes ($CD33^+$, $CD14^+$) to all monocytes ($CD14^+$) as determined by FACS.

The percentage compared to baseline (i.e. 100%) of absolute circulating CD33-positive monocyte counts at the end of treatment with CD33-AF5 VH-VL x I2C VH-VL in 4 cohorts of 2 cynomolgus monkeys with inter-cohort dose escalation from 30 over 60 and 240 to 1000 $\mu g/m^2/24h$ are shown in FIG 26 A.

As shown in FIG 26 A, continuous intravenous infusion of CD33-AF5 VH-VL x I2C VH-VL induces depletion of circulating CD33-positive monocytes in a dose-

dependent manner. While there was still no detectable depletion of circulating CD33-positive monocytes at 30 µg/m^2/24h, a first trend towards a reduction of CD33-positive monocyte counts became visible at 60 µg/m^2/24h after 7 days of treatment. At 240 µg/m^2/24h circulating CD33-positive monocytes were almost completely depleted from the peripheral blood after 3 days of treatment. This was reached even faster at 1000 µg/m^2/24h, where depletion of the circulating CD33-positive monocytes from the peripheral blood was completed already after 1 day of treatment. This finding was confirmed by the results shown in Figure 26 B demonstrating depletion of circulating CD33-positive monocytes by two thirds and 50% compared to the respective baseline in two cynomolgus monkeys treated by continuous infusion with CD33-AF5 VH-VL x I2C VH-VL at 120 µg/m^2/24h for 14 days.

This outcome is a clear signal clinical efficacy of the CD3 binding molecules of the invention in general and of bispecific CD33-directed CD3 binding molecules of the invention for the treatment of CD33-positive malignomas like AML in particularly. Moreover, the T cell redistribution during the starting phase of treatment with CD33-AF5 VH-VL x I2C VH-VL in the presence of circulating target cells (i.e. CD33-positive monocytes) seems to be less pronounced than T cell redistribution during the starting phase of treatment with conventional CD19xCD3 constructs, as described in WO99/54440 in B-NHL patients with a significant number of circulating target cells (i.e. CD19-positive B cells) as shown in Fig 22. While T cells disappear completely from the circulation upon start of CD19xCD3 infusion and do not reappear until the circulating CD19-positive target B cells are depleted from the peripheral blood (FIG 22), initial disappearance of circulating T cells is incomplete upon infusion start with CD33-AF5 VH-VL x I2C VH-VL and T cell counts recover still during the presence of circulating CD33-positive target cells (FIG 26 B). This confirms that CD3 binding molecules of the invention (directed against and generated against an epitope of human and non-chimpanzee primates CD3ε (epsilon) chain and being a part or fragment or the full length of the amino acid sequence as provided in SEQ ID Nos. 2, 4, 6, or 8) by recognizing a context-independent CD3 epitope show a more favorable T cell redistribution profile than conventional CD3 binding molecules recognizing a context-dependent CD3 epitope, like the binding molecules provided in WO99/54440.

15. CD3 binding molecules of the invention directed at essentially context independent CD3 epitopes by inducing less redistribution of circulating T cells

in the absence of circulating target cells reduce the risk of adverse events related to the initiation of treatment

Reduced T cell redistribution in cynomolgus monkeys following initiation of treatment with a representative cross-species specific CD3 binding molecule of the invention

MCSP-G4 VH-VL x I2C VH-VL (amino acid sequence: SEQ ID NO. 193) was produced by expression in CHO cells using the coding nucleotide sequence SEQ ID NO. 194. The coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His6-tag followed by a stop codon were both attached in frame to the nucleotide sequence SEQ ID NO. 194 prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). Stable transfection of DHFR-deficient CHO cells, selection for DHFR-positive transfectants secreting the CD3 binding molecule MCSP-G4 VH-VL x I2C VH-VL into the culture supernatant and gene amplification with methotrexat for increasing expression levels were carried out as described (Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025). Test material for treatment of cynomolgus monkeys was produced in a 200-liter fermenter. Protein purification from the harvest was based on IMAC affinity chromatography targeting the C-terminal His6-tag of MCSP-G4 VH-VL x I2C VH-VL followed by preparative size exclusion chromatography (SEC). The total yield of final endotoxin-free test material was 40 mg. The test material consisted of 70 % monomer, 30% dimer and a small contamination of higher multimer. The potency of the test material was measured in a cytotoxicity assay as described in example 11 using CHO cells transfected with cynomolgus MCSP as target cells and the macaque T cell line 4119LnPx as source of effector cells (FIG 27). The concentration of MCSP-G4 VH-VL x I2C VH-VL required for half-maximal target cell lysis by the effector T cells (EC50) was determined to be 1.9 ng/ml.

Young (approx. 3 years old) adult cynomolgus monkeys (Macaca fascicularis) were treated by continuous intravenous infusion of CD3 binding molecule MCSP-G4 VH-VL x I2C VH-VL at different flow-rates (i.e. dose levels) to study redistribution of circulating T cells following initiation of treatment in the absence of circulating target cells. Although the CD3 binding molecule MCSP-G4 VH-VL x I2C VH-VL can recognize both cynomolgus MCSP and cynomolgus CD3, there are no circulating

blood cells expressing MCSP. Therefore, the only interaction possible in the circulating blood is binding of the CD3-specific arm of MCSP-G4 VH-VL x I2C VH-VL to CD3 on T cells. This situation is equivalent to the treatment with the conventional CD3 binding molecule (CD19xCD3 binding molecule specific for CD19 on B cells and CD3 on T cells) of those B-NHL patients, who have no circulating CD19-positive target B cells as described in example 13.

Continuous infusion was carried out according to the Swivel method as follows: The monkeys are catheterized via the vena femoralis into the vena cava caudalis using a vein catheter. The catheter is tunneled subcutaneously to the dorsal shoulder region and exteriorized at the caudal scapula. Then a tube is passed through a jacket and a protection spring. The jacket is fastened around the animal and the catheter, via the tube, is connected to an infusion pump.

Administration solution (1.25 M lysine, 0.1% tween 80, pH 7) without test material was infused continuously at 48 ml/24h for 7 days prior to treatment start to allow acclimatization of the animals to the infusion conditions. Treatment was started by adding MCSP-G4 VH-VL x I2C VH-VL test material to the administration solution at the amount required for each individual dose level to be tested (i.e. flow rate of MCSP-G4 VH-VL x I2C VH-VL). The infusion reservoir was changed every day throughout the whole acclimatization and treatment phase. Treatment duration was 7 days.

Time courses of absolute T-cell counts in peripheral blood were determined by four color FACS analysis as follows:

Collection of blood samples and routine analysis

Blood samples (1 ml) were obtained before and 0.75, 2, 6, 12, 24, 30, 48, 72 hours after start of continuous infusion with MCSP-G4 VH-VL x I2C VH-VL as well as after 7 days of treatment using EDTA-containing Vacutainer™ tubes (Becton Dickinson) which were shipped for analysis at 4°C. In some cases slight variations of these time points occurred for operational reasons. FACS analysis of lymphocyte subpopulations was performed within 24 – 48 h after blood sample collection. Absolute numbers of leukocyte subpopulations in the blood samples were determined through differential blood analysis in a routine veterinary lab.

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Flowcytometric detection of stained lymphocytes by FACS

Data collection was performed with a 4 color BD FACSCalibur™ (Becton Dickinson). For each measurement $1x10^4$ cells of defined lymphocyte subpopulations were acquired. Statistical analysis was performed with the program CellQuest Pro™ (Becton Dickinson) to obtain lymphocyte subpopulation percentages and to classify cell surface molecule expression intensity. Subsequently, percentages of single lymphocyte subsets related to total lymphocytes (i.e. B plus T plus NK cells excluding myeloid cells via CD14-staining) as determined by FACS were correlated with the lymphocyte count from the differential blood analysis to calculate absolute cell numbers of T cells ($CD3^+$, $CD56^-$, $CD14^-$).

T cell redistribution during the starting phase of treatment with MCSP-G4 VH-VL x I2C VH-VL in cynomolgus monkeys at dose levels of 60, 240 and 1000 $\mu g/m^2/24h$ is shown in Fig 28. These animals showed no signs at all of any T cell redistribution during the starting phase of treatment, i.e. T cell counts rather increased than decreased upon treatment initiation. Given that T cell redistribution is consistently observed in 100% of all patients without circulating target cells, upon treatment initiation with the conventional CD3 binding molecule (e.g. CD19xCD3 construct as described in WO 99/54440) against a context dependent CD3 epitope, it was demonstrated that substantially less T cell redistribution in the absence of circulating target cells upon treatment initiation can be observed with a CD3 binding molecule of the invention directed and generated against an epitope of human an non-chimpanzee primate CD3 epsilon chain as defined by the amino acid sequence of anyone of SEQ ID NOs: 2, 4, 6, or 8 or a fragment thereof. This is in clear contrast to CD3-binding molecules directed against a context-dependent CD3 epitope, like the constructs described in WO 99/54440, The binding molecules against context-independent CD3 epitopes, as (inter alia) provided in any one of SEQ ID NOs: 2, 4,

6, or 8 (or fragments of these sequences) provide for this substantially less (detrimental and non-desired) T cell redistribution. Because T cell redistribution during the starting phase of treatment with CD3 binding molecules is a major risk factor for CNS adverse events, the CD3 binding molecules provided herein and capable of recognizing a context independent CD3 epitope have a substantial advantage over the CD3 binding molecules known in the art and directed against context-dependent CD3 epitopes. Indeed none of the cynomolgus monkeys treated with MCSP-G4 VH-VL x I2C VH-VL showed any signs of CNS symptoms.

The context-independence of the CD3 epitope is provided in this invention and corresponds to the first 27 N-terminal amino acids of CD3 epsilon) or fragments of this 27 amino acid stretch. This context-independent epitope is taken out of its native environment within the CD3 complex and fused to heterologous amino acid sequences without loss of its structural integrity. Anti-CD3 binding molecules as provided herein and generated (and directed) against a context-independent CD3 epitope provide for a surprising clinical improvement with regard to T cell redistribution and, thus, a more favorable safety profile. Without being bound by theory, since their CD3 epitope is context-independent, forming an autonomous selfsufficient subdomain without much influence on the rest of the CD3 complex, the CD3 binding molecules provided herein induce less allosteric changes in CD3 conformation than the conventional CD3 binding molecules (like molecules provided in WO 99/54440), which recognize context-dependent CD3 epitopes like molecules provided in WO 99/54440. As a consequence (again without being bound by theory), the induction of intracellular NcK2 recruitment by the CD3 binding molecules provided herein is also reduced resulting in less isoform switch of T cell integrins and less adhesion of T cells to endothelial cells. It is preferred that preparations of CD3 binding molecules of the invention (directed against and generated against a context-independent epitope as defined herein) essentially consists of monomeric molecules. These monomeric molecules are even more efficient (than dimeric or multimeric molecules) in avoiding T cell redistribution and thus the risk of CNS adverse events during the starting phase of treatment.

16. Generation and characterization of CD33 and CD3 cross-species specific bispecific single chain molecules

16.1. Generation of CHO cells expressing human CD33

The coding sequence of human CD33 as published in GenBank (Accession number NM_001772) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by a 19 amino acid immunoglobulin leader peptide, followed in frame by the coding sequence of the mature human CD33 protein, followed in frame by the coding sequence of serine glycine dipeptide, a histidine$_6$-tag and a stop codon (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 305 and 306). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methothrexate (MTX) to a final concentration of up to 20 nM MTX.

16.2. Generation of CHO cells expressing the extracellular domain of macaque CD33

The cDNA sequence of macaque CD33 was obtained by a set of 3 PCRs on cDNA from macaque monkey bone marrow prepared according to standard protocols. The following reaction conditions: 1 cycle at 94°C for 3 minutes followed by 35 cycles with 94°C for 1 minute, 53°C for 1 minute and 72°C for 2 minutes followed by a terminal cycle of 72°C for 3 minutes and the following primers were used:

1. forward primer:

   5'-gaggaattcaccatgccgctgctgctactgctgcccctgctgtgggcaggggccctggctatgg-3'

(SEQ ID No. 369)

reverse primer: 5'-gatttgtaactgtatttggtacttcc-3' (SEQ ID No. 370)

2. forward primer: 5'-attccgcctccttggggatcc-3' (SEQ ID No. 371)

   reverse primer: 5'-gcataggagacattgagctggatgg-3' (SEQ ID No. 372)

3. forward primer: 5'-gcaccaacctgacctgtcagg-3' (SEQ ID No. 373)

   reverse primer: 5'-agtgggtcgactcactgggtcctgacctctgagtattcg-3' (SEQ ID No. 374)

Those PCRs generate three overlapping fragments, which were isolated and sequenced according to standard protocols using the PCR primers, and thereby provided a portion of the cDNA sequence of macaque CD33 from the second nucleotide of codon +2 to the third nucleotide of codon +340 of the mature protein. To generate a construct for expression of macaque CD33 a cDNA fragment was obtained by gene synthesis according to standard protocols (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 307 and 308). In this construct the coding sequence of macaque CD33 from amino acid +3 to +340 of the mature CD33 protein was fused into the coding sequence of human CD33 replacing the human coding sequence of the amino acids +3 to +340. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the fragment containing the cDNA coding for essentially the whole extracellular domain of macaque CD33, the macaque CD33 transmembrane domain and a macaque-human chimeric intracellular CD33 domain. The introduced restriction sites XbaI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was then cloned via XbaI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). A sequence verified clone of this plasmid was used to transfect CHO/dhfr- cells as described above.

16.3. Generation of CD33 and CD3 cross-species specific bispecific antibody molecules

Cloning of cross-species specific binding molecules

Generally, bispecific antibody molecules, each comprising a domain with a binding specificity cross-species specific for human and non-chimpanzee primate CD3 epsilon as well as a domain with a binding specificity cross-species specific for

human and non-chimpanzee primate CD33, were designed as set out in the following Table 5:

Table 5: Formats of anti-CD3 and anti-CD33 cross-species specific bispecific molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
276/275	AH11HLxH2CHL
258/257	AH3HLxH2CHL
270/269	AC8HLxH2CHL
264/263	AF5HLxH2CHL
288/287	F2HLxH2CHL
300/299	E11HLxH2CHL
282/281	B3HLxH2CHL
294/293	B10HLxH2CHL
278/277	AH11HLxF12QHL
260/259	AH3HLxF12QHL
272/271	AC8HLxF12QHL
266/265	AF5HLxF12QHL
290/289	F2HLxF12QHL
302/301	E11HLxF12QHL
284/283	B3HLxF12QHL
296/295	B10HLxF12QHL
280/279	AH11HLxI2CHL
262/261	AH3HLxI2CHL
274/273	AC8HLxI2CHL
268/267	AF5HLxI2CHL
292/291	F2HLxI2CHL
304/303	E11HLxI2CHL
286/285	B3HLxI2CHL
298/297	B10HLxI2CHL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains cross-species specific for human and macaque CD33 and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed and eukaryotic protein expression was performed similar as described in example 9 for the MCSP and CD3 cross-species specific single chain molecules.
The same holds true for the expression and purification of the CD33 and CD3 cross-species specific single chain molecules.

In the Western Blot a single band was detected at 52 kD corresponding to the purified bispecific antibody.

16.4. Flow cytometric binding analysis of the CD33 and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs regarding the capability to bind to human and macaque CD33 and CD3, respectively, a FACS analysis was performed similar to the analysis described for the analysis of the MCSP and CD3 cross-species specific bispecific antibodies in example 10 using CHO cells expressing the human or macaque CD33 extracellular domains (see example 16.1 and 16.2).

The specific binding of human and non-chimpanzee primate CD3 of the CD3 binding molecules of the invention was clearly detectable as shown in Figure 29. In the FACS analysis all constructs show binding to CD3 and CD33 as compared to the respective negative controls. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and CD33 antigens is demonstrated.

16.5. Bioactivity of CD33 and CD3 cross-species specific bispecific antibodies

Bioactivity of the generated bispecific antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the CD33 positive cell lines described in Examples 16.1 and 16.2. As effector cells stimulated human CD4/CD56 depleted PBMC or the macaque T cell line 4119LnPx were used as specified in the respective figures. The cytotoxicity assays were performed similar to the setting described for the bioactivity analysis of the MCSP and CD3 cross-species specific bispecific antibodies in example 11 using CHO cells expressing the human or macaque CD33 extracellular domains (see example 16.1 and 16.2) as target cells.

As shown in Figure 30, all of the generated cross-species specific bispecific constructs demonstrate cytotoxic activity against human CD33 positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and against macaque CD33 positive target cells elicited by the macaque T cell line 4119LnPx.

17. Purification of cross-species specific bispecific single chain molecules by an affinity procedure based on the context independent CD3 epsilon epitope corresponding to the N-terminal amino acids 1-27

17.1 Generation of an affinity column displaying the isolated context independent human CD3 epsilon epitope corresponding to the N-terminal amino acids 1-27

The plasmid for expression of the construct 1-27 CD3-Fc consisting of the 1-27 N-terminal amino acids of the human CD3 epsilon chain fused to the hinge and Fc gamma region of human immunoglobulin IgG1 described above (Example 3; cDNA sequence and amino acid sequence of the recombinant fusion protein are listed under SEQ ID NOs 230 and 229) was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX. After two passages of stationary culture the cells were grown in roller bottles with nucleoside-free HyQ PF CHO liquid soy medium (with 4.0 mM L-Glutamine with 0.1% Pluronic F – 68; HyClone) for 7 days before harvest. The cells were removed by centrifugation and the supernatant containing the expressed protein was stored at -20°C. For the isolation of the fusion protein a goat anti-human fc affinity column was prepared according to standard protocols using a commercially available affinity purified goat anti-human IgG fc fragment specific antibody with minimal cross-reaction to bovine, horse, and mouse serum proteins (Jackson ImmunoResearch Europe Ltd.). Using this affinity column the fusion protein was isolated out of cell culture supernatant on an Äkta Explorer System (GE Amersham) and eluted by citric acid. The eluate was neutralized and concentrated. After dialysis against amine free coupling buffer the purified fusion protein was coupled to an N-Hydroxy-Succinimide NHS activated 1 ml HiTrap column (GE Amersham).

After coupling remaining NHS groups were blocked and the column was washed and stored at 5°C in storage buffer containing 0.1% sodium azide.

17.2 Purification of cross-species specific bispecific single chain molecules using a human CD3 peptide affinity column

200 ml cell culture supernatant of cells expressing cross-species specific bispecific single chain molecules were 0.2 µm sterile filtered and applied to the CD3 peptide affinity column using an Äkta Explorer system (GE Amersham).

The column was then washed with phosphate buffered saline PBS pH 7.4 to wash out unbound sample. Elution was done with an acidic buffer pH 3.0 containing 20 mM Citric acid and 1 M sodium chloride. Eluted protein was neutralized immediately by 1 M Trishydroxymethylamine TRIS pH 8.3 contained in the collection tubes of the fraction collector.

Protein analysis was done by SDS PAGE and Western Blot.

For SDS PAGE BisTris Gels 4-12% are used (Invitrogen). The running buffer was 1 x MES-SDS-Puffer (Invitrogen). As protein standard 15 µl prestained Sharp Protein Standard (Invitrogen) was applied. Electrophoresis was performed for 60 minutes at 200 volts 120 mA max. Gels were washed in demineralised water and stained with Coomassie for one hour. Gels are destained in demineralised water for 3 hours. Pictures are taken with a Syngene Gel documentation system.

For Western Blot a double of the SDS PAGE gel was generated and proteins were electroblotted onto a nitrocellulose membrane. The membrane was blocked with 2% bovine serum albumin in PBS and incubated with a biotinylated murine Penta His antibody (Qiagen). As secondary reagent a streptavidin alkaline phosphatase conjugate (DAKO) was used. Blots were developed with BCIP/NBT substrate solution (Pierce).

As demonstrated in Figures 31, 32 and 33 the use of a human CD3 peptide affinity column as described above allows the highly efficient purification of the bispecific single chain molecules from cell culture supernatant. The cross-species specific anti-CD3 single chain antibodies contained in the bispecific single chain molecules therefore enable via their specific binding properties an efficient generic one-step method of purification for the cross-species specific bispecific single chain molecules, without the need of any tags solely attached for purification purposes.

18. Generic pharmacokinetic assay for cross-species specific bispecific single chain molecules

18.1 Production of 1-27 CD3-Fc for use in the pharmacokinetic assay

The coding sequence of the 1-27 N-terminal amino acids of the human CD3 epsilon chain fused to the hinge and Fc gamma region of human immunoglobulin IgG1 was obtained by gene synthesis according to standard protocols (cDNA sequence and amino acid sequence of the recombinant fusion protein are listed under SEQ ID NOs 309 and 310). The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by a 19 amino acid immunoglobulin leader peptide, followed in frame by the coding sequence of the first 27 amino acids of the extracellular portion of the mature human CD3 epsilon chain, followed in frame by the coding sequence of the hinge region and Fc gamma portion of human IgG1 and a stop codon. The gene synthesis fragment was also designed and cloned as described in example 3.1, supra. A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described in example 9, supra. For the isolation of the fusion protein a goat anti-human fc affinity column was prepared according to standard protocols using a commercially available affinity purified goat anti-human IgG fc fragment specific antibody with minimal cross-reaction to bovine, horse, and mouse serum proteins (Jackson ImmunoResearch Europe Ltd.). Using this affinity column the fusion protein was isolated out of cell culture supernatant on an Äkta Explorer System (GE Amersham) and eluted by citric acid. The eluate was neutralized and concentrated.

18.2 Pharmacokinetic assay for cross-species specific bispecific single chain molecules

The assay is based on the ECL-ELISA technology using ruthenium labelled detection on carbon plates measured on a Sektor Imager device (MSD). In a first step, carbon plates (MSD High Bind Plate 96 well Cat: L15xB-3) were coated with 5 µl/well at 50 ng/ml of the purified 1-27 CD3-Fc described in Example 18.1. The plate was then dried overnight at 25°C. Subsequently plates were blocked with 5% BSA (Paesel&Lorei #100568) in PBS at 150 µl/well for 1h at 25°C in an incubator while

shaking (700 rpm). In the next step plates were washed three times with 0.05% Tween in PBS. A standard curve in 50% macaque serum in PBS was generated by serial 1:4 dilution starting at 100 ng/ml of the respective cross-species specific bispecific single chain molecule to be detected in the assay. Quality control (QC) samples were prepared in 50% macaque serum in PBS ranging from 1 ng/ml to 50 ng/ml of the respective cross-species specific bispecific single chain molecule dependent on the expected sample serum concentrations. Standard, QC or unknown samples were transferred to the carbon plates at 10 µl/well and incubated for 90 min at 25°C in the incubator while shaking (700 rpm). Subsequently plates were washed three times with 0.05% Tween in PBS. For detection 25 µl/well of penta-His-Biotin antibody (Qiagen, 200 µg/ml in 0.05% Tween in PBS) was added and incubated for 1 h at 25°C in an incubator while shaking (700 rpm). In a second detection step 25 µl/well Streptavidin-SulfoTag solution (MSD; Cat: R32AD-1; Lot: W0010903) was added and incubated for 1 h at 25°C in an incubator while shaking (700 rpm). Subsequently plates were washed three times with 0.05% Tween in PBS. Finally 150 µl/well MSD Reading Buffer (MSD, Cat: R9ZC-1) was added and plates were read in the Sektor Imager device.

Figures 34 and 35 demonstrate the feasibility of detection of cross-species specific bispecific single chain molecules in serum samples of macaque monkeys for cross-species specific bispecific single chain molecules. The cross-species specific anti-CD3 single chain antibodies contained in the bispecific single chain molecules enable therefore via their specific binding properties a highly sensitive generic assay for detection of the cross-species specific bispecific single chain molecules. The assay set out above can be used in the context of formal toxicological studies that are needed for drug development and can be easily adapted for measurement of patient samples in connection with the clinical application of cross-species specific bispecific single chain molecules.

19. Generation of recombinant transmembrane fusion proteins of the N-terminal amino acids 1-27 of CD3 epsilon from different non-chimpanzee primates fused to EpCAM from cynomolgus monkey (1-27 CD3-EpCAM).

19.1 Cloning and expression of 1-27 CD3-EpCAM

CD3 epsilon was isolated from different non-chimpanzee primates (marmoset, tamarin, squirrel monkey) and swine. The coding sequences of the 1-27 N-terminal

amino acids of CD3 epsilon chain of the mature human, common marmoset (*Callithrix jacchus*), cottontop tamarin (*Saguinus oedipus),* common squirrel monkey (*Saimiri sciureus*) and domestic swine (*Sus scrofa*; used as negative control) fused to the N-terminus of Flag tagged cynomolgus EpCAM were obtained by gene synthesis according to standard protocols (cDNA sequence and amino acid sequence of the recombinant fusion proteins are listed under SEQ ID NOs 231 to 240). The gene synthesis fragments were designed as to contain first a BsrGI site to allow for fusion in correct reading frame with the coding sequence of a 19 amino acid immunoglobulin leader peptide already present in the target expression vector, which was followed in frame by the coding sequence of the N-terminal 1-27 amino acids of the extracellular portion of the mature CD3 epsilon chains, which was followed in frame by the coding sequence of a Flag tag and followed in frame by the coding sequence of the mature cynomolgus EpCAM transmembrane protein. The gene synthesis fragments were also designed to introduce a restriction site at the end of the cDNA coding for the fusion protein. The introduced restriction sites BsrGI at the 5' end and SalI at the 3' end, were utilized in the following cloning procedures. The gene synthesis fragments were then cloned via BsrGI and SalI into a derivative of the plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150), which already contains the coding sequence of the 19 amino acid immunoglobulin leader peptide following standard protocols. Sequence verified plasmids were used to transfect DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

Transfectants were tested for cell surface expression of the recombinant transmembrane protein via an FACS assay according to standard protocols. For that purpose a number of $2.5x10^5$ cells were incubated with 50 µl of the anti-Flag M2 antibody (Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany) at 5 µg/ml in PBS with 2% FCS. Bound antibody was detected with an R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). Flow cytometry was performed on a FACS-Calibur apparatus, the

CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).
Expression of the Flag tagged recombinant transmembrane fusion proteins consisting of cynomolgus EpCAM and the 1-27 N-terminal amino acids of the human, marmoset, tamarin, squirrel monkey and swine CD3 epsilon chain respectively on transfected cells is clearly detectable (Figure 36).

19.2 Cloning and expression of the cross-species specific anti-CD3 single chain antibody I2C HL in form of an IgG1 antibody

In order to provide improved means of detection of binding of the cross-species specific single chain anti-CD3 antibody the I2C VHVL specificity is converted into an IgG1 antibody with murine IgG1 and murine kappa constant regions. cDNA sequences coding for the heavy chain of the IgG antibody were obtained by gene synthesis according to standard protocols. The gene synthesis fragments were designed as to contain first a Kozak site to allow for eukaryotic expression of the construct, which is followed by an 19 amino acid immunoglobulin leader peptide, which is followed in frame by the coding sequence of the heavy chain variable region or light chain variable region, followed in frame by the coding sequence of the heavy chain constant region of murine IgG1 as published in GenBank (Accession number AB097849) or the coding sequence of the murine kappa light chain constant region as published in GenBank (Accession number D14630), respectively.
Restriction sites were introduced at the beginning and the end of the cDNA coding for the fusion protein. Restriction sites EcoRI at the 5' end and SalI at the 3' end were used for the following cloning procedures. The gene synthesis fragments were cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) for the heavy chain construct and pEFADA (pEFADA is described in Raum et al. loc cit.) for the light chain construct according to standard protocols. Sequence verified plasmids were used for co-transfection of respective light and heavy chain constructs into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) loc cit. Gene amplification of the constructs was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX

and deoxycoformycin (dCF) to a final concentration of up to 300 nM dCF. After two passages of stationary culture cell culture supernatant was collected and used in the subsequent experiment.

19.3 Binding of the cross-species specific anti-CD3 single chain antibody I2C HL in form of an IgG1 antibody to 1-27 CD3-EpCAM

Binding of the generated I2C IgG1 construct to the 1-27 N-terminal amino acids of the human, marmoset, tamarin and squirrel monkey CD3 epsilon chains respectively fused to cynomolgus Ep-CAM as described in Example 19.1 was tested in a FACS assay according to standard protocols. For that purpose a number of $2.5x10^5$ cells were incubated with 50 µl of cell culture supernatant containing the I2C IgG1 construct as described in Example 19.2. The binding of the antibody was detected with an R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

As shown in Figure 37 binding of the I2C IgG1 construct to the transfectants expressing the recombinant transmembrane fusion proteins consisting of the 1-27 N-terminal amino acids of CD3 epsilon of human, marmoset, tamarin or squirrel monkey fused to cynomolgus EpCAM as compared to the negative control consisting of the 1-27 N-terminal amino acids of CD3 epsilon of swine fused to cynomolgus EpCAM was observed. Thus multi-primate cross-species specificity of I2C was demonstrated. Signals obtained with the anti Flag M2 antibody and the I2C IgG1 construct were comparable, indicating a strong binding activity of the cross-species specific specificity I2C to the N-terminal amino acids 1-27 of CD3 epsilon.

20. Binding of the cross-species specific anti-CD3 binding molecule I2C to the human CD3 epsilon chain with and without N-terminal His6 tag

A chimeric IgG1 antibody with the binding specificity I2C as described in Example 19.2 specific for CD3 epsilon was tested for binding to human CD3 epsilon with and without N-terminal His6 tag. Binding of the antibody to the EL4 cell lines transfected

with His6-human CD3 epsilon as described in Example 6.1 and wild-type human CD3 epsilon as described in Example 5.1 respectively was tested by a FACS assay according to standard protocols. $2.5x10^5$ cells of the transfectants were incubated with 50 µl of cell culture supernatant containing the I2C IgG1 construct or 50 µl of the respective control antibodies at 5µg/ml in PBS with 2% FCS. As negative control an appropriate isotype control and as positive control for expression of the constructs the CD3 specific antibody UCHT-1 were used respectively. Detection of the His6 tag was performed with the penta His antibody (Qiagen). The binding of the antibodies was detected with a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific, diluted 1:100 in PBS with 2% FCS (Jackson ImmunoResearch Europe Ltd., Newmarket, Suffolk, UK). Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

Comparable binding of the anti-human CD3 antibody UCHT-1 to both transfectants demonstrates approximately equal levels of expression of the constructs. The binding of the penta His antibody confirmed the presence of the His6 tag on the His6-human CD3 construct but not on the wild-type construct.

Compared to the EL4 cell line transfected with wild-type human CD3 epsilon a clear loss of binding of the I2C IgG1 construct to human-CD3 epsilon with an N-terminal His6 tag was detected. These results show that a free N-terminus of CD3 epsilon is essential for binding of the cross-species specific anti-CD3 binding specificity I2C to the human CD3 epsilon chain (Figure 28).

21. Generation of CD33 and CD3 cross-species specific bispecific single chain molecules

21.1 Generation of CD33 and CD3 cross-species specific bispecific single chain molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity cross-species specific for human and macaque CD3epsilon as well as a domain with a binding specificity cross-species specific for human and macaque CD33, were designed as set out in the following Table 6:

Table 6: Formats of anti-CD3 and anti-CD33 cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
316/315	I2CHLxAF5HL
314/313	F12QHLxAF5HL
312/311	H2CHLxAF5HL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains cross-species specific for human and macaque CD33 and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed in analogy to the procedure described in example 9 for the MCSP and CD3 cross-species specific single chain molecules. A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as also described in example 9 for the MCSP and CD3 cross-species specific single chain molecules and used in the subsequent experiments.

21.2 Flow cytometric binding analysis of the CD33 and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs regarding the capability to bind to human and macaque CD33 and CD3, respectively, a FACS analysis is performed similar to the analysis described for the analysis of the MCSP and CD3 cross-species specific bispecific antibodies in example 10 using CHO cells expressing the human or macyque CD33 extracellular domains (see examples 16.1 and 16.2).

The bispecific binding of the single chain molecules listed above, which were cross-species specific for CD33 and cross-species specific for human and non-chimpanzee primate CD3 was clearly detectable as shown in Figure 41. In the FACS analysis all constructs showed binding to CD3 and CD33 as compared to the respective negative controls. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and CD33 antigens was demonstrated.

21.3. Bioactivity of CD33 and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the CD33 positive cell lines described in Examples 16.1 and 16.2. As effector cells stimulated human CD4/CD56 depleted PBMC or the macaque T cell line 4119LnPx were used as specified in the respective figures. The cytotoxicity assays were performed similar to the procedure described for the bioactivity analysis of the MCSP and CD3 cross-species specific bispecific antibodies in example 11 using CHO cells expressing the human or macaque CD33 extracellular domains (see example 16.1 and 16.2) as target cells.

As shown in Figure 42, all of the generated cross-species specific bispecific single chain antibody constructs demonstrate cytotoxic activity against human CD33 positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and against macaque CD33 positive target cells elicited by the macaque T cell line 4119LnPx.

22. Redistribution of circulating chimpanzee T cells upon exposure to a conventional bispecific CD3 binding molecule directed at a target molecule which is absent from circulating blood cells

A single male chimpanzee was subjected to dose escalation with intravenous single-chain EpCAM/CD3-bispecific antibody construct (Schlereth (2005) Cancer Res 65: 2882). Like in the conventional single-chain CD19/CD3-bispecific antibody construct (Loffler (2000, Blood, Volume 95, Number 6) or WO 99/54440), the CD3 arm of said EpCAM/CD3-construct is also directed against a conventional context dependent epitope of human and chimpanzee CD3. At day 0, the animal received 50ml PBS/5% HSA without test material, followed by 50ml PBS/5% HSA plus single-chain EpCAM/CD3-bispecific antibody construct at 1.6, 2.0, 3.0 and 4.5 µg/kg on days 7, 14, 21 and 28, respectively. The infusion period was 2 hours per administration. For each weekly infusion the chimpanzee was sedated with 2-3 mg/kg Telazol intramuscularly, intubated and placed on isoflurane/O_2 anesthesia with stable mean blood pressures. A second intravenous catheter was placed in an opposite limb to collect (heparinized) whole blood samples at the time points indicated in Figure 43 for FACS analysis of circulating blood cells. After standard erythrocyte lysis, T cells were

stained with a FITC-labeled antibody reacting with chimpanzee CD2 (Becton Dickinson) and the percentage of T cells per total lymphocytes determined by flowcytometry. As shown in Figure 43, every administration of single-chain EpCAM/CD3-bispecific antibody construct induced a rapid drop of circulating T cells as observed with single-chain CD19/CD3-bispecific antibody construct in B-NHL patients, who had essentially no circulating target B (lymphoma) cells. As there are no EpCAM-positive target cells in the circulating blood of humans and chimpanzees, the drop of circulating T cells upon exposure to the single-chain EpCAM/CD3-bispecific antibody construct can be attributed solely to a signal, which the T cells receive through pure interaction of the CD3 arm of the construct with a conventional context dependent CD3 epitope in the absence of any target cell mediated crosslinking. Like the redistribution of T cells induced through their exposure to single-chain CD19/CD3-bispecific antibody construct in B-NHL patients, who had essentially no circulating target B (lymphoma) cells, the T cell redistribution in the chimpanzee upon exposure to the single-chain EpCAM/CD3-bispecific antibody construct can be explained by a conformational change of CD3 following the binding event to a context dependent CD3 epitope further resulting in the transient increase of T cell adhesiveness to blood vessel endothelium (see Example 13). This finding confirms, that conventional CD3 binding molecules directed to context dependent CD3 epitopes – solely through this interaction – can lead to a redistribution pattern of peripheral blood T cells, which is associated with the risk of CNS adverse events in humans as describe in Example 13.

23. Specific binding of scFv clones to the N-terminus of human CD3 epsilon

23.1 Bacterial expression of scFv constructs in E. coli XL1 Blue

As previously mentioned, *E. coli* XL1 Blue transformed with pComb3H5Bhis/Flag containing a VL- and VH-segment produce soluble scFv in sufficient amounts after excision of the gene III fragment and induction with 1 mM IPTG. The scFv-chain is exported into the periplasma where it folds into a functional conformation.

The following scFv clones were chosen for this experiment:

i) ScFvs 4-10, 3-106, 3-114, 3-148, 4-48, 3-190 and 3-271 as described in WO 2004/106380.

ii) ScFvs from the human anti-CD3epsilon binding clones H2C, F12Q and I2C as described herein.

For periplasmic preparations, bacterial cells transformed with the respective scFv containing plasmids allowing for periplasmic expression were grown in SB-medium supplemented with 20 mM $MgCl_2$ and carbenicillin 50 µg/ml and redissolved in PBS after harvesting. By four rounds of freezing at -70°C and thawing at 37°C, the outer membrane of the bacteria was destroyed by osmotic shock and the soluble periplasmic proteins including the scFvs were released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the human anti-human CD3-scFvs was collected and used for further examination. These crude supernatants containing scFv will be further termed periplasmic preparations (PPP).

23.2 Binding of scFvs to human CD3 epsilon (aa 1-27)-Fc fusion protein

ELISA experiments were carried out by coating the human CD3 epsilon (aa 1-27)- Fc fusion protein to the wells of 96 well plastic plates (Nunc, maxisorb) typically at 4° C over night. The antigen coating solution was then removed, wells washed once with PBS/0.05 % Tween 20 and subsequently blocked with PBS/3 % BSA for at least one hour. After removal of the blocking solution, PPPs and control solutions were added to the wells and incubated for typically one hour at room temperature. The wells were then washed three times with PBS/0.05 % Tween 20. Detection of scFvs bound to immobilized antigen was carried out using a Biotin-labeled anti FLAG-tag antibody (M2 anti Flag-Bio, Sigma, typically at a final concentration of 1µg/ml PBS) and detected with a peroxidase-labeled Streptavidine (Dianova, 1µg/ml PBS). The signal was developed by adding ABTS substrate solution and measured at a wavelength of 405 nm. Unspecific binding of the test-samples to the blocking agent and/or the human IgG1 portion of the human CD3 epsilon (aa 1-27)- Fc fusion protein was examined by carrying out the identical assay with the identical reagents and identical timing on ELISA plates which were coated with human IgG1 (Sigma). PBS was used as a negative control.

As shown in Figure 44, scFvs H2C, F12Q and I2C show strong binding signals on human CD3 epsilon (aa 1-27)- Fc fusion protein. The human scFvs 3-106, 3-114, 3-148, 3-190, 3-271, 4-10 and 4-48 (as described in WO 2004/106380) do not show any significant binding above negative control level.

To exclude the possibility that the positive binding of scFvs H2C, F12Q and I2C to wells coated with human CD3 epsilon (aa 1-27)- Fc fusion protein might be due to binding to BSA (used as a blocking agent) and/or the human IgG1 Fc-gamma-portion

of the human CD3 epsilon (aa 1-27)- Fc fusion protein, a second ELISA experiment was performed in parallel. In this second ELISA experiment, all parameters were identical to those in the first ELISA experiment, except that in the second ELISA experiment human IgG1 (Sigma) was coated instead of human CD3 epsilon (aa 1-27)- Fc fusion protein. As shown in Figure 45, none of the scFvs tested showed any significant binding to BSA and/or human IgG1 above background level.

Taken together, these results allow the conclusion that conventional CD3 binding molecules recognizing a context-dependent epitope of CD3 epsilon (e.g. as disclosed in WO 2004/106380) do not bind specifically to the human CD3 epsilon (aa 1-27)-region, whereas the scFvs H2C, F12Q and I2C binding a context-independent epitope of CD3 epsilon clearly show specific binding to the N-terminal 27 amino acids of human CD3 epsilon.

24. Generation and characterization of PSCA and CD3 cross-species specific bispecific single chain antibody molecules

24.1 Generation of CHO cells expressing human PSCA

The coding sequence of human PSCA as published in GenBank (Accession number NM_005672) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by a 19 amino acid immunoglobulin leader peptide, followed in frame by the coding sequence of a FLAG tag, followed in frame by the coding sequence of the mature human PSCA protein and a stop codon (the corresponding sequences of the construct are listed under SEQ ID NOs. 443 and 444). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in

DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

24.2 Generation of CHO cells expressing macaque PSCA

The cDNA sequence of macaque PSCA was obtained by a PCR on cDNA from macaque monkey (cynomolgus) prostate prepared according to standard protocols. The following reaction conditions: 1 cycle at 94°C for 2 minutes followed by 40 cycles with 94°C for 1 minute, 55°C for 1 minute and 72°C for 1 minute followed by a terminal cycle of 72°C for 3 minutes and the following primers were used:

forward primer: 5'- CACCACAGCCCACCAGTGACC -3' (SEQ ID NO. 447)

reverse primer: 5'- GAGGCCTGGGGCACCACACCC -3' (SEQ ID NO. 448)

The PCR reactions were performed under addition of PCR grade betain to a final concentration of 1M. This PCR generated a DNA fragment, which was isolated and sequenced according to standard protocols using the PCR primers, and thereby provided the cDNA sequence coding macaque PSCA. To generate a construct for expression of macaque PSCA a cDNA fragment was obtained by gene synthesis according to standard protocols (the corresponding sequences are listed under SEQ ID NOs: 445 and 446). The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by a 19 amino acid immunoglobulin leader peptide, followed in frame by the coding sequence of a FLAG tag, followed in frame by the coding sequence of the mature macaque PSCA protein and a stop codon. The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990)

Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

24.3 Generation of PSCA and CD3 cross-species specific bispecific single chain antibody molecules

Cloning of cross-species specific PSCAxCD3 bispecific single chain antibody molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity cross-species specific for human and non-chimpanzee primate CD3 epsilon as well as a domain with a binding specificity cross-species specific for human and non-chimpanzee primate PSCA, were designed as set out in the following Table 7:

Table 7: Formats of anti-CD3 and anti-PSCA cross-species specific bispecific single chain antibody molecules

SEQ ID NO. (nucl/prot)	Formats of protein constructs (N → C)
390/389	PSCA1HLxI2CHL
422/421	PSCA3HLxI2CHL
440/439	PSCA4HLxI2CHL
392/391	PSCA1LHxI2CHL
406/405	PSCA2LHxI2CHL
424/423	PSCA3LHxI2CHL
442/441	PSCA4LHxI2CHL
1227/1226	PC16E12HLxI2CHL
1199/1198	PC32D5HLxI2CHL
1185/1184	PC32B8HLxI2CHL
1241/1240	PC08F4HLxI2CHL
1213/1212	PC17D10HLxI2CHL
1269/1268	PC17H10HLxI2CHL
1255/1254	PC16F5HLxI2CHL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains cross-species specific for human and macaque PSCA and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed and eukaryotic protein expression was performed in analogy to the

procedure described in example 9 for the MCSP and CD3 cross-species specific single chain molecules.

24.4 Expression and purification of the PSCAxCD3 bispecific single chain antibody molecules

The bispecific single chain antibody molecules were expressed in Chinese hamster ovary cells (CHO) or HEK293 cells as described herein above for the MCSPxCD3 bispecific single chan antibodies.

The isolation and analysis of the expressed bispecific single chan antibodies has also been described herein above in Example 9.

24.5 Flow cytometric binding analysis of the PSCA and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs regarding the capability to bind to human and macaque PSCA and CD3, respectively, a FACS analysis was performed. For this purpose CHO cells transfected with human PSCA as described in Example 24.1 and the human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used to test the binding to human antigens. The binding reactivity to macaque antigens was tested by using the generated macaque PSCA transfectant described in Example 24.2 and a macaque T cell line 4119LnPx (kindly provided by Prof Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; published in Knappe A, et al., and Fickenscher H., Blood 2000, 95, 3256-61). 200.000 cells of the respective cell lines were incubated for 30 min on ice with 50 µl of cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The cells were washed twice in PBS with 2% FCS and binding of the construct was detected with a murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Supernatant of untransfected cells was used as a negative control.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were

performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

The bispecific binding of the single chain molecules listed above, which are cross-species specific for PSCA and CD3 was clearly detectable as shown in Figure 46 and 48. In the FACS analysis all constructs showed binding to CD3 and PSCA compared to the negative control. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and PSCA antigens, respectively, was demonstrated.

24.6 Bioactivity of PSCA and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the CHO cells transfected with human PSCA described in Example 24.1 and the CHO cells transfected with macaque PSCA described in Example 24.2. As effector cells stimulated human CD4/CD56 depleted PBMC or the macaque T cell line 4119LnPx were used, respectively.

The generation of stimulated human PBMC was described herein above in Example 11.

Target cells were prepared and the assay was performed in analogy to the procedure described for the MCSPxCD3 bispecific single chain antibodies in example 11.

As shown in Figure 47 and 49 all of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against human PSCA positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and macaque PSCA positive target cells elicited by the macaque T cell line 4119LnPx.

24.7 Bispecific single chain antibody constructs directed against human and non-chimpanzee primate CD3 and PSCA

The human antibody germline VH sequence VH1 1-f (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRH1 (SEQ ID NO. 414), CDRH2 (SEQ ID NO. 415) and CDRH3 (SEQ ID NO. 416). Likewise the same human antibody germline VH sequence is chosen as framework context for CDRH1 (SEQ ID NO. 400), CDRH2 (SEQ ID NO. 401) and CDRH3 (SEQ ID NO. 402). For each human VH several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every

second primer is an antisense primer. For VH1 1-f the following set of oligonucleotides is used:

5' P3-VH-A-XhoI
CCT GAT CTC GAG AGC GGC SCA GAS STG RAA AAG CCA GGC GCC ACG GTG AAG ATT (SEQ ID NO. 449)
5' P3-VH-B
GGC GCC ACG GTG AAG ATT TCC TGC AAG SYC AGC GGC WAC ACG TTC ACC GGC TAC TAC ATC CAC TGG GTG (SEQ ID NO. 450)
3' P3-VH-C
GTA GGA GGT GAA GCC GTT GTT GGG GTC CAC TCT GCC SAT CCA TTC CAG GCY CTT CCC GKG GGM CTG TTK CAC CCA GTG GAT GTA GTA (SEQ ID NO. 451)
5' P3-VH-D
AAC GGC TTC ACC TCC TAC AAC CAG AAG TTC AAG GGC ARG GYC AYA MTK ACC GYG GAC AMG AGC ACC RRC ACC GCC TAC ATG GAA CTG (SEQ ID NO. 452)
3' P3-VH-E
GCT GTC GAA GAA GTT GCC CRC GCA ATA GTA CAC GGC GGT GTC CTC GCT GSK CAG GCT KCT CAG TTC CAT GTA GGC GGT (SEQ ID NO. 453)
3' P3-VH-F-BstEII
CAC GTC GGT GAC CGT GGT TCC CTG GCC CCA GCT GTC GAA GAA GTT GCC (SEQ ID NO. 454)
As another set of oligonucleotides for VH1 1-f the following primers are used:

5'-PSCA2VH-A-XHO1
CAG GTG CTCGAG YCA GGC GCC GAA STG RWG AAG CCT GGC GCC MCA GTG AAG MTA TCC TGC AAG GYC AGC GGC TAC ACC TTC ACC AAC (SEQ ID NO. 455)
3'-PSCA2VH-B
GCT GTC GCT GGG GTC GAT CCT GCC YAT CCA TTC CAG GCC CYT GCC GGG CSY CTG TTK CAC CCA GTT CAG CCA GTA GTT GGT GAA GGT GTA GCC (SEQ ID NO. 456)
5'-PSCA2VH-C
AGG ATC GAC CCC AGC GAC AGC GAG ATC CAC TAC GAC CAG AAG TTC AAG GAC ARA GYC ACC MTA ACC GYG GAC AMG AGC ACC RRC ACC GCC TAC (SEQ ID NO. 457)
3'-PSCA2VH-D
GGC CAG GGC GCA ATA GTA CAC GGC GGT GTC CTC GCT TST CAG GCT GGA CAG CTS SAT GTA GGC GGT GYY GGT GCT C (SEQ ID NO. 458)
3'-PSCA2VH-E-BSTE2
AGA CAC GGT GAC CGT GGT GCC CTG GCC CCA GTA GGC CAT GGC GTA GAT GCC GGT CAG GGC GCA ATA GTA CAC (SEQ ID NO. 459)
Each of these primer sets spans over the whole corresponding VH sequence.

Within each set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR

cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

Each VH PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VH approximately 350 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VH DNA fragment is amplified.

The human antibody germline VL sequence VkII A1 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID NO. 409), CDRL2 (SEQ ID NO. 410) and CDRL3 (SEQ ID NO. 411). Likewise human antibody germline VL sequence VkII A19 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID NO. 395), CDRL2 (SEQ ID NO. 396) and CDRL3 (SEQ ID NO. 397). For each human VL several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. Restriction sites needed for later cloning within the oligonucleotides are deleted. For VkII A1 the following oligonucleotides are used:

5' P3-VL-A-SacI
CCT GTA GAG CTC GTC ATG ACC CAG TCC CCC CTG TCC CTG MSC GTG ACC MTC GGC CAG CCA GCC AGC ATC (SEQ ID NO. 460)
3' P3-VL-B
CCA GTT CAG GTA GGT CTT GCC GTC GCT GTC CAG CAG GGA CTG GCT GGA CTT GCA AGA GAT GCT GGC TGG CTG GCC (SEQ ID NO. 461)
5' P3-VL-C
AAG ACC TAC CTG AAC TGG YTS CWG CAG AGG CCA GGC CAG AGC CCC ARG AGG CTG ATC TAC CTG GTG TCC ACC CTG (SEQ ID NO. 462)
3' P3-VL-D
GGT GAA GTC GGT GCC GGA GCC GCT GCC GGA GAA TCT GTC TGG CAC GCC GCT GTC CAG GGT GGA CAC CAG GTA (SEQ ID NO. 463)
5' P3-VL-E
TCC GGC ACC GAC TTC ACC CTG AAG ATC AGC AGG GTG GAG GCC GAG GAC STG GGC GTG TAC TAC TGC TGG CAG GGC ACC (SEQ ID NO. 464)
3' P3-VL-F-BsiWI/SpeI
CCA GAC ACT AGT CGT ACG CTT GAT TTC CAG CTT GGT CCC TCC GCC GAA GGT CCT TGG GAA GTG GGT GCC CTG CCA GCA GTA (SEQ ID NO. 465)
For VkII A19 the oligonucleotides are as follows:

5'-PSCA2VL-a-SAC1
CAG ACA GAG CTC GTG ATG ACC CAG KCA SCT CYA AGC STG CCA GTG ACC CCA GGC GAG YCA GYG TCC ATC AGC TGC AGG TCC AGC (SEQ ID NO. 466)
3'-PSCA2VL-b

CTG GGG GCT CTG GCC TGG CYT CTG CAG AWA CCA GTA CAG GTA GGT GTT GCC GTT GCT GTG CAG CAG GCT CTT GCT GGA CCT GCA GCT GAT G (SEQ ID NO. 467)
5'-PSCA2VL-c
CCA GGC CAG AGC CCC CAG CTG CTG ATC TAC AGG ATG AGC AAC CTG GCT AGC GGC GTG CCA GAC AGA TTC AGC GGC AGC GGC TCT GGA ACC (SEQ ID NO. 468)
3'-PSCA2VL-d
CAG GCA GTA GTA CAC GCC CAC GTC CTC GGC CTC CAC CCT GCT GAT CYT CAG GGT GAA GKC GGT TCC AGA GCC GCT GCC (SEQ ID NO. 469)
3'-PSCA2VL-e-BsiW1-Spe1
GTG CTG ACT AGT CGT ACG CTT GAT TTC CAG CTT GGT CCC TTG GCC GAA GGT GTA GGG GTA TTC CAG GTG CTG CAG GCA GTA GTA CAC GCC (SEQ ID NO. 470)
Each of these primer sets spans over the whole corresponding VL sequence.

Within each set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

Each VL PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VL approximately 330 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VL DNA fragment is amplified.

The final VH1 1-f (P3)-based VH PCR product (i.e. the repertoire of human/humanized VH) is then combined with the final VkII A1 -based VL PCR product (i.e. the repertoire of human/humanized VL) and the final VH1 1-f (PSCA2)-based VH PCR product (i.e. the repertoire of human/humanized VH) with the final VkII A19-based VL PCR product (i.e. the repertoire of human/humanized VL) in the phage display vector pComb3H5Bhis to form two different libraries of functional scFvs from which – after display on filamentous phage - anti-PSCA binders are selected, screened, identified and confirmed as described as follows:

450 ng of the light chain fragments (SacI-SpeI digested) are ligated with 1400 ng of the phagemid pComb3H5Bhis (SacI-SpeI digested; large fragment). The resulting combinatorial antibody library is then transformed into 300 ul of electrocompetent

Escherichia coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 uFD, 200 Ohm, Biorad gene-pulser) resulting in a library size of more than 10^7 independent clones. After one hour of phenotype expression, positive transformants are selected for carbenicilline resistance encoded by the pComb3H5BHis vector in 100 ml of liquid super broth (SB)-culture over night. Cells are then harvested by centrifugation and plasmid preparation is carried out using a commercially available plasmid preparation kit (Qiagen).

2800 ng of this plasmid-DNA containing the VL-library (XhoI-BstEII digested; large fragment) are ligated with 900 ng of the heavy chain V-fragments (XhoI-BstEII digested) and again transformed into two 300 ul aliquots of electrocompetent E. coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 uFD, 200 Ohm) resulting in a total VH-VL scFv (single chain variable fragment) library size of more than 10^7 independent clones.

After phenotype expression and slow adaptation to carbenicillin, the E. coli cells containing the antibody library are transferred into SB-Carbenicillin (50 ug/mL) selection medium. The E. coli cells containing the antibody library is then infected with an infectious dose of 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein phage particle contains single stranded pComb3H5BHis-DNA encoding a scFv-fragment and displayed the corresponding scFv-protein as a translational fusion to phage coat protein III. This pool of phages displaying the antibody library is used for the selection of antigen binding entities.

For this purpose the phage library carrying the cloned scFv-repertoire is harvested from the respective culture supernatant by PEG8000/NaCl precipitation and centrifugation. Approximately $10^{11}$to 10^{12} scFv phage particles are resuspended in 0.4 ml of PBS/0.1% BSA and incubated with 10^5 to 10^7 PSCA transfected CHO cells (see example 24.1) for 1 hour on ice under slow agitation. These PSCA transfected CHO cells are harvested beforehand by centrifugation, washed in PBS and resuspended in PBS/1 % FCS (containing Na Azide). scFv phage which do not specifically bind to the PSCA transfected CHO cells are eliminated by up to five washing steps with PBS/1 % FCS (containing Na Azide). After washing, binding entities are eluted from the cells by resuspending the cells in HCl-glycine pH 2.2 (10 min incubation with subsequent vortexing) and after neutralization with 2 M Tris pH 12, the eluate is used for infection of a fresh uninfected E. coli XL1 Blue culture

(OD600 > 0.5). The E. coli culture containing E. coli cells successfully transduced with a phagemid copy, encoding a human/humanized scFv-fragment, are again selected for carbenicillin resistance and subsequently infected with VCMS 13 helper phage to start the second round of antibody display and in vitro selection. A total of 4 to 5 rounds of selections are carried out, normally.

In order to screen for PSCA specific binders plasmid DNA corresponding to 4 and 5 rounds of panning is isolated from E. coli cultures after selection. For the production of soluble scFv-protein, VH-VL-DNA fragments are excised from the plasmids (XhoI-SpeI). These fragments are cloned via the same restriction sites into the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis in that the expression construct (e.g. scFv) includes a Flag-tag (DYKDDDDK) between the scFv and the His6-tag and the additional phage proteins are deleted. After ligation, each pool (different rounds of panning) of plasmid DNA is transformed into 100 µl heat shock competent E. coli TG1 or XLI blue and plated onto carbenicillin LB-agar. Single colonies are picked into 100 ul of LB carb (50 ug/ml).

E. coli transformed with pComb3H5BHis containing a VL- and VH-segment produce soluble scFv in sufficient amounts after excision of the gene III fragment and induction with 1 mM IPTG. Due to a suitable signal sequence, the scFv-chain is exported into the periplasma where it folds into a functional conformation.

Single E. coli TG1 bacterial colonies from the transformation plates are picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM $MgCl_2$ and carbenicillin 50µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. By four rounds of freezing at –70°C and thawing at 37°C, the outer membrane of the bacteria is destroyed by temperature shock and the soluble periplasmic proteins including the scFvs are released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the anti-PSCA scFvs is collected and used for the identification of PSCA specific binders as follows:

Binding of scFvs to PSCA is tested by flow cytometry on PSCA transfected CHO cells (see example 24.1); untransfected CHO cell are used as negative control.

For flow cytometry $2,5x10^5$ cells are incubated with 50 ul of scFv periplasmic preparation or with 5 µg/ml of purified scFv in 50 µl PBS with 2% FCS. The binding of scFv is detected with an anti-His antibody (Penta-His Antibody, BSA free, Qiagen GmbH, Hilden, FRG) at 2 µg/ml in 50 µl PBS with 2% FCS. As a second step reagent

a R-Phycoerythrin-conjugated affinity purified F(ab')$_2$ fragment, goat anti-mouse IgG (Fc-gamma fragment specific), diluted 1:100 in 50 µl PBS with 2% FCS (Dianova, Hamburg, FRG) is used. The samples are measured on a FACSscan (BD biosciences, Heidelberg, FRG).

Single clones are then analyzed for favourable properties and amino acid sequence. PSCA specific scFvs are converted into recombinant bispecific single chain antibodies by joining them via a Gly_4Ser_1-linker with the CD3 specific scFv I2C (SEQ ID NO. 185) or any other CD3 specific scFv of the invention to result, for example, in constructs with the domain arrangement VH_{PSCA} - $(Gly_4Ser_1)_3$ –VL_{PSCA}- Gly_4Ser_1-VH_{CD3} - $(Gly_4Ser_1)_3$ - VL_{CD3} or VL_{PSCA} - $(Gly_4Ser_1)_3$ –VH_{PSCA}- Gly_4Ser_1-VH_{CD3} - $(Gly_4Ser_1)_3$ - VL_{CD3} or alternative domain arrangements. For expression in CHO cells the coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His_6-tag followed by a stop codon are both attached in frame to the nucleotide sequence encoding the bispecific single chain antibodies prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). Stable transfection of DHFR-deficient CHO cells, selection for DHFR-positive transfectants secreting the bispecific single chain antibodies into the culture supernatant and gene amplification with methotrexat for increasing expression levels are carried out as described (Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025). All other state of the art procedures are carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)).

Identification of functional bispecific single-chain antibody constructs is carried out by flowcytometric analysis of culture supernatant from transfected CHO cells. For this purpose CD3 binding is tested on the human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) and on the macaque T cell line 4119LnPx. Binding to tumor specific PSCA epitopes is tested on PSCA transfected CHO cells (see example 24.1). 200.000 cells of the respective cell line are incubated for 30 min. on ice with 50 µl of cell culture supernatant. The cells are washed twice in PBS with 2% FCS and bound bispecific single-chain antibody construct is detected with a murine anti-His antibody (Penta His antibody; Qiagen; diluted 1:20 in 50 µl

PBS with 2% FCS). After washing, bound anti-His antibodies are detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Supernatant of untransfected CHO cells is used as negative control.

Flow cytometry is performed on a FACS-Calibur apparatus; the CellQuest software is used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity are performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

Only those constructs showing bispecific binding to human and macaque CD3 as well as to human and macaque PSCA are selected for further use.

For protein production CHO cells expressing fully functional bispecific single chain antibody and adapted to nucleoside-free HyQ PF CHO liquid soy medium (with 4.0 mM L-Glutamine with 0.1% Pluronic F – 68; HyClone) are grown in roller bottles with nucleoside-free HyQ PF CHO liquid soy medium (with 4.0 mM L-Glutamine with 0.1% Pluronic F – 68; HyClone) for 7 days. Culture supernatant is cleared from cells by centrifugation and stored at –20°C until purification. As chromatography equipment for purification of bispecific single chain antibody from culture supernatant Äkta® Explorer System (GE Health Systems) and Unicorn® Software are used. Immobilized metal affinity chromatography ("IMAC") is performed using a Fractogel EMD chelate® (Merck) which is loaded with $ZnCl_2$ according to the protocol provided by the manufacturer. The column is equilibrated with buffer A (20 mM sodium phosphate buffer pH 7.2, 0.1 M NaCl) and the cell culture supernatant (500 ml) is applied to the column (10 ml) at a flow rate of 3 ml/min. The column is washed with buffer A to remove unbound sample. Bound protein is eluted using a two step gradient of buffer B (20 mM sodium phosphate buffer pH 7.2, 0.1 M NaCl, 0.5 M Imidazole) according to the following:

Step 1: 20% buffer B in 6 column volumes

Step 2: 100% buffer B in 6 column volumes

Eluted protein fractions from step 2 are pooled for further purification. All chemicals are of research grade and purchased from Sigma (Deisenhofen) or Merck (Darmstadt).

Gel filtration chromatography is performed on a HiLoad 16/60 Superdex 200 prep grade column (GE/Amersham) equilibrated with Equi-buffer (25 mM Citrate, 200 mM

Lysine, 5% Glycerol, pH 7.2). Eluted protein samples (flow rate 1 ml/min) are subjected to standard SDS-PAGE and Western Blot for detection. Prior to purification, the column is calibrated for molecular weight determination (molecular weight marker kit, Sigma MW GF-200). Protein concentrations are determined using OD280 nm.

Purified bispecific single chain antibody protein is analyzed in SDS PAGE under reducing conditions performed with pre-cast 4-12% Bis Tris gels (Invitrogen). Sample preparation and application are performed according to the protocol provided by the manufacturer. The molecular weight is determined with MultiMark protein standard (Invitrogen). The gel is stained with colloidal Coomassie (Invitrogen protocol). The purity of the isolated protein is >95% as determined by SDS-PAGE.

The bispecific single chain antibody has a molecular weight of about 52 kDa under native conditions as determined by gel filtration in PBS. All constructs are purified according to this method.

Western Blot is performed using an Optitran® BA-S83 membrane and the Invitrogen Blot Module according to the protocol provided by the manufacturer. For detection of the bispecific single chain antibody protein antibodies an anti-His Tag antibody is used (Penta His, Qiagen). A Goat-anti-mouse Ig antibody labeled with alkaline phosphatase (AP) (Sigma) is used as secondary antibody and BCIP/NBT (Sigma) as substrate. A single band is detected at 52 kD corresponding to the purified bispecific single chain antibody.

The potency in the human and the non-chimpanzee primate system of bispecific single chain antibodies interacting with human and macaque CD3 and with human and macaque PSCA is determined by a cytotoxicity assay based on chromium 51 (^{51}Cr) release using PSCA transfected CHO cells as target cells (see example 24.1) and stimulated human CD4/CD56 depleted PBMC or the macaque T cell line 4119LnPx as effector cells.

Generation of stimulated human PBMC is performed as follows:

A Petri dish (85 mm diameter, Nunc) is coated with a commercially available anti-CD3 specific antibody (e.g. OKT3, Othoclone) in a final concentration of 1 µg/ml for 1 hour at 37°C. Unbound protein is removed by one washing step with PBS. The fresh PBMC are isolated from peripheral blood (30 – 50 ml human blood) by Ficoll gradient centrifugation according to standard protocols. 3 – 5 x 10^7 PBMC are added to the precoated petri dish in 50 ml of RPMI 1640 with stabilized glutamine / 10%

FCS / IL-2 20 U/ml (Proleukin, Chiron) and stimulated for 2 days. On the third day the cells are collected and washed once with RPMI 1640. IL-2 is added to a final concentration of 20 U/ml and the cells are cultivated again for one day in the same cell culture medium as above.

Target cells are washed twice with PBS and labelled with 11.1 MBq ^{51}Cr in a final volume of 100 µl RPMI with 50% FCS for 45 minutes at 37°C. Subsequently the labelled target cells are washed 3 times with 5 ml RPMI and then used in the cytotoxicity assay. The assay is performed in a 96 well plate in a total volume of 250µl supplemented RPMI (as above) with an E:T ratio of 10:1. 1 µg/ml of the cross-species specific bispecific single chain antibody molecules and 20 threefold dilutions thereof are applied. The assay time is 18 hours and cytotoxicity is measured as relative values of released chromium in the supernatant related to the difference of maximum lysis (addition of Triton-X) and spontaneous lysis (without effector cells). All measurements are done in quadruplicates. Measurement of chromium activity in the supernatants is performed with a Wizard 3" gamma counter (Perkin Elmer Life Sciences GmbH, Köln, Germany). Analysis of the experimental data is performed with Prism 4 for Windows (version 4.02, GraphPad Software Inc., San Diego, California, USA). Sigmoidal dose response curves typically have R^2 values >0.90 as determined by the software. EC_{50} values as measure of potency are calculated by the analysis program.

25. Generation and characterization of CD19 and CD3 cross-species specific bispecific single chain antibody molecules

25.1. Cloning and expression of human CD19 antigen on CHO cells

The sequence of the human CD19 antigen (NM_001770 Homo sapiens CD19 molecule (CD19), mRNA, National Center for Biotechnology Information, http://www.ncbi.nlm.nih.gov/entrez) was used to obtain a synthetic molecule by gene synthesis according to standard protocols. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the DNA. The introduced restriction sites EcoRI at the 5' end and SalI at the 3' end were utilised during the cloning step into the expression plasmid designated pEFDHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). After sequence verification the plasmid was used to transfect CHO/dhfr- cells as follows. A sequence verified plasmid was used to

transfect CHO/dhfr- cells (ATCC No. CRL 9096; cultured in RPMI 1640 with stabilized glutamine obtained from Biochrom AG Berlin, Germany, supplemented with 10% FCS, 1% penicillin/streptomycin all obtained from Biochrom AG Berlin, Germany and nucleosides from a stock solution of cell culture grade reagents obtained from Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany, to a final concentration of 10 µg/ml Adenosine, 10 µg/ml Deoxyadenosine and 10 µg/ml Thymidine, in an incubator at 37 C, 95% humidity and 7% CO2). Transfection was performed using the PolyFect Transfection Reagent (Qiagen GmbH, Hilden, Germany) and 5 µg of plasmid DNA according to the manufacturer's protocol. After culture period of 24 hours cells were washed once with PBS and again cultured in the aforementioned cell culture medium except that the medium was not supplemented with nucleosides and dialysed FCS (obtained from Biochrom AG Berlin, Germany) was used. Thus the cell culture medium did not contain nucleosides and thereby selection was applied on the transfected cells. Approximately 14 days after transfection the outgrowth of resistant cells was observed. After an additional 7 to 14 days the transfectants were tested positive for expression of the construct via FACS. Eukaryotic protein expression in DHFR deficient CHO cells is performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct is induced by increasing concentrations of methothrexate (MTX) to a final concentration of up to 20 nM MTX.

25.2. Generation of CD19 and CD3 cross-species specific bispecific single chain molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity for the human and the macaque CD3 antigen as well as a domain with a binding specificity for the human CD19 antigen, were designed as set out in the following Table 8:

Table 8: Formats of anti-CD3 and anti-CD19 cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
482/481	HD37 LH x I2C HL
486/485	HD37 LH x F12Q HL
484/483	HD37 LH x H2C HL
534/533	hCD19 47-A3 LH x I2C HL
522/521	hCD19 46-B11LH x I2C HL
510/509	hCD19 45-A10 LH x I2C HL
498/497	hCD19 26-D6 LH x I2C HL
546/545	HD37-DT LH x I2C HL
558/557	HD37-A LH x I2C HL
570/569	HD37-G LH x I2C HL
582/581	HD37-S LH x I2C HL
594/593	HD37-T LH x I2C HL
606/605	HD37-I LH x I2C HL
618/617	HD37-L LH x I2C HL
630/629	HD37-V LH x I2C HL
642/641	HD37-E LH x I2C HL
654/653	HD37-Q LH x I2C HL
666/665	HD37-N LH x I2C HL
678/677	HD37-K LH x I2C HL
690/689	HD37-R LH x I2C HL
702/701	HD37-H LH x I2C HL
714/713	HD37-Y LH x I2C HL
726/725	HD37-P LH x I2C HL
738/737	HD37-F LH x I2C HL
750/749	HD37-W LH x I2C HL
762/761	HD37-M LH x I2C HL
1283/1282	hCD19 5-A9 LH x I2C HL
1297/1296	hCD19 2-C6 LH x I2C HL
1311/1310	hCD19 4-C7 LH x I2C HL
1325/1324	hCD19 2-D7 LH x I2C HL
1339/1338	hCD19 2-D4 LH x I2C HL
1353/1352	hCD19 5-G3 LH x I2C HL
1367/1366	hCD19 4-E10 LH x I2C HL
1381/1380	hCD19 4-E3 LH X I2C HL
1395/1394	hCD19 3-H7 LH X I2C HL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains specific for human CD19 and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed and eukaryotic protein expression was performed in analogy to the procedure described in example 9 for the MCSPxCD3 cross-species specific single chain molecules.

25.3. Expression and purification of the bispecific single chain antibody molecules

The bispecific single chain antibody molecules were expressed in chinese hamster ovary cells (CHO) or HEK 293 cells as described herein above for the MCSPxCD3 bispecific single chain antibodies.

The isolation and analysis of the expressed bispecific single chain antibodies has also been described herein above in Example 9.

25.4. Flow cytometric binding analysis of the CD19 and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs with regard to binding capability to human CD19 as well as to human and macaque CD3, a FACS analysis was performed. For this purpose the CHO cells transfected with human CD19 as described in example 25.1 and human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used to check the binding to human antigens. The binding reactivity to macaque CD3 was tested by using a macaque T cell line 4119LnPx (kindly provided by Prof Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; Knappe A, et al., and Fickenscher H: Herpesvirus saimiri-transformed macaque T cells are tolerated and do not cause lymphoma after autologous reinfusion. Blood 2000;95:3256-61.) 200,000 cells of the respective cell population were incubated for 30 min on ice with 50 µl of the purified protein of the cross-species specific bispecific antibody constructs (e. g. 2 µg/ml) Alternatively the cell culture supernatant of transiently produced proteins was used. The cells were washed twice in PBS and binding of the construct was detected with an unlabeled murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in 50 µl PBS with 2% FCS. Fresh culture medium was used as a negative control.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to aquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

In the FACS analysis shown in Figure 50 all tested constructs showed binding to human and macaque CD3 and to human CD19.

25.5. Bioactivity of CD19 and CD3 cross-species specific bispecific single chain antibodies

The bioactivity of bispecific single chain antibodies was analyzed by chromium 51 release in vitro cytotoxicity assays using the CD19 positive cell line described in example 25.1. As effector cells stimulated human CD8 positive T cells or the macaque T cell line 4119LnPx were used.

The generation of stimulated human PBMC was described herein above in Example 11.

Target cells prepared and the assay was performed in analogy to the procedure described for the MCSPxCD3 bispecific single chain antibodies in example 11.

In the T cell cytotoxicity assay shown in Figure 51 all tested bispecific single chain antibody constructs revealed cytotoxic activity against human CD19 positive target cells elicited by human CD8+ cells and against human CD19 positive target cells elicited by the macaque T cell line 4119LnPx. As a negative control, an irrelevant bispecific single chain antibody was used.

25.6. Generation of additional CD19 and CD3 cross-species specific bispecific single chain molecules

The human antibody germline VH sequence VH1 1-46 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRH1 (SEQ ID NO 473), CDRH2 (SEQ ID NO 474) and CDRH3 (SEQ ID NO 475). For the human VH several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. For VH1 1-46 the following oligonucleotides are used (5'- to 3'):

5'-37VH-aXho1

CAG CTG CTC GAG TCT GGG GCT GAG STG RWG ARG CCT GGG KCC TCA GTG AAG RTT TCC TGC AAG GCT TCT GGC (SEQ ID NO 763)

3'-37VH-b

cca ctc aag acc ctg tcc agg GSS ctg cYt cac cca gtt cat cca gta gct aGw gaa tgY ata gcc aga agc ctt gca gga (SEQ ID NO 764)

5'-37VH-c

GGA CAG GGT CTT GAG TGG ATK GGA CAG ATT TGG CCT GGA GAT GGT GAT ACT AAC TAC AAT GGA AAG TTC AAG (SEQ ID NO 765)

3'-37VH-d

cag gct gct gag ttS cat gta gRc tgt gct ggt gga tKY gtc ASS agt caK agt gRc tYt acc ctt gaa ctt tcc att gta g (SEQ ID NO 766)

5'-37VH-e

C ATG SAA CTC AGC AGC CTG SSA TCT GAG GAC ACT GCG GTC TAT TWC TGT GCA AGA CGG GAG ACT ACG ACG G (SEQ ID NO 767)

3'-37VH-fBstE2

gga gac ggt gac cgt ggt ccc ttg gcc cca gta gtc cat agc ata gta ata acg gcc tac cgt cgt agt ctc ccg tct tgc (SEQ ID NO 768)

This primer set spans over the whole corresponding VH sequence.

Within the set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

The VH PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VH approximately 350 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VH DNA fragment is amplified.

The human antibody germline VL sequence VkI O12 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID NO 478), CDRL2 (SEQ ID NO 479) and CDRL3 (SEQ ID NO 480). For the human VL several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. Restriction sites needed for later cloning within the oligonucleotides are deleted. For VkI O12 the following oligonucleotides are used (5'- to 3'):

5'-37VL-A-SacI

CAG CTG GAG CTC CAG ATG ACC CAG TCT CCA KCT TCT TTG KCT GYG TCT STA GGG SAS AGA GYC ACC ATC WCC TGC AAG GCC AGC (SEQ ID NO 769)

3'-37VL-B

ctg ttg gta cca gtt caa ata aSt SNN acc atc ata atc aac act ttg gct ggc ctt gca ggt gat ggt (SEQ ID NO 770)

5'-37VL-C

TTG AAC TGG TAC CAA CAG AWA CCA GGA MAG SCA CCC AAA CTC CTC ATC TAT GAT GCA TCC AAT CTA GTT TCT (SEQ ID NO 771)

3'-37VL-D

gag ggt gaa gtc tgt ccc aga ccc act gcc act aaa cct ggR tgg gaY ccc aga aac tag att gga tgc (SEQ ID NO 772)

5'-37VL-E

GGG ACA GAC TTC ACC CTC AMC ATC MRT YCT STG SAG MMG GWG GAT KYC GCA ACC TAT YAC TGT CAG CAA AGT ACT GAG (SEQ ID NO 773)

3'-37VL-F-BsiW1Spe1

ACT CAG ACT AGT CGT ACG ttt gat ctc cac ctt ggt ccc ttg acc gaa cgt cca cgg atc ctc agt act ttg ctg aca g (SEQ ID NO 774)

This primer sets spans over the whole corresponding VL sequence.

Within the set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

The VL PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VL approximately 330 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VL DNA fragment is amplified.

The final VH1 1-46 -based VH PCR product (i.e. the repertoire of human/humanized VH) is then combined with the final Vkl O12 -based VL PCR product (i.e. the repertoire of human/humanized VL) in the phage display vector pComb3H5Bhis to

form a library of functional scFvs from which – after display on filamentous phage - anti-CD19 binders are selected, screened, identified and confirmed as described in the following:

450 ng of the light chain fragments (SacI-SpeI digested) are ligated with 1400 ng of the phagemid pComb3H5Bhis (SacI-SpeI digested; large fragment). The resulting combinatorial antibody library is then transformed into 300 µl of electrocompetent Escherichia coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm, Biorad gene-pulser) resulting in a library size of more than 107 independent clones. After one hour of phenotype expression, positive transformants are selected for carbenicilline resistance encoded by the pComb3H5BHis vector in 100 ml of liquid super broth (SB)-culture over night. Cells are then harvested by centrifugation and plasmid preparation is carried out using a commercially available plasmid preparation kit (Qiagen).

2800 ng of this plasmid-DNA containing the VL-library (XhoI-BstEII digested; large fragment) are ligated with 900 ng of the heavy chain V-fragments (XhoI-BstEII digested) and again transformed into two 300 µl aliquots of electrocompetent E. coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm) resulting in a scFv library with a size of more than 107 independent clones.

After phenotype expression and slow adaptation to carbenicilline, the E. coli cells containing the antibody library are transferred into SB-carbenicilline (SB with 50 µg/mL carbenicilline) selection medium. The E. coli cells containing the antibody library are then infected with an infectious dose of 1012 particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein each phage particle contains single stranded pComb3H5BHis-DNA encoding a scFv-fragment and displays the corresponding scFv-protein as a translational fusion to phage coat protein III. This pool of phages displaying the antibody library is used for the selection of antigen binding entities.

For this purpose the phage library carrying the cloned scFv-repertoire is harvested from the respective culture supernatant by PEG8000/NaCl precipitation and centrifugation. Approximately 1011to 1012 scFv phage particles are resuspended in 0.4 ml of PBS/0.1% BSA and incubated with 105 to 107 CD19 transfected CHO cells (see example 1) for 1 hour on ice under slow agitation. These CD19 transfected CHO cells are harvested beforehand by centrifugation, washed in PBS and resuspended in PBS/1 % FCS (containing Na Azide). scFv phage which do not specifically bind to the

CD19 transfected CHO cells are eliminated by up to five washing steps with PBS/1 % FCS (containing Na Azide). After washing, binding entities are eluted from the cells by resuspending the cells in HCl-glycine pH 2.2 (10 min incubation with subsequent vortexing) and after neutralization with 2 M Tris pH 12, the eluate is used for infection of a fresh uninfected E. coli XL1 Blue culture (OD600 > 0.5). The E. coli culture containing E. coli cells successfully transduced with a phagemid copy, encoding a human/humanized scFv-fragment, are again selected for carbenicilline resistance and subsequently infected with VCMS 13 helper phage to start the second round of antibody display and in vitro selection. A total of 4 to 5 rounds of selections are carried out, normally.

In order to screen for CD19 specific binders plasmid DNA corresponding to 4 and 5 rounds of panning is isolated from E. coli cultures after selection. For the production of soluble scFv-protein, the scFv-DNA fragments are excised from the plasmids (XhoI-SpeI). These fragments are cloned via the same restriction sites into the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis in that the expression construct (i.e. the scFv) includes a Flag-tag (DYKDDDDK, SEQ ID NO 775) at its C-terminus before the His6-tag and that phage protein III/N2 domain and protein III/CT domain had been deleted. After ligation, each pool (different rounds of panning) of plasmid DNA is transformed into 100 µl heat shock competent E. coli TG1 or XLI blue and plated onto carbenicilline LB-agar. Single colonies are picked into 100 µl of LB carb (LB with 50 µg/ml carbenicilline).

E. coli transformed with pComb3H5BFlag/His containing a scFv-DNA fragment produce soluble scFv-protein in sufficient amounts after induction with 1 mM IPTG. Due to a suitable signal sequence, the scFv is exported into the periplasma where it folds into a functional conformation.

Single E. coli TG1 bacterial colonies from the transformation plates are picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM MgCl2 and carbenicilline 50µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. A temperature shock is applied by four rounds of freezing at –70°C and thawing at 37°C whereby the outer membrane of the bacteria is destroyed and the soluble periplasmic proteins including the scFvs are released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the anti-CD19 scFvs is collected and used for the identification of CD19 specific binders as follows:

Binding of scFvs to CD19 is tested by flow cytometry on CD19 transfected CHO cells (see example 25.1); untransfected CHO cells are use as negative control.

For flow cytometry 2.5x105 cells are incubated with 50 µl of scFv periplasmic preparation or with 5 µg/ml of purified scFv in 50 µl PBS with 2% FCS. The binding of scFv is detected with an anti-His antibody (Penta-His Antibody, BSA free, Qiagen GmbH, Hilden, FRG) at 2 µg/ml in 50 µl PBS with 2% FCS. As a second step reagent a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG (Fc-gamma fragment specific), diluted 1:100 in 50 µl PBS with 2% FCS (Dianova, Hamburg, FRG) is used. The samples are measured on a FACSscan (BD biosciences, Heidelberg, FRG).

Single clones are then analyzed for favourable properties and amino acid sequence. CD19 specific scFvs are converted into recombinant bispecific single chain antibodies by joining them via a Gly4Ser1-linker with the CD3 specific scFv I2C (amino acid sequence SEQ ID NO 185, nucleic acid sequence SEQ ID NO 186) or any other CD3 specific scFv of the invention to result in constructs with the domain arrangement VLCD19 - (Gly4Ser1)3 –VHCD19- Gly4Ser1-VHCD3 - (Gly4Ser1)3 - VLCD3. For expression in CHO cells the coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His6-tag followed by a stop codon are both attached in frame to the nucleotide sequence encoding the bispecific single chain antibodies prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). Transfection of the generated expression plasmids, protein expression and purification of cross-species specific bispecific antibody constructs are performed as described in Examples 25.2 and 25.3. All other state of the art procedures are carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)).

Identification of functional bispecific single-chain antibody constructs is carried out by flow cytometric binding analysis of culture supernatant from transfected cells expressing the cross-species specific bispecific antibody constructs. Analysis is perfomed as described in Example 25.4.

Only those constructs showing bispecific binding to human and macaque CD3 as well as to CD19 are selected for further use.

The cytotoxic activity of cross-species specific bispecific single chain antibody constructs against CD19 positive target cells elicited by effector T cells is analyzed as described in Example 25.5. CHO-cells transfected with human CD19 are used as target cells and stimulated CD4/CD56-depleted human PBMCs or the macaque T cell line 4119LnPx as effector T cells. Only those constructs showing potent redirected T cell cytotoxicity against CD19-positive target cells are selected for further use.

26. Generation and characterization of C-MET and CD3 cross-species specific bispecific single chain antibody molecules

26.1 Generation of CHO cells expressing human C-MET

The coding sequence of human C-MET as published in GenBank (Accession number NM_000245) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct followed by the coding sequence of the human C-MET protein and a stop codon (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 776 and 777). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. Internal restriction sites were removed by silent mutation of the coding sequence in the gene synthesis fragment (SalI: nucleotide 366 from C to G; EcoRI and XbaI: nucleotides 2059 to 2061 from TCT to AGC; EcoRI: nucleotide 2304 from T to C). The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

26.2 Generation of CHO cells expressing macaque C-MET

The cDNA sequence of macaque C-MET (cynomolgus) was obtained by a set of 5 PCRs on cDNA from macaque monkey Liver prepared according to standard protocols. The following reaction conditions: 1 cycle at 94°C for 2 minutes followed by 40 cycles with 94°C for 1 minute, 56°C for 1 minute and 72°C for 3 minutes followed by a terminal cycle of 72°C for 3 minutes and the following primers were used:

4. forward primer: 5'-aggaattcaccatgaaggcccccgctgtgcttgcacc-3' (SEQ ID NO: 778)
   reverse primer: 5'-ctccagaggcatttccatgtagg-3' (SEQ ID NO: 779)
5. forward primer: 5'-gtccaaagggaaactctagatgc-3' (SEQ ID NO: 780)
   reverse primer: 5'-ggagacactggatgggagtccagg-3' (SEQ ID NO: 781)
6. forward primer: 5'-catcagagggtcgcttcatgcagg-3' (SEQ ID NO: 782)
   reverse primer: 5'-gctttggttttcaggggagttgc-3' (SEQ ID NO: 783)
7. forward primer: 5'-atccaaccaaatcttttattagtggtgg-3' (SEQ ID NO: 784)
   reverse primer: 5'-gacttcattgaaatgcacaatcagg-3' (SEQ ID NO: 785)
8. forward primer: 5'-tgctctaaatccagagctggtcc-3' (SEQ ID NO: 786)
   reverse primer: 5'-gtcagataagaaattccttagaatcc-3' (SEQ ID NO: 787)

These PCRs generated five overlapping fragments, which were isolated and sequenced according to standard protocols using the PCR primers, and thereby provided a portion of the cDNA sequence coding macaque C-MET from codon 10 of the leader peptide to the last codon of the mature protein. To generate a construct for expression of macaque C-MET a cDNA fragment was obtained by gene synthesis according to standard protocols (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 788 and 789). In this construct the coding sequence of macaque C-MET from amino acid 10 of the leader peptide to the last amino acid of the mature C-MET protein followed by a stop codon was fused in frame to the coding sequence of the amino acids 1 to 9 of the leader peptide of the human C-MET protein. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the fragment containing the cDNA. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. Internal restriction sites were removed by silent mutation of the coding sequence in the gene synthesis fragment (SalI: nucleotide 366 from C to G; EcoRI: nucleotide 2055 from G to C). The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer

Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

26.3 Generation of C-MET and CD3 cross-species specific bispecific single chain molecules

Cloning of cross-species specific binding molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity cross-species specific for human and non-chimpanzee primate CD3epsilon as well as a domain with a binding specificity for C-MET, were designed as set out in the following Table 9:

Table 9: Formats of anti-C-MET and anti-CD3 cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
830/829	MET1HLxI2CHL
854/853	MET4HLxI2CHL
872/871	MET5HLxI2CHL
890/889	MET6HLxI2CHL
832/831	MET1LHxI2CHL
856/855	MET4LHxI2CHL
874/873	MET5LHxI2CHL
892/891	MET6LHxI2CHL
906/905	MET7LHxI2CHL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains specific for C-MET and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed and eukaryotic protein expression was performed in analogy to the procedure described in example 9 for the MCSPxCD3 cross-species specific single chain molecules. The bispecific single

chain antibody molecules were expressed in chinese hamster ovary cells (CHO) or HEK 293 cells as described herein above for the MCSPxCD3 bispecific single chain antibodies.

The isolation and analysis of the expressed bispecific single chain antibodies has also been described herein above in Example 9.

As shown in Figure 55 all of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against macaque cMET positive target cells elicited by the macaque T cell line 4119LnPx.

26.5 Flow cytometric binding analysis of the C-MET and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs regarding the capability to bind to C-MET and human and macaque CD3, respectively, a FACS analysis was performed. For this purpose the human C-MET positive breast cancer cell line MDA-MB-231 (ATCC No. HTB-26) and the human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used to test the binding to human antigens. The binding reactivity to macaque CD3 was tested by using the macaque T cell line 4119LnPx (kindly provided by Prof Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; published in Knappe A, et al., and Fickenscher H., Blood 2000, 95, 3256-61). 200.000 cells of the respective cell lines were incubated for 30 min on ice with with 50 µl of cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The cells were washed twice in PBS with 2% FCS and binding of the construct was detected with a murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Supernatant of untransfected cells was used as a negative control.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

The bispecific binding of the single chain molecules listed above, which are specific for C-MET and cross-species specific for human and non-chimpanzee primate CD3

was clearly detectable as shown in Figure 52. In the FACS analysis all constructs showed binding to CD3 and C-MET compared to the negative control. Cross-species specificity of the bispecific antibodies for human and macaque CD3 was demonstrated.

26.6 Bioactivity of C-MET and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the MDA-MB-231 cell line. As effector cells stimulated human CD4/CD56 depleted PBMC were used.

The generation of stimulated human PBMC was described herein above in Example 11. Target cells prepared and the assay was performed in analogy to the procedure described for the MCSPxCD3 bispecific single chain antibodies in example 11.

As shown in Figure 53 all of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against C-MET positive target cells elicited by stimulated human CD4/CD56 depleted PBMC.

26.7 Generation of additional C-MET and CD3 cross-species specific bispecific single chain molecules

The human antibody germline VH sequence VH1 1-03 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRH1 (SEQ ID NO 821), CDRH2 (SEQ ID NO 822) and CDRH3 (SEQ ID NO 823). Likewise human antibody germline VH sequence VH1 1-46 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRH1 (SEQ ID NO 836), CDRH2 (SEQ ID NO 837) and CDRH3 (SEQ ID NO 838). For each human VH several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. For VH1 1-03 the following oligonucleotides are used:

5'CM1-VH-A-XhoI (SEQ ID NO: 790)
CCA TGT CTC GAG TCT GGG SCT GAA STG RWG ARG CCT GGG GCT TCA GTG AAA RTG TCC TGC ARG GCT TCG GGC TAT ACC TTC

3'CM1-VH-B (SEQ ID NO: 791)
AT CCA CTC AAG CCY TTG TCC AGG CSY CTG TYT AAC CCA GTG CAA CCA GTA GCT GGT GAA GGT ATA GCC CGA AGC

5'CM1-VH-C (SEQ ID NO: 792)
GG CTT GAG TGG ATK GGC ATG ATT GAT CCT TCC AAT AGT GAC ACT AGG TTT AAT CCG AAC TTC AAG GAC

3'CM1-VH-D (SEQ ID NO: 793)

GCT GCT GAG CWS CAT GTA GGC TGT GYT GGM AGA TST GTC TMY AKT SAW TGT GRC CYT GTC CTT GAA GTT CGG ATT

5'CM1-VH-E (SEQ ID NO: 794)

GCC TAC ATG SWA CTC AGC AGC CTG ASA TCT GMG GAC ACT GCA GTC TAT TAC TGT GCC ASA TAT GGT AGC TAC GTT

3'CM1-VH-F-BstEII (SEQ ID NO: 795)

CAT GTA GGT GAC CGA GGT TCC TTG ACC CCA GTA GTC CAG AGG GGA AAC GTA GCT ACC ATA

For VH1 1-46 the oligonucleotides are as follows:

5' CM3-VH-A-XhoI (SEQ ID NO: 796)

CCA TGT CTC GAG TCT GGG RCT GAA STG RWG AAG CCT GGG GCT TCA GTG AAG STG TCC TGC AAG GCT TCT

3' CM3-VH-B (SEQ ID NO: 797)

CTC AAG GCC TTG TCC AGG CSY CTG CYT CAC CCA GTG TAT CCA GTA ACT GGT GAA GGT GTA GCC AGA AGC CTT GCA GGA

5' CM3-VH-C (SEQ ID NO: 798)

CCT GGA CAA GGC CTT GAG TGG ATK GGA GAG ATT AAT CCT AGC AGC GGT CGT ACTA AC TAC AAC GAG AAA TTC

3' CM3-VH-D (SEQ ID NO: 799)

C TGT GGA GGT AGA TKT GTC TMY AGT CAY TGT GAC CYT GTT CTT GAA TTT CTC GTT GTA GTT

5' CM3-VH-E (SEQ ID NO: 800)

A TCT ACC TCC ACA GYC TAC ATG SAA CTC AGC ARC CTG ASA TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA

3' CM3-VH-F-BstEII (SEQ ID NO: 801)

CAT GTA GGT GAC CGT GGT GCC TTG GCC CCA GTA GCC CCT WCT TGC ACA GTA ATA GAC CGC

Each of these primer sets spans over the whole corresponding VH sequence.

Within each set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

Each VH PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VH approximately 350 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VH DNA fragment is amplified.

The human antibody germline VL sequence VkII O11 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID NO 816), CDRL2 (SEQ ID NO 817) and CDRL3 (SEQ ID NO 818). Likewise human antibody germline VL sequence VkII A1 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID NO 833), CDRL2 (SEQ ID NO 834) and CDRL3 (SEQ ID NO 835). For each human VL several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. Restriction sites needed for later cloning within the oligonucleotides are deleted. For VkII O11 the following oligonucleotides are used:

5' CM1-VL-A-SacI (SEQ ID NO: 802)
CCT GTA GAG CTC GTG ATG ACC CAG ACT CCA YYC TCC CTA MCT GTG
ACA SYT GGA GAG MMG GYT TCT RTC AGC TGC AAG TCC AGT
3' CM1-VL-B (SEQ ID NO: 803)
GTA CCA GGC CAA GTA GTT CTT CTG ACT GCT AGT ATA TAA AAG GGA
CTG ACT GGA CTT GCA GCT GA
5' CM1-VL-C (SEQ ID NO: 804)
TAC TTG GCC TGG TAC CWG CAG AAA CCA GGT CAG TCT CCT MAA CTG
CTG ATT TAC TGG GCA TCC ACT AGG
3' CM1-VL-D (SEQ ID NO: 805)
GAG AGT GAA ATC TGT CCC AGA TCC ACT GCC TGA GAA GCG ATC AGG
GAC CCC AGA TTC CC TAGT GGA TGC CCA GTA
5' CM1-VL-E (SEQ ID NO: 806)
ACA GAT TTC ACT CTC AMA ATC TCC AGW GTG RAG GCT GAS GAC STG
GSA GTT TAT TAC TGT CAG CAA TAT
3' CM1-VL-F-BsiWI/SpeI (SEQ ID NO: 807)
CCT CAG ACT AGT CGT ACG TTT GAT CTC CAA CTT TGT GCC TCC ACC
GAA CGT CCA CGG ATA GGC ATA ATA TTG CTG ACA GTA ATA

For VkII A1 the oligonucleotides are as follows:

5' CM3-VL-A-SacI (SEQ ID NO: 808)
CCT GTA GAG CTC GTG ATG ACC CAA TCT CCA SYT TCT TTG SCT GTG
ACT CTA GGG CAG CSG GCC TCC ATC TCC TGC
3' CM3-VL-Ba (SEQ ID NO: 809)
GAA CCA ACT CAT ATA ACT ACC ACC ATC ATA ATC AAC ACT TTG GCT
GGC CTT GCA GGA GAT GGA GGC
3' CM3-VL-Bb (SEQ ID NO: 810)
GAA CCA ACT CAT ATA ACT ACC ACC ATC ATA ATC AAC ACT AGA TTG
GCT GGC CTT GCA GGA GAT GGA GGC
5' CM3-VL-C (SEQ ID NO: 811)
AGT TAT ATG AGT TGG TTC CAA CAG AGA CCA GGA CAG YCA CCC ARA
CKC CTC ATC TMT GCT GCA TCC AAT CTA
3' CM3-VL-D (SEQ ID NO: 812)
GGT GAA GTC TGT CCC AGA GCC ACT GCC ACT AAA CCT GKC TGG GAY
CCC AGA TTC TAG ATT GGA TGC AGC
5' CM3-VL-E (SEQ ID NO: 813)

TCT GGG ACA GAC TTC ACC CTC AAK ATC YMT CST GTG GAG GMG GAG
GAT GTT GSA RYC TAT TACT GT CAG CAA AGT

3' CM3-VL-F-BsiWI/SpeI (SEQ ID NO: 814)

CCT CAG ACT AGT CGT ACG TTT GAT CTC CAG CTT GGT CCC CTG ACC
GAA CGT GAG CGG ATC CTC ATA ACT TTG CTG ACA GTA ATA

Each of these primer sets spans over the whole corresponding VL sequence.

Within each set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

Each VL PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VL approximately 330 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VL DNA fragment is amplified.

The final VH1 1-03 -based VH PCR product (i.e. the repertoire of human/humanized VH) is then combined with the final VkII O11 -based VL PCR product (i.e. the repertoire of human/humanized VL) and the final VH1 1-46-based VH PCR product (i.e. the repertoire of human/humanized VH) with the final VkII A1-based VL PCR product (i.e. the repertoire of human/humanized VL) in the phage display vector pComb3H5Bhis to form two different libraries of functional scFvs from which – after display on filamentous phage - anti-C-MET binders are selected, screened, identified and confirmed as described in the following:

450 ng of the light chain fragments (SacI-SpeI digested) are ligated with 1400 ng of the phagemid pComb3H5Bhis (SacI-SpeI digested; large fragment). The resulting combinatorial antibody library is then transformed into 300 µl of electrocompetent Escherichia coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm, Biorad gene-pulser) resulting in a library size of more than 10^7 independent clones. After one hour of phenotype expression, positive transformants are selected for carbenicilline resistance encoded by the pComb3H5BHis vector in 100 ml of liquid super broth (SB)-culture over night. Cells are then harvested by

centrifugation and plasmid preparation is carried out using a commercially available plasmid preparation kit (Qiagen).

2800 ng of this plasmid-DNA containing the VL-library (XhoI-BstEII digested; large fragment) are ligated with 900 ng of the heavy chain V-fragments (XhoI-BstEII digested) and again transformed into two 300 µl aliquots of electrocompetent E. coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm) resulting in a total VH-VL scFv (single chain variable fragment) library size of more than 10^7 independent clones.

After phenotype expression and slow adaptation to carbenicillin, the E. coli cells containing the antibody library are transferred into SB-carbenicillin (SB with 50 µg/mL carbenicillin) selection medium. The E. coli cells containing the antibody library are then infected with an infectious dose of 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein each phage particle contains single stranded pComb3H5BHis-DNA encoding a scFv-fragment and displays the corresponding scFv-protein as a translational fusion to phage coat protein III. This pool of phages displaying the antibody library is used for the selection of antigen binding entities.

For this purpose the phage library carrying the cloned scFv-repertoire is harvested from the respective culture supernatant by PEG8000/NaCl precipitation and centrifugation. Approximately $10^{11}$to 10^{12} scFv phage particles are resuspended in 0.4 ml of PBS/0.1% BSA and incubated with 10^5 to 10^7 C-MET transfected CHO cells (see example 26.1) for 1 hour on ice under slow agitation. These C-MET transfected CHO cells are harvested beforehand by centrifugation, washed in PBS and resuspended in PBS/1 % FCS (containing Na Azide). scFv phage which do not specifically bind to the C-MET transfected CHO cells are eliminated by up to five washing steps with PBS/1 % FCS (containing Na Azide). After washing, binding entities are eluted from the cells by resuspending the cells in HCl-glycine pH 2.2 (10 min incubation with subsequent vortexing) and after neutralization with 2 M Tris pH 12, the eluate is used for infection of a fresh uninfected E. coli XL1 Blue culture (OD600 > 0.5). The E. coli culture containing E. coli cells successfully transduced with a phagemid copy, encoding a human/humanized scFv-fragment, are again selected for carbenicillin resistance and subsequently infected with VCMS 13 helper phage to start the second round of antibody display and in vitro selection. A total of 4 to 5 rounds of selections are carried out, normally.

In order to screen for C-MET specific binders plasmid DNA corresponding to 4 and 5 rounds of panning is isolated from E. coli cultures after selection. For the production of soluble scFv-protein, VH-VL-DNA fragments are excised from the plasmids (XhoI-SpeI). These fragments are cloned via the same restriction sites into the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis in that the expression construct (e.g. scFv) includes a Flag-tag (DYKDDDDK) between the scFv and the His6-tag and the additional phage proteins are deleted. After ligation, each pool (different rounds of panning) of plasmid DNA is transformed into 100 µl heat shock competent E. coli TG1 or XLI blue and plated onto carbenicillin LB-agar. Single colonies are picked into 100 µl of LB carb (LB with 50 µg/ml carbenicillin).

E. coli transformed with pComb3H5BHis containing a VL-and VH-segment produce soluble scFv in sufficient amounts after excision of the gene III fragment and induction with 1 mM IPTG. Due to a suitable signal sequence, the scFv is exported into the periplasma where it folds into a functional conformation.

Single E. coli TG1 bacterial colonies from the transformation plates are picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM $MgCl_2$ and carbenicillin 50µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. A temperature shock is applied by four rounds of freezing at –70°C and thawing at 37°C whereby the outer membrane of the bacteria is destroyed and the soluble periplasmic proteins including the scFvs are released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the anti-C-MET scFvs is collected and used for the identification of C-MET specific binders as follows:

Binding of scFvs to C-MET is tested by flow cytometry on C-MET transfected CHO cells (see example 247.1); untransfected CHO cells are use as negative control.

For flow cytometry $2.5x10^5$ cells are incubated with 50 µl of scFv periplasmic preparation or with 5 µg/ml of purified scFv in 50 µl PBS with 2% FCS. The binding of scFv is detected with an anti-His antibody (Penta-His Antibody, BSA free, Qiagen GmbH, Hilden, FRG) at 2 µg/ml in 50 µl PBS with 2% FCS. As a second step reagent a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG (Fc-gamma fragment specific), diluted 1:100 in 50 µl PBS with 2% FCS (Dianova, Hamburg, FRG) is used. The samples are measured on a FACSscan (BD biosciences, Heidelberg, FRG).

Single clones are then analyzed for favourable properties and amino acid sequence.

C-MET specific scFvs are converted into recombinant bispecific single chain antibodies by joining them via a Gly_4Ser_1-linker with the CD3 specific scFv I2C (SEQ ID: 185) or any other CD3 specific scFv of the invention to result in constructs with the domain arrangement $VH_{C\text{-}MET}$ - $(Gly_4Ser_1)_3$ –$VL_{C\text{-}MET}$- $Ser_1Gly_4Ser_1$-VH_{CD3} - $(Gly_4Ser_1)_3$ - VL_{CD3} or alternative domain arrangements. For expression in CHO cells the coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His_6-tag followed by a stop codon are both attached in frame to the nucleotide sequence encoding the bispecific single chain antibodies prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). Transfection of the generated expression plasmids, protein expression and purification of cross-species specific bispecific antibody constructs are performed as described in Examples 26.3 and 26.4. All other state of the art procedures are carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)).

Identification of functional bispecific single-chain antibody constructs is carried out by flow cytometric binding analysis of culture supernatant from transfected cells expressing the cross-species specific bispecific antibody constructs. Analysis is perfomed as described in Example 26.5 except that in addition C-MET transfected CHO cells as described in examples 26.1 and 26.2 are used.

Only those constructs showing bispecific binding to human and macaque CD3 as well as to C-MET are selected for further use.

Cytotoxic activity of the generated cross-species specific bispecific single chain antibody constructs against C-MET positive target cells elicited by effector cells is analyzed as described in Example 26.6 except that in addition C-MET transfected CHO cells as described in examples 26.1 and 26.2 are used as target cells and the macaque T cell line 4119LnPx is used as effector cells. Only those constructs showing potent recruitment of cytotoxic activity of effector cells against cells positive for C-MET are selected for further use.

27. Generation and characterization of additional cMET and CD3 cross-species specific bispecific single chain molecules

27.1 Generation of CHO cells with enhanced expression of human cMET and CHO cells with enhanced expression of macaque cMET extracellular domains

The modified coding sequences of human cMET and macaque cMET as described above were used for the construction of artificial cDNA sequences encoding fusion proteins of the extracellular domains of human cMET and macaque cMET, respectively, with a truncated variant of human EpCAM. To generate a construct for expression of these cMET fusion proteins cDNA fragments were obtained by gene synthesis according to standard protocols (the cDNA and amino acid sequence of the constructs is listed under SEQ ID NOs 767 and 777 for human cMET and SEQ ID NOs 788 and 789 for macaque cMET). The gene synthesis fragments were designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by the coding sequence of a 19 amino acid immunoglobulin leader peptide, followed in frame by the the coding sequence of the human cMET or macaque cMET protein from amino acid 1 to 908 of the mature protein corresponding to the extracellular domains of human cMET and macaque cMET, respectively, followed in frame by the coding sequence of an artificial Ser_1-Gly_4-Ser_1-Gly_1-linker, followed in frame by the coding sequence of the transmembrane domain and intracellular domain of human EpCAM (as published in GenBank; Accession number NM_002354; amino acids 266 to 314 [as counted from the start codon] except for a point mutation at position 279 with isoleucine instead of valine) and a stop codon. The gene synthesis fragments were also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilized in the following cloning procedures. The gene synthesis fragments were cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. Clones with sequence-verified nucleotide sequence were transfected into DHFR deficient CHO cells for eukaryotic expression of the constructs. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the constructs was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

27.2 Generation of cMET and CD3 cross-species specific bispecific single chain molecules

Cloning of cross-species specific binding molecules

Bispecific single chain antibody molecules, with a binding specificity cross-species specific for human and non-chimpanzee primate CD3epsilon as well as a binding specificity cross-species specific for human and non-chimpanzee primate cMET, were designed as set out in the following Table 10:

Table 10: Formats of anti-CD3 and anti-cMET cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
1413/1412/	ME86H11HLxI2CHL
1427/1426/	ME62A12HLxI2CHL
1441/1440	ME63F2HLxI2CHL
1455/1454	ME62D11HLxI2CHL
1469/1468	ME62C10HLxI2CHL
1483/1482	ME62A4HLxI2CHL

Generation, expression and purification of these cross-species specific bispecific single chain molecules was performed as described above.

The flow cytometric binding analysis of the cMET and CD3 cross-species specific bispecific antibodies was performed as described above. The bispecific binding of the single chain molecules listed above, which are cross-species specific for cMET and cross-species specific for human and non-chimpanzee primate CD3 was clearly detectable as shown in Figure 54. In the FACS analysis all constructs showed binding to CD3 and cMET compared to the negative control. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and cMET antigens was demonstrated. Analysis of bioactivity by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays is performed as described above. Based on demonstrated cross-species specific bispecific binding and recruited cytotoxicity cross-species specific binding molecules are selected for further use.

27.3 Generation and flow cytometric binding analysis of cross-species specific single chain antibody fragments (scFv) binding to cMET

scFv cross-species specific for cMET were generated as described above and designated as set out in the following Table 11:

Table 11: Designation of cross-species specific single chain antibody fragments

SEQ ID (nucl/prot)	Designation
1649/1648	ME06F2HL
1635/1634	ME06E10HL
1621/1620	ME06D2HL
1607/1606	ME06D1HL
1579/1578	ME06C7HL
1565/1564	ME06C6HL
1593/1592	ME06B7HL
1551/1550	ME05F6HL
1523/1522	ME05D7HL
1537/1536	ME05B7HL
1509/1508	ME99B1HL
1495/1494	ME75H6HL

The flow cytometric binding analysis of periplasmic preparations containing scFv cross-species specific for cMET using CHO cells expressing human cMET as described in Example 27.1 and CHO cells expressing macaque cMET as described in Example 27.1 was performed as described above. The binding of the scFv listed above, which are cross-species specific for cMET was clearly detectable as shown in Figure 56. In the FACS analysis all constructs showed binding to cMET compared to the negative control. Cross-species specificity of the scFv antibodies to human and macaque cMET antigens was demonstrated.

Cloning of cross-species specific binding molecules based on the scFvs and expression and purification of these cross-species specific bispecific single chain molecules is performed as described above. Flow cytometric analysis of cross-species specific bispecific binding and analysis of bioactivity by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays is performed as described above. Based on demonstrated cross-species specific bispecific binding and recruited cytotoxicity cross-species specific binding molecules are selected for further use.

Human/humanized equivalents of non-human scFvs cross-species specific for cMET contained in the selected cross-species specific bispecific single chain molecules are generated as described herein. Cloning of cross-species specific binding molecules based on these human/humanized scFvs and expression and purification of these cross-species specific bispecific single chain molecules is performed as described above. Flow cytometric analysis of cross-species specific bispecific binding and analysis of bioactivity by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays is performed as described above. Based on demonstrated cross-species specific bispecific binding and recruited cytotoxicity cross-species specific binding molecules are selected for further use.

28. Generation and characterization of Endosialin and CD3 cross-species specific bispecific single chain antibody molecules

28.1 Generation of CHO cells expressing human Endosialin

The coding sequence of human Endosialin as published in GenBank (Accession number NM_020404) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by the coding sequence of human Endosialin, followed in frame by the coding sequence of a FLAG tag and a stop codon (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 913 and 914). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and XbaI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and XbaI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by

increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

28.2 Generation of CHO cells expressing macaque Endosialin

The cDNA sequence of macaque Endosialin was obtained by a set of 2 PCRs on cDNA from macaque monkey (cynomolgus) colon prepared according to standard protocols. The following reaction conditions: 1 cycle at 95°C for 5 minutes followed by 40 cycles with 95°C for 45 seconds, 50°C for 45 seconds and 72°C for 2 minutes followed by a terminal cycle of 72°C for 5 minutes and the following primers were used for the first PCR:

forward primer: 5'-atatgaattcgccaccatgctgctgcgcctgttgctggcc-3' SEQ ID NO 917

reverse primer: 5'-gtcttcatcttcctcatcctcccc-3' SEQ ID NO 918

The following reaction conditions: 1 cycle at 95°C for 5 minutes followed by 40 cycles with 95°C for 45 seconds, 58°C for 45 seconds and 72°C for 2 minutes followed by a terminal cycle of 72°C for 5 minutes and the following primers were used for the second PCR:

forward primer: 5'-gtcaactacgttggtggcttcgagtg-3' SEQ ID NO 919

reverse primer: 5'-ggtctagatcacttatcgtcatcatctttgtagtccacgctggttctgcaggtctgc-3' SEQ ID NO 920

The PCR reactions were performed under addition of PCR grade betain to a final concentration of 1M. Those PCRs generated two overlapping fragments, which were isolated and sequenced according to standard protocols using the PCR primers, and thereby provided a portion of the cDNA sequence coding macaque Endosialin from codon 9 of the leader peptide to codon 733 of the mature protein. To generate a construct for expression of macaque Endosialin a cDNA fragment was obtained by gene synthesis according to standard protocols (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 915 and 916). In this construct the coding sequence of macaque Endosialin from amino acid 9 of the leader peptide to amino acid 733 of the mature Endosialin protein, followed in frame by the coding sequence of amino acid 734 to the last amino acid of the mature human Endosialin protein, followed in frame by the coding sequence of a FLAG tag and a stop codon was fused in frame to the coding sequence of the amino acids 1 to 8 of the leader peptide of the human Endosialin protein. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the fragment containing the cDNA. The introduced

restriction sites, EcoRI at the 5' end and XbaI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and XbaI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

28.3 Cross-species specific binding to Endosialin of a scFv-antibody fragment

The cDNA of a scFv-antibody fragment was obtained by gene synthesis according to standard protocols. The cDNA fragment was cloned via suitable restriction sites into the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis (described below) in that the expression construct (e.g. scFv) includes a Flag-tag (DYKDDDDK SEQ ID NO 933) between the scFv-fragment and the His6-tag and the additional phage proteins are deleted. After ligation, a sequence verified clone of the plasmid DNA was transformed into 100 µl heat shock competent E. coli TG1 or XLI blue and plated onto carbenicillin LB-agar. Single colonies were picked into 100 µl of LB carb (LB with 50 µg/ml carbenicillin).

After induction with 1 mM IPTG E. coli transformed with pComb3H5BFlag/His containing the coding sequence of the cross-species specific single-chain antibody produced soluble scFv in sufficient amounts. Due to a suitable signal sequence, the scFv-chain is exported into the periplasma where it folds into a functional conformation.

Single E. coli bacterial colonies from the transformation plates were picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM $MgCl_2$ and carbenicillin 50µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. A temperature shock was applied by four rounds of freezing at –70°C and thawing at 37°C whereby the outer membrane of the bacteria is destroyed and the soluble periplasmic proteins including the scFv-molecules are

released into the supernatant. After elimination of intact cells and cell-debris by centrifugation the supernatant containing the scFv-antibody fragment was collected and used in the subsequent flow cytometric binding analysis with the CHO cells transfected with human Endosialin as described in Example 28.1 and the macaque Endosialin transfectant described in Example 28.2.

To this end 200.000 cells of the respective cell lines were incubated for 30 min on ice with 50 µl of the periplasmic preparation containing the cross-species specific single-chain antibody. The cells were washed twice in PBS with 2% FCS and binding of the construct was detected with a murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Untransfected CHO cells were used as a negative control.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

As shown in Figure 46, specific binding of the scFv-antibody fragment to both, human and macaque Endosialin could be demonstrated compared to the negative control.

28.4 Generation of Endosialin and CD3 cross-species specific bispecific single chain molecules

The human antibody germline VH sequence VH1 1-03 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRH1 (SEQ ID 910), CDRH2 (SEQ ID 911) and CDRH3 (SEQ ID 912). For the human VH several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. For VH1 1-03 the following set of oligonucleotides is used:

5'ED-VH-A-XhoI
CCA GCT CTC GAG TCA GGA SCT GAG STG RWG AAG CCT GGG GCT TCA GTG AAG RTG TCC TGC AAG GCT TCT GGA TAC ACA TTC ACT SEQ ID NO 921

3'ED-VH-B
AAT ATA TCC MAT CCA CTC AAG GCK CTK TCC AKK TSY CTG CYT CAY CCA GTG TAT AAC ATA GTC AGT GAA TGT GTA TCC AGA SEQ ID NO 922

5'ED-VH-C
CTT GAG TGG ATK GGA TAT ATT AAT CCT TAT GAT GAT GAT ACTA CC TAC AAC CAG AAG TTC AAG GGC SEQ ID NO 923

3'ED-VH-D
T GAG CTS CAT GTA GGC TGT GYT GGM GGA TKT GWC TMS AGT MAW TGT GRC CYG GCC CTT GAA CTT CTG GTT SEQ ID NO 924
5'ED-VH-E
C ACA GCC TAC ATG SAA CTC ARC AGC CTG ASA TCT GAG GAC ACT GCA GTC TAT TAC TGT GCA AGA AGG GGG SEQ ID NO 925
3'ED-VH-F-BstEII
CCT GAT GGT GAC CAA GGT TCC TTG ACC CCA GTA GTC CAT AGA ATA GTC GAA GTA ACC ATC ATA GGA GTT CCC CCT TCT TGC ACA GTA SEQ ID NO 926
This primer set spans over the whole corresponding VH sequence.

Within the set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

The VH PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VH approximately 350 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VH DNA fragment is amplified.

The human antibody germline VL sequence VkI L8 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID 907), CDRL2 (SEQ ID 908) and CDRL3 (SEQ ID 909). For the human VL several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. Restriction sites needed for later cloning within the oligonucleotides are deleted. For VkI L8 the following oligonucleotides are used:

5'ED-VL-A-SacI
CCA GTC GAG CTC CAG CTG ACC CAG TCT CMA ARM TTC MTG TCC RCA TCA GTA GGA GAC AGA GTC NNS ATC ACC TGC AGG GCC AG (SEQ ID NO 927)
3'ED-VL-B
TCC TGG TTT CTG TTG ATA CCA GGC TAC AGC AGT ACC CAC ATT CTG ACT GGC CCT GCA GGT GAT (SEQ ID NO 928)
5'ED-VL-C

TAT CAA CAG AAA CCA GGA MAA KCC CCT AAA TTA CTG ATT TACT CG GCA TCG AAT CGG TAC ACT GGA GTC CCT (SEQ ID NO 929)

3'ED-VL-D

GCT GAT GGT GAG AGT GAA MTC TGT CCC AGA TCC ACT GCC TGA GAA GCG AYY AGG GAC TCC AGT GTA CCG (SEQ ID NO 930)

5'ED-VL-E

TTC ACT CTC ACC ATC AGC ART MTG CAG YCT GAA GAC YTS GCA RMT TAT TWC TGC CAG CAA TAT ACC AAC (SEQ ID NO 931)

3'ED-VL-F-BsiWI/SpeI

CCT GAT ACT AGT CGT ACG TTT TAT TTC CAG CTT GGT CCC CTG TCC AAA CGT ATA CAT GGG ATA GTT GGT ATA TTG CTG GCA (SEQ ID NO 932)

This primer set spans over the whole corresponding VL sequence.

Within the set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

The VL PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VL approximately 330 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VL DNA fragment is amplified.

The final VH1 1-03 -based VH PCR product (i.e. the repertoire of human/humanized VH) is then combined with the final VkI L8 -based VL PCR product (i.e. the repertoire of human/humanized VL) in the phage display vector pComb3H5Bhis to form a library of functional scFvs from which – after display on filamentous phage - anti-Endosialin binders are selected, screened, identified and confirmed as described in the following:

450 ng of the light chain fragments (SacI-SpeI digested) are ligated with 1400 ng of the phagemid pComb3H5Bhis (SacI-SpeI digested; large fragment). The resulting combinatorial antibody library is then transformed into 300 µl of electrocompetent Escherichia coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm, Biorad gene-pulser) resulting in a library size of more than 10^7 independent clones. After one hour of phenotype expression, positive transformants

are selected for carbenicillin resistance encoded by the pComb3H5BHis vector in 100 ml of liquid super broth (SB)-culture over night. Cells are then harvested by centrifugation and plasmid preparation is carried out using a commercially available plasmid preparation kit (Qiagen).

2800 ng of this plasmid-DNA containing the VL-library (XhoI-BstEII digested; large fragment) are ligated with 900 ng of the heavy chain V-fragments (XhoI-BstEII digested) and again transformed into two 300 µl aliquots of electrocompetent E. coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm) resulting in a total VH-VL scFv (single chain variable fragment) library size of more than 10^7 independent clones.

After phenotype expression and slow adaptation to carbenicillin, the E. coli cells containing the antibody library are transferred into SB-carbenicillin (SB with 50 µg/mL carbenicillin) selection medium. The E. coli cells containing the antibody library are then infected with an infectious dose of 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein each phage particle contains single stranded pComb3H5BHis-DNA encoding a scFv-fragment and displays the corresponding scFv-protein as a translational fusion to phage coat protein III. This pool of phages displaying the antibody library is used for the selection of antigen binding entities.

For this purpose the phage library carrying the cloned scFv-repertoire is harvested from the respective culture supernatant by PEG8000/NaCl precipitation and centrifugation. Approximately 10^{11} to 10^{12} scFv phage particles are resuspended in 0.4 ml of PBS/0.1% BSA and incubated with 10^5 to 10^7 Endosialin transfected CHO cells (see example 28.1) for 1 hour on ice under slow agitation. These Endosialin transfected CHO cells are harvested beforehand by centrifugation, washed in PBS and resuspended in PBS/1 % FCS (containing Na Azide). scFv phage which do not specifically bind to the Endosialin transfected CHO cells are eliminated by up to five washing steps with PBS/1 % FCS (containing Na Azide). After washing, binding entities are eluted from the cells by resuspending the cells in HCl-glycine pH 2.2 (10 min incubation with subsequent vortexing) and after neutralization with 2 M Tris pH 12, the eluate is used for infection of a fresh uninfected E. coli XL1 Blue culture (OD600 > 0.5). The E. coli culture containing E. coli cells successfully transduced with a phagemid copy, encoding a human/humanized scFv-fragment, are again selected for carbenicillin resistance and subsequently infected with VCMS 13 helper

phage to start the second round of antibody display and in vitro selection. A total of 4 to 5 rounds of selections are carried out, normally.

In order to screen for Endosialin specific binders plasmid DNA corresponding to 4 and 5 rounds of panning is isolated from E. coli cultures after selection. For the production of soluble scFv-protein, VH-VL-DNA fragments are excised from the plasmids (XhoI-SpeI). These fragments are cloned via the same restriction sites into the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis in that the expression construct (e.g. scFv) includes a Flag-tag (DYKDDDDK) between the scFv and the His6-tag and the additional phage proteins are deleted. After ligation, each pool (different rounds of panning) of plasmid DNA is transformed into 100 µl heat shock competent E. coli TG1 or XLI blue and plated onto carbenicillin LB-agar. Single colonies are picked into 100 µl of LB carb (50 µg/ml).

After induction with 1 mM IPTG E. coli transformed with pComb3H5BFlag/His containing a VL-and VH-segment produce soluble scFv in sufficient amounts. Due to a suitable signal sequence, the scFv-chain is exported into the periplasma where it folds into a functional conformation.

Single E. coli TG1 bacterial colonies from the transformation plates are picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM $MgCl_2$ and carbenicillin 50 µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. A temperature shock is applied by four rounds of freezing at –70°C and thawing at 37°C whereby the outer membrane of the bacteria is destroyed and the soluble periplasmic proteins including the scFvs are released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the anti-Endosialin scFvs is collected and used for the identification of Endosialin specific binders as follows:

Binding of scFvs to Endosialin is tested by flow cytometry on Endosialin transfected CHO cells (see example 28.1); untransfected CHO cells are use as negative control.

For flow cytometry $2.5x10^5$ cells are incubated with 50 µl of scFv periplasmic preparation or with 5 µg/ml of purified scFv in 50 µl PBS with 2% FCS. The binding of scFv is detected with an anti-His antibody (Penta-His Antibody, BSA free, Qiagen GmbH, Hilden, FRG) at 2 µg/ml in 50 µl PBS with 2% FCS. As a second step reagent a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG (Fc-gamma fragment specific), diluted 1:100 in 50 µl PBS with 2% FCS (Dianova,

Hamburg, FRG) is used. The samples are measured on a FACSscan (BD biosciences, Heidelberg, FRG).

Single clones are then analyzed for favourable properties and amino acid sequence. Endosialin specific scFvs are converted into recombinant bispecific single chain antibodies by joining them via a Gly4Ser1-linker with the CD3 specific scFv I2C (SEQ ID NO: 185) or any other CD3 specific scFv of the invention to result in constructs with the domain arrangement VH Endosialin - (Gly4Ser1)3 –VL Endosialin - Ser1Gly4Ser1-VHCD3 - (Gly4Ser1)3 - VLCD3 or alternative domain arrangements. For expression in CHO cells the coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His6-tag followed by a stop codon are both attached in frame to the nucleotide sequence encoding the bispecific single chain antibodies prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). A clone with sequence-verified nucleotide sequence is transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells is performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct is induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

28.5 Expression and purification of bispecific single chain antibody molecules

Bispecific single chain antibody molecules are expressed in Chinese hamster ovary cells (CHO or HEK 293 cells as described herein above for the MCSPxCD3 bispecific single chain antibodies.

The isolation and analysis of the expressed bispecific single chain antibodies has also been described herein above in Example 9.

28.6 Flow cytometric binding analysis of the Endosialin and CD3 cross-species specific bispecific antibodies

In order to test the functionality of cross-species specific bispecific antibody constructs regarding the capability to bind to human and macaque Endosialin and CD3, respectively, a FACS analysis is performed. For this purpose CHO cells transfected with human Endosialin as described in Example 28.1 and the human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) are

used to test the binding to human antigens. The binding reactivity to macaque antigens is tested by using the generated macaque Endosialin transfectant described in Example 28.2 and a macaque T cell line 4119LnPx (kindly provided by Prof Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; published in Knappe A, et al., and Fickenscher H., Blood 2000, 95, 3256-61). 200.000 cells of the respective cell lines are incubated for 30 min on ice with 50 µl of cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The cells are washed twice in PBS with 2% FCS and binding of the construct is detected with a murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies are detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Supernatant of untransfected cells is used as a negative control.
Flow cytometry is performed on a FACS-Calibur apparatus, the CellQuest software is used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity are performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).
Only those constructs showing bispecific binding to human and macaque CD3 as well as to Endosialin are selected for further use.

28.7 Bioactivity of Endosialin and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of generated bispecific single chain antibodies is analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the CHO cells transfected with human Endosialin described in Example 28.1 and the CHO cells transfected with macaque Endosialin described in Example 28.2. As effector cells stimulated human CD4/CD56 depleted PBMC or the macaque T cell line 4119LnPx are used, respectively.
The generation of stimulated human PBMC was described herein above in Example 11.
Target cells prepared and the assay was performed in analogy to the procedure described for the MCSPxCD3 bispecific single chain antibodies in example 11.
Only those constructs showing potent recruitment of cytotoxic activity of effector cells against cells positive for Endosialin are selected for further use.

29. Generation and characterization of CD248 (Endosialin) and CD3 cross-species specific bispecific single chain molecules

29.1 Generation of CD248 and CD3 cross-species specific bispecific single chain molecules

Cloning of cross-species specific binding molecules

Bispecific single chain antibody molecules, with a binding specificity cross-species specific for human and non-chimpanzee primate CD3epsilon as well as a binding specificity cross-species specific for human and non-chimpanzee primate CD248, were designed as set out in the following Table 13:

Table 13: Formats of anti-CD3 and anti-CD248 cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
1665/1664	EN00B12HLxI2CHL
1679/1678	EN00C3HLxI2CHL
1693/1692	EN01D5HLxI2CHL
1707/1706	EN00E4HLxI2CHL
1721/1720	EN00F7HLxI2CHL
1735/1734	EN00H6HLxI2CHL

Generation, expression and purification of these cross-species specific bispecific single chain molecules was performed as described above.

The flow cytometric binding analysis of the CD248 and CD3 cross-species specific bispecific antibodies was performed as described above. The bispecific binding of the single chain molecules listed above, which are cross-species specific for CD248 and cross-species specific for human and non-chimpanzee primate CD3 was clearly detectable as shown in Figure 58. In the FACS analysis all constructs showed binding to CD3 and CD248 compared to the negative control. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and CD248 antigens was demonstrated.

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays as described above. As shown in Figure 59 all of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against human CD248 positive

target cells elicited by stimulated human CD4/CD56 depleted PBMC and macaque CD248 positive target cells elicited by the macaque T cell line 4119LnPx.

30. Generation and characterization of EpCAM and CD3 cross-species specific bispecific single chain antibody molecules

30.1 Cloning and expression of human EpCAM antigen on CHO cells

The sequence of the human EpCAM antigen ('NM_002354, Homo sapiens tumor-associated calcium signal transducer 1 (TACSTD1), mRNA, National Center for Biotechnology Information, http://www.ncbi.nlm.nih.gov/entrez) was used to obtain a synthetic molecule by gene synthesis according to standard protocols. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and and restriction sites at the beginning and the end of the DNA. The introduced restriction sites XbaI at the 5' end and SalI at the 3' end were utilised during the cloning step into the expression plasmid designated pEFDHFR as described in Raum et al. (loc cit.). After sequence verification the plasmid was used to transfect CHO/dhfr- cells as follows. A sequence verified plasmid was used to transfect CHO/dhfr- cells (ATCC No. CRL 9096; cultivated in RPMI 1640 with stabilized glutamine obtained from Biochrom AG Berlin, Germany, supplemented with 10% FCS, 1% penicillin/streptomycin all obtained from Biochrom AG Berlin, Germany and nucleosides from a stock solution of cell culture grade reagents obtained from Sigma-Aldrich Chemie GmbH, Taufkirchen, Germany, to a final concentration of 10 µg/ml Adenosine, 10 µg/ml Deoxyadenosine and 10 µg/ml Thymidine, in an incubator at 37°C, 95% humidity and 7% CO_2). Transfection was performed using the PolyFect Transfection Reagent (Qiagen GmbH, Hilden, Germany) and 5 µg of plasmid DNA according to the manufacturer's protocol. After culturing for 24 hours cells were washed once with PBS and again cultured in the aforementioned cell culture medium except that the medium was not supplemented with nucleosides and dialysed FCS (obtained from Biochrom AG Berlin, Germany) was used. Thus the cell culture medium did not contain nucleosides and thereby selection was applied on the transfected cells. Approximately 14 days after transfection the outgrowth of resistant cells was observed. After an additional 7 to 14 days the transfectants were tested positive for EpCAM-expression by FACS. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene

amplification of the construct was induced by increasing concentrations of methothrexate (MTX) to a final concentration of up to 20 nM MTX.

30.2 Generation of EpCAM and CD3 cross-species specific bispecific single chain molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity for the human and the macaque CD3 antigen as well as a domain with a binding specificity for the human EPCAM antigen, were designed as set out in the following Table 14:

Table 14: Formats of anti-CD3 and anti-EpCAM cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
945/944	Ep 5-10 LH x I2C HL
949/948	Ep 5-10 LH x F12Q HL
947/946	Ep 5-10 LH x H2C HL
961/960	hEp 14-A1 LH x I2C HL
973/972	hEp 14-D2 LH x I2C HL
985/984	hEp 14-H8 LH x I2C HL
997/996	hEp 14-A6 LH x I2C HL
1009/1008	hEp 14-D1 LH x I2C HL
1033/1032	hEp 14-H4 LH x I2C HL
1045/1044	hEp 17-A6 LH x I2C HL
1057/1056	hEp 17-E9 LH x I2C HL
1079/1078	hEp 18-E3 LH x I2C HL
1091/1090	hEp 18-F11 LH x I2C HL
1103/1102	hEp 18-F12 LH x I2C HL
1115/1114	hEp 18-G1 LH x I2C HL
1127/1126	hEp 18-G9 LH x I2C HL
1021/1020	hEp 14-G6 LH x I2C HL
1777/1776	hEp 18-A6 LH x I2C HL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains specific for human EpCAM and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed and eukaryotic protein expression was performed in analogy to the procedure described in example 9 for the MCSPxCD3 cross-species specific single chain molecules.

30.3 Expression and purification of the single domain bispecific single chain antibody molecules

The single domain bispecific single chain antibody molecules were expressed in chinese hamster ovary cells (CHO) or HEK 293 cells as described herein above for the MCSPxCD3 bispecific single chain antibodies.

The isolation and analysis of the expressed bispecific single chain antibodies has also been described herein above in Example 9.

30.4 Flow cytometric binding analysis of the EpCAM and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs with regard to binding capability to human EpCAM and human / macaque CD3, a FACS analysis was performed. For this purpose the CHO cells transfected with human EpCAM as described in Example 30.1 and human CD3 positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used to check the binding to human antigens. The binding reactivity to macaque CD3 was tested by using a macaque T cell line 4119LnPx (kindly provided by Prof Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; Knappe A, et al., and Fickenscher H: Herpesvirus saimiri-transformed macaque T cells are tolerated and do not cause lymphoma after autologous reinfusion. Blood 2000;95:3256-61.) 200,000 cells of the respective cell population were incubated for 30 min on ice with 50 µl of the purified protein of the cross-species specific bispecific antibody constructs (e. g. 2 µg/ml) Alternatively the cell culture supernatant of transiently produced proteins was used. The cells were washed twice in PBS and binding of the construct was detected with an unlabeled murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in 50 µl PBS with 2% FCS. Fresh culture medium was used as a negative control.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

The binding ability of all EpCAM-directed bispecific single chain molecules were clearly detectable as shown in Figure 60. In the FACS analysis, all constructs showed binding to human and macaque CD3 and to human EpCAM compared to the negative control using culture medium and 1. and 2. detection antibody. In summary, the cross-species specificity of the bispecific antibody to human and macaque CD3 and human EpCAM could clearly be demonstrated.

30.5 Bioactivity of EpCAM and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 release in vitro cytotoxicity assays using the EpCAM positive cell line described in example 30.1. As effector cells stimulated human CD8 positive T cells or the macaque T cell line 4119LnPx were used.

Stimulated CD8+ T cells were obtained as follows:

The generation of stimulated human PBMC was described herein above in Example 11.

Target cells prepared and the assay was performed in analogy to the procedure described for the MCSPxCD3 bispecific single chain antibodies in example 11.

As shown in Figures 61 to 66, all of the indicated cross-species specific bispecific single chain antibody constructs revealed cytotoxic activity against human EpCAM positive target cells elicited by human CD8+ cells and against human EpCAM positive target cells elicited by the macaque T cell line 4119LnPx. As a negative control, an irrelevant bispecific single chain antibody was used.

30.6 Cloning and expression of murine EpCAM antigen and a human-murine EpCAM hybrid antigen on CHO cells

The sequence of the mouse EpCAM antigen ('NM 008532, Mus musculus tumor-associated calcium signal transducer 1 (Tacstd1), mRNA., National Center for Biotechnology Information, http://www.ncbi.nlm.nih.gov/entrez) was used to obtain a synthetic molecule by gene synthesis according to standard protocols. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the DNA. The introduced restriction sites XbaI at the 5' end and SalI at the 3' end were utilised during the cloning step into the expression plasmid designated pEFDHFR. After sequence verification the plasmid was used to transfect CHO/DHFR$^-$ cells as

described in example 30.1. The human-murine EpCAM hybrid antigen was generated by exchanging the murine Exon 2 (amino acids no 26 – 61) for the human Exon 2 amino acids to enable the identification of the epitopes recognised by the cross-species specific bispecific antibody constructs. The deduced sequence was used to obtain a synthetic molecule by gene synthesis and CHO cells were transfected as described above.

30.7 Flow cytometric binding analysis of the EpCAM and CD3 cross-species specific bispecific antibodies to different EpCAM antigens

In order to analyze the binding ability of the cross-species specific bispecific antibody constructs with regard to binding abilities to different epitopes on human or murine or on a human-mouse hybrid EpCAM, a FACS flow cytometry was performed. For this purpose the CHO cells transfected with human EpCAM as described in example 1, Cho cells transfected with murine EpCAM (example 30.6) and CHO cells transfected with a human-mouse EpCAM hybrid (example 30.6) were used to check the different binding patterns. 200,000 cells of the respective cell population were incubated for 30 min on ice with 50 µl of the cell culture supernatant of transiently produced proteins. The cells were washed twice in PBS and binding of the construct was detected with an unlabeled murine Penta His antibody (Qiagen; diluted 1:20 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in 50 µl PBS with 2% FCS. Fresh culture medium was used instead of cell culture supernatant from CHO cells transfected with the respective bispecific single chain antibody molecules as a negative control. As positive control for the expression of the murine EpCAM the detection with a rat derived unlabeled antibody specific for murine EpCAM (BD Pharmingen, #552370, Rat IgG2a,k) followed by PE labelled anti Rat IgG2a, κ specific antibody (BD Pharmingen, Heidelberg, #553930) was used.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002). For the purpose of comparison the median values of the fluorescence intensity was used to generate a bar chart.

The binding ability of all EpCAM-directed bispecific single chain molecules to CHO cells transfected with human EpCAM was clearly detectable as shown in Figure 67. None of the human EpCAM specific molecules elicited a median value significantly above the negative control when binding to murine EpCAM was analysed. The binding properties of the human EpCAM specific single chain bispecific antibody molecules to human-mouse EpCAM hybrid antigen revealed two subsets of molecules: Those without a detectable binding to the human-mouse EpCAM hybrid antigen (HD69 HL x I2C HL) and those with a median fluorescence intensity nearly at the level of the binding strength to the human EpCAM antigen (hEp 14-A1 LH x I2C HL; hEp 14-H8 LH x I2C HL; hEp 14-A6 LH x I2C HL; hEp 14-D1 LH x I2C HL; hEp 14-H4 LH x I2C HL; hEp 17-A6 LH x I2C HL; hEp 17-E9 LH x I2C HL; hEp 18-E3 LH x I2C HL; hEp 18-F11 LH x I2C HL; hEp 18-F12 LH x I2C HL; hEp 18-G1 LH x I2C HL; hEp 18-G9 LH x I2C HL; for SEQ ID NOs of the constructs see table 14). The divergent binding patterns of these two subsets of human EpCAM specific single chain bispecific antibody molecules demonstrate different epitopes on the human EpCAM antigen. Transplantation of the human EpCAM Exon 2 domain into the backbone of murine EpCAM led to gain of binding by the EpCAM-directed bispecific single chain molecules of this invention but not by the HD69 HL x I2C HL molecule.

Thus, the second binding domain of the EpCAM-CD3 bispecific single chain antibody of the invention binds to an epitope localized in amino acid residues 26 to 61 of the EGF-like domain 1 of EpCAM which is encoded by Exon 2 of the EpCAM gene. Said amino acid residues 26 to 61 of the EGF-like domain 1 of human EpCAM encoded by exon 2 of the EpCAM gene are shown in SEQ ID NO. 1130.

Accordingly the epitope of the EpCAM-directed bispecific single chain molecules of this invention is mapped to the Exon 2 region of human EpCAM, while other regions of EpCAM participate in forming the epitope of the HD69 HL x I2C HL molecule. Thus, the EpCAM-directed bispecific single chain molecules of this invention form a unique own class of EpCAM-binding molecules, that is clearly differentiated from former EpCAM-binding molecules based on the EpCAM-binder HD69.

31. Generation and characterization of FAP alpha and CD3 cross-species specific bispecific single chain antibody molecules

31.1 Generation of CHO cells expressing human FAP alpha

The coding sequence of human FAPalpha as published in GenBank (Accession number NM_004460) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct, followed by the coding sequence of the human FAPalpha protein and a stop codon (the cDNA and amino acid sequence of the construct is listed under SEQ ID NOs. 1149 and 1150). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, XmaI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via XmaI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

31.2 Generation of CHO cells expressing macaque FAP alpha

The cDNA sequence of macaque FAP alpha (Cynomolgus) was obtained by a set of four PCRs on cDNA from macaque monkey skin prepared according to standard protocols. The following reaction conditions: 1 cycle at 94°C for 3 minutes followed by 40 cycles with 94°C for 0.5 minutes, 56°C for 0.5 minutes and 72°C for 3 minutes followed by a terminal cycle of 72°C for 3 minutes and the following primers were used:

forward primer: 5'-cagcttccaactacaaagacagac-3' (SEQ ID NO. 1153)

reverse primer: 5'-tttcctcttcataaacccagtctgg-3' (SEQ ID NO. 1154)

forward primer: 5'-ttgaaacaaagaccaggagatccacc-3' (SEQ ID NO. 1155)
reverse primer: 5'-agatggcaagtaacacacttcttgc-3' (SEQ ID NO. 1156)
forward primer: 5'-gaagaaacatctacagaattagcattgg-3' (SEQ ID NO. 1157)
reverse primer: 5'-cacatttgaaaagaccagttccagatgc-3' (SEQ ID NO. 1158)
forward primer: 5'-agattacagctgtcagaaaattcatagaaatgg-3' (SEQ ID NO. 1159)
reverse primer: 5'-atataaggttttcagattctgatacaggc-3' (SEQ ID NO. 1160)

These PCRs generated four overlapping fragments, which were isolated and sequenced according to standard protocols using the PCR primers, and thereby provided the cDNA sequence coding macaque FAPalpha. To generate a construct for expression of macaque FAPalpha a cDNA fragment was obtained by gene synthesis according to standard protocols (the cDNA and amino acid sequence of the construct is listed under SEQ ID NOs. 1151 and 1152). This construct contains the complete coding sequence of macaque FAPalpha followed by a stop codon. The gene synthesis fragment was also designed as to contain a Kozak site for eukaryotic expression of the construct and restriction sites at the beginning and the end of the fragment containing the cDNA. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilised in the following cloning procedures. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

31.3 Generation of FAP alpha and CD3 cross-species specific bispecific single chain molecules

Cloning of cross-species specific binding molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity cross-species specific for human and non-chimpanzee primate

CD3 epsilon as well as a domain with a binding specificity cross-species specific for human and non-chimpanzee primate FAP alpha, were designed as set out in the following Table 15:

Table 15: Formats of anti-CD3 and anti-FAP alpha cross-species specific bispecific single chain antibody molecules

SEQ ID NO. (nucl/prot)	Formats of protein constructs (N → C)
1144/1143	FAPA-1 LH x I2C HL
1148/1147	FAPA-1 LH x F12Q HL
1146/1145	FAPA-1 LH x H2C HL

The aforementioned constructs containing the variable light-chain (L) and variable heavy-chain (H) domains cross-species specific for human and macaque FAP alpha and the CD3 specific VH and VL combinations cross-species specific for human and macaque CD3 were obtained by gene synthesis. The gene synthesis fragments were designed and eukaryotic protein expression was performed in analogy to the procedure described in example 9 for the MCSPxCD3 cross-species specific single chain molecules.

31.4 Expression and purification of the bispecific single chain antibody molecules

The bispecific single chain antibody molecules were expressed in Chinese hamster ovary cells (CHO) or HEK 293 cells as described herein above for the MCSPxCD3 bispecific single chain antibodies.

The isolation and analysis of the expressed bispecific single chain antibodies has also been described herein above in Example 9.

31.5 Flow cytometric binding analysis of the FAP alpha and CD3 cross-species specific bispecific antibodies

In order to test the functionality of the cross-species specific bispecific antibody constructs regarding the capability to bind to human and macaque FAPalpha and CD3, respectively, a FACS analysis was performed. For this purpose CHO cells transfected with human FAPalpha as described in Example 31.1 and the human CD3

positive T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used to test the binding to human antigens. The binding reactivity to macaque antigens was tested by using the generated macaque FAPalpha transfectant described in Example 31.2 and a macaque T cell line 4119LnPx (kindly provided by Prof Fickenscher, Hygiene Institute, Virology, Erlangen-Nuernberg; published in Knappe A, et al., and Fickenscher H., Blood 2000, 95, 3256-61). 200.000 cells of the respective cell lines were incubated for 30 min on ice with 50 µl of cell culture supernatant of transfected cells expressing the cross-species specific bispecific antibody constructs. The cells were washed twice in PBS with 2% FCS and binding of the construct was detected with a murine Penta His antibody (Qiagen; diluted 1:100 in 50 µl PBS with 2% FCS). After washing, bound anti His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS with 2% FCS. Supernatant of untransfected cells was used as a negative control.

Flow cytometry was performed on a FACS-Calibur apparatus, the CellQuest software was used to acquire and analyze the data (Becton Dickinson biosciences, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

The bispecific binding of the single chain molecules listed above, which are cross-species specific for FAPalpha and cross-species specific for human and non-chimpanzee primate CD3 was clearly detectable as shown in Figure 68. In the FACS analysis all constructs showed binding to CD3 and FAPalpha compared to the negative control. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and FAPalpha antigens was demonstrated.

31.6 Bioactivity of FAPalpha and CD3 cross-species specific bispecific single chain antibodies

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays using the CHO cells transfected with human FAPalpha described in Example 31.1 and the CHO cells transfected with macaque FAPalpha described in Example 31.2. As effector cells stimulated human CD4/CD56 depleted PBMC or the macaque T cell line 4119LnPx were used, respectively.

The generation of stimulated human PBMC was described herein above in Example 11.

Target cells prepared and the assay was performed in analogy to the procedure described for the MCSPxCD3 bispecific single chain antibodies in example 11.

As shown in Figure 69 all of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against human FAPalpha positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and macaque FAPalpha positive target cells elicited by the macaque T cell line 4119LnPx.

31.7 Generation of additional FAP alpha and CD3 cross-species specific bispecific single chain antibody molecules

The human antibody germline VH sequence VH1 1-03 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRH1 (SEQ ID NO. 1137), CDRH2 (SEQ ID NO. 1138) and CDRH3 (SEQ ID NO. 1139). For the human VH several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. For VH1 1-03 the following oligonucleotides are used:

5'FAP-VH-A-XhoI
CCG CTA CTC GAG TCT GGA SCT GAG STG RWG AAG CCT GGG GCT TCA GTA AAG (SEQ ID NO. 1161)
3'FAP-VH-B
CTG TCT CAC CCA GTG TAT GGT GTA TTC AGT GAA TGT GTA TCY AGA AGY CTT GCA GGA CAY CTT TAC TGA AGC CCC (SEQ ID NO. 1162)
5'FAP-VH-C
CAC TGG GTG AGA CAG KCC CMT GGA MAG AGM CTT GAG TGG ATK GGA GGT ATT AAT CCT AAC AAT GGT ATT CCT AAC TAC (SEQ ID NO. 1163)
3'FAP-VH-D
CAT GTA GGC GGT GCT GGM GGA CKT GYC TMY AGT TAW TGT GRC CCT GCC CTT GAA CTT CTG ATT GTA GTT AGG AAT ACC (SEQ ID NO. 1164)
5'FAP-VH-E
AGC ACC GCC TAC ATG GAG CTC MGC AGC CTG ASA TCT GAG GAT ACT GCG GTC TAT TWC TGT GCA AGA AGA AGA ATC GCC (SEQ ID NO. 1165)
3'FAP-VH-F-BstEII
CCA GTA GGT GAC CAG GGT TCC TTG ACC CCA GTA GTC CAT AGC ATG GCC CTC GTC GTA ACC ATA GGC GAT TCT TCT TCT TGC ACA (SEQ ID NO. 1166)

This primer set spans over the whole corresponding VH sequence.

Within the set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of

PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

The VH PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VH approximately 350 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VH DNA fragment is amplified.

The human antibody germline VL sequence VkII O11 (http://vbase.mrc-cpe.cam.ac.uk/) is chosen as framework context for CDRL1 (SEQ ID NO. 1132), CDRL2 (SEQ ID NO. 1133) and CDRL3 (SEQ ID NO. 1134). For this human VL several degenerated oligonucleotides have to be synthesized that overlap in a terminal stretch of approximately 15-20 nucleotides. To this end every second primer is an antisense primer. Restriction sites needed for later cloning within the oligonucleotides are deleted. For VkII O11 the following oligonucleotides are used:

5'FAP-VL-A-SacI
CGA CCT GAG CTC GTG ATG ACA CAG ACT CCA YYC TCC CTA SCT GTG ACA SYT GGA GAG MMG GYT TCT ATS AGC TGC AAG TCC AGT CAG (SEQ ID NO. 1167)

3'FAP-VL-B
AGA CTG CCC TGG CTT CTG CWG GWA CCA GGC CAA GTA GTT CTT TTG ATT ACG ACT ATA TAA AAG GCT CTG ACT GGA CTT GCA GCT (SEQ ID NO. 1168)

5'FAP-VL-C
CAG AAG CCA GGG CAG TCT CCT MAA CTG CTG ATT TWC TGG GCA TCC ACTA GG GAA TCT GGG GTC CCT GAT CGC TTC TCA GGC AGT GGA (SEQ ID NO. 1169)

3'FAP-VL-D
ATA TTG CTG ACA GTM ATA AAC TSC CAS GTC CTC AGC CTS CAC WCT GCT GAT CKT GAG AKT GAA ATC CGT CCC ARA TCC ACT GCC TGA GAA (SEQ ID NO. 1170)

3'FAP-VL-E-BsiWI/SpeI
CCA GTA ACT AGT CGT ACG TTT GAT CTC CAC CTT GGT CCC ACC ACC GAA CGT GAG CGG ATA GCT AAA ATA TTG CTG ACA GT (SEQ ID NO. 1171)

This primer set spans over the whole corresponding VL sequence.

Within the set primers are mixed in equal amounts (e.g. 1 µl of each primer (primer stocks 20 to 100 µM) to a 20 µl PCR reaction) and added to a PCR mix consisting of

PCR buffer, nucleotides and Taq polymerase. This mix is incubated at 94 °C for 3 minutes, 65 °C for 1 minute, 62°C for 1 minute, 59 °C for 1 minute, 56 °C for 1 minute, 52 °C for 1 minute, 50 °C for 1 minute and at 72°C for 10 minutes in a PCR cycler. Subsequently the product is run in an agarose gel electrophoresis and the product of a size from 200 to 400 isolated from the gel according to standard methods.

The VL PCR product is then used as a template for a standard PCR reaction using primers that incorporate N-terminal and C-terminal suitable cloning restriction sites. The DNA fragment of the correct size (for a VL approximately 330 nucleotides) is isolated by agarose gel electrophoresis according to standard methods. In this way sufficient VL DNA fragment is amplified.

The final VH1 1-03 -based VH PCR product (i.e. the repertoire of human/humanized VH) is then combined with the final VkII O11 -based VL PCR product (i.e. the repertoire of human/humanized VL) in the phage display vector pComb3H5Bhis to form a library of functional scFvs from which – after display on filamentous phage - anti-FAPalpha binders are selected, screened, identified and confirmed as described in the following:

450 ng of the light chain fragments (SacI-SpeI digested) are ligated with 1400 ng of the phagemid pComb3H5Bhis (SacI-SpeI digested; large fragment). The resulting combinatorial antibody library is then transformed into 300 µl of electrocompetent Escherichia coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm, Biorad gene-pulser) resulting in a library size of more than 10^7 independent clones. After one hour of phenotype expression, positive transformants are selected for carbenicillin resistance encoded by the pComb3H5BHis vector in 100 ml of liquid super broth (SB)-culture over night. Cells are then harvested by centrifugation and plasmid preparation is carried out using a commercially available plasmid preparation kit (Qiagen).

2800 ng of this plasmid-DNA containing the VL-library (XhoI-BstEII digested; large fragment) are ligated with 900 ng of the heavy chain V-fragments (XhoI-BstEII digested) and again transformed into two 300 µl aliquots of electrocompetent E. coli XL1 Blue cells by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 µFD, 200 Ohm) resulting in a total VH-VL scFv (single chain variable fragment) library size of more than 10^7 independent clones.

After phenotype expression and slow adaptation to carbenicillin, the E. coli cells containing the antibody library are transferred into SB-carbenicillin (SB with 50 µg/mL carbenicillin) selection medium. The E. coli cells containing the antibody library are then infected with an infectious dose of 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein each phage particle contains single stranded pComb3H5BHis-DNA encoding a scFv-fragment and displays the corresponding scFv-protein as a translational fusion to phage coat protein III. This pool of phages displaying the antibody library is used for the selection of antigen binding entities.

For this purpose the phage library carrying the cloned scFv-repertoire is harvested from the respective culture supernatant by PEG8000/NaCl precipitation and centrifugation. Approximately 10^{11} to 10^{12} scFv phage particles are resuspended in 0.4 ml of PBS/0.1% BSA and incubated with 10^5 to 10^7 FAPalpha transfected CHO cells (see example 31.1) for 1 hour on ice under slow agitation. These FAPalpha transfected CHO cells are harvested beforehand by centrifugation, washed in PBS and resuspended in PBS/1 % FCS (containing 0.05% Na Azide). scFv phage which do not specifically bind to the FAPalpha transfected CHO cells are eliminated by up to five washing steps with PBS/1 % FCS (containing 0.05% Na Azide). After washing, binding entities are eluted from the cells by resuspending the cells in HCl-glycine pH 2.2 (10 min incubation with subsequent vortexing) and after neutralization with 2 M Tris pH 12, the eluate is used for infection of a fresh uninfected E. coli XL1 Blue culture (OD600 > 0.5). The E. coli culture containing E. coli cells successfully transduced with a phagemid copy, encoding a human/humanized scFv-fragment, are again selected for carbenicillin resistance and subsequently infected with VCMS 13 helper phage to start the second round of antibody display and in vitro selection. Typically a total of 4 to 5 rounds of selections are carried out.

In order to screen for FAPalpha specific binders plasmid DNA corresponding to 4 and 5 rounds of panning is isolated from E. coli cultures after selection. For the production of soluble scFv-protein, VH-VL-DNA fragments are excised from the plasmids (XhoI-SpeI). These fragments are cloned via the same restriction sites into the plasmid pComb3H5BFlag/His differing from the original pComb3H5BHis in that the expression construct (e.g. scFv) includes a Flag-tag (DYKDDDDK) between the scFv and the His6-tag and the additional phage proteins are deleted. After ligation, each pool (different rounds of panning) of plasmid DNA is transformed into 100 µl heat

shock competent E. coli TG1 or XLI blue and plated onto carbenicillin LB-agar. Single colonies are picked into 100 µl of LB carb (LB with 50 µg/ml carbenicillin).

E. coli transformed with pComb3H5BFlag/His containing a VL-and VH-segment produce soluble scFv in sufficient amounts after induction with 1 mM IPTG. Due to a suitable signal sequence, the scFv is exported into the periplasma where it folds into a functional conformation.

Single E. coli bacterial colonies from the transformation plates are picked for periplasmic small scale preparations and grown in SB-medium (e.g. 10 ml) supplemented with 20 mM $MgCl_2$ and carbenicillin 50µg/ml (and re-dissolved in PBS (e.g. 1 ml) after harvesting. A temperature shock is applied by four rounds of freezing at –70°C and thawing at 37°C whereby the outer membrane of the bacteria is destroyed and the soluble periplasmic proteins including the scFvs are released into the supernatant. After elimination of intact cells and cell-debris by centrifugation, the supernatant containing the anti-FAPalpha scFvs is collected and used for the identification of FAPalpha specific binders as follows:

Binding of scFvs to FAPalpha is tested by flow cytometry on FAPalpha transfected CHO cells (see example 31.1); untransfected CHO cells are use as negative control.

For flow cytometry $2.5x10^5$ cells are incubated with 50 µl of scFv periplasmic preparation or with 5 µg/ml of purified scFv in 50 µl PBS with 2% FCS. The binding of scFv is detected with an anti-His antibody (Penta-His Antibody, BSA free, Qiagen GmbH, Hilden, FRG) at 2 µg/ml in 50 µl PBS with 2% FCS. As a second step reagent a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG (Fc-gamma fragment specific), diluted 1:100 in 50 µl PBS with 2% FCS (Dianova, Hamburg, FRG) is used. The samples are measured on a FACSscan (BD biosciences, Heidelberg, FRG).

Single clones are then analyzed for favorable properties and amino acid sequence.

FAPalpha specific scFvs are converted into recombinant bispecific single chain antibodies by joining them via a Gly_4Ser_1-linker with the CD3 specific scFv I2C (SEQ ID NO. 185) or any other CD3 specific scFv of the invention to result in constructs with the domain arrangement $VL_{FAPalpha}$ - $(Gly_4Ser_1)_3$ –$VH_{FAPalpha}$- $Ser_1Gly_4Ser_1$-VH_{CD3} - $(Gly_4Ser_1)_3$ - VL_{CD3} or alternative domain arrangements. For expression in CHO cells the coding sequences of (i) an N-terminal immunoglobulin heavy chain leader comprising a start codon embedded within a Kozak consensus sequence and (ii) a C-terminal His_6-tag followed by a stop codon are both attached in frame to the

nucleotide sequence encoding the bispecific single chain antibodies prior to insertion of the resulting DNA-fragment as obtained by gene synthesis into the multiple cloning site of the expression vector pEF-DHFR (Raum et al. Cancer Immunol Immunother 50 (2001) 141-150). Transfection of the generated expression plasmids, protein expression and purification of cross-species specific bispecific antibody constructs are performed as described in Examples 31.3 and 31.4. All other state of the art procedures are carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)).

Identification of functional bispecific single-chain antibody constructs is carried out by flow cytometric binding analysis of culture supernatant from transfected cells expressing the cross-species specific bispecific antibody constructs. Analysis is performed as described in Example 31.5. Only those constructs showing bispecific binding to human and macaque CD3 as well as to FAPalpha are selected for further use.

Cytotoxic activity of the generated cross-species specific bispecific single chain antibody constructs against FAPalpha positive target cells elicited by effector cells is analyzed as described in Example 31.6. Only those constructs showing potent recruitment of cytotoxic activity of effector cells against cells positive for FAPalpha are selected for further use.

32. Generation and characterization of additional FAPalpha and CD3 cross-species specific bispecific single chain molecules

32.1 Generation of FAPalpha and CD3 cross-species specific bispecific single chain molecules

Cloning of cross-species specific binding molecules

Bispecific single chain antibody molecules, with a binding specificity cross-species specific for human and non-chimpanzee primate CD3epsilon as well as a binding specificity cross-species specific for human and non-chimpanzee primate FAPalpha, were designed as set out in the following Table 16:

Table 16: Formats of anti-CD3 and anti-FAPalpha cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
1861/1860	FA19D12HLxI2CHL
1847/1846	FA20H3HLxI2CHL
1791/1790	FA22A9HLxI2CHL
1805/1804	FA22C11HLxI2CHL
1875/1874	FA19D9HLxI2CHL
1819/1818	FA22D8HLxI2CHL
1833/1832	FA22E8HLxI2CHL

Generation, expression and purification of these cross-species specific bispecific single chain molecules was performed as described above.

The flow cytometric binding analysis of the FAPalpha and CD3 cross-species specific bispecific antibodies was performed as described above. The bispecific binding of the single chain molecules listed above, which are cross-species specific for FAPalpha and cross-species specific for human and non-chimpanzee primate CD3 was clearly detectable as shown in Figure 70. In the FACS analysis all constructs showed binding to CD3 and FAPalpha compared to the negative control. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and FAPalpha antigens was demonstrated.

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays as described above. As shown in Figure 71 all of the generated cross-species specific bispecific single chain antibody constructs demonstrated cytotoxic activity against human FAPalpha positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and macaque FAPalpha positive target cells elicited by the macaque T cell line 4119LnPx.

32.2 Generation and flow cytometric binding analysis of cross-species specific single chain antibody fragments (scFv) binding to FAPalpha

scFv cross-species specific for FAPalpha were generated as described above and designated as set out in the following Table 17:

Table 17: Designation of cross-species specific single chain antibody fragments

SEQ ID (nucl/prot)	Designation

1901/1900	86C12HL
1887/1886	87G9HL
1971/1970	86F12HL
1957/1956	86F10HL
1985/1984	86F2HL
1943/1942	86E5HL
1929/1928	86D6HL
1915/1914	86D2HL

The flow cytometric binding analysis of periplasmic preparations containing scFv cross-species specific for FAPalpha using CHO cells transfected with human FAPalpha and CHO cells transfected with macaque FAPalpha was performed as described above. The binding of the scFv listed above, which are cross-species specific for FAPalpha was clearly detectable as shown in Figure 72. In the FACS analysis all constructs showed binding to FAPalpha compared to the negative control. Cross-species specificity of the scFv antibodies to human and macaque FAPalpha antigens was demonstrated.

Cloning of cross-species specific binding molecules based on the scFvs and expression and purification of these cross-species specific bispecific single chain molecules is performed as described above. Flow cytometric analysis of cross-species specific bispecific binding and analysis of bioactivity by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays is performed as described above. Based on demonstrated cross-species specific bispecific binding and recruited cytotoxicity cross-species specific binding molecules are selected for further use.

Human/humanized equivalents of non-human scFvs cross-species specific for FAPalpha contained in the selected cross-species specific bispecific single chain molecules are generated as described herein. Cloning of cross-species specific binding molecules based on these human/humanized scFvs and expression and purification of these cross-species specific bispecific single chain molecules is performed as described above. Flow cytometric analysis of cross-species specific bispecific binding and analysis of bioactivity by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays is performed as described above. Based on demonstrated cross-species specific bispecific binding and recruited cytotoxicity cross-species specific binding molecules are selected for further use.

33. Generation and characterization of IGF-1R and CD3 cross-species specific bispecific single chain molecules

33.1 Generation of CHO cells expressing human IGF-1R

The coding sequence of human IGF-1R as published in GenBank (Accession number NM_000875) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct followed by the coding sequence of the human IGF-1R protein and a stop codon (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 2011 and 2012). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI at the 3' end, were utilized in the following cloning procedures. Undesirable internal restriction sites were removed by silent mutation of the coding sequence in the gene synthesis fragment. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

33.2 Generation of CHO cells expressing macaque IGF-1R

The coding sequence of macaque IGF-1R as published in GenBank (Accession number XM_001100407) was obtained by gene synthesis according to standard protocols. The gene synthesis fragment was designed as to contain first a Kozak site for eukaryotic expression of the construct followed by the coding sequence of the macaque IGF-1R protein and a stop codon (the cDNA and amino acid sequence of the construct is listed under SEQ ID Nos 2013 and 2014). The gene synthesis fragment was also designed as to introduce restriction sites at the beginning and at the end of the fragment. The introduced restriction sites, EcoRI at the 5' end and SalI

at the 3' end, were utilized in the following cloning procedures. Undesirable internal restriction sites were removed by silent mutation of the coding sequence in the gene synthesis fragment. The gene synthesis fragment was cloned via EcoRI and SalI into a plasmid designated pEF-DHFR (pEF-DHFR was described in Raum et al. Cancer Immunol Immunother 50 (2001) 141-150) following standard protocols. The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). A clone with sequence-verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described by Kaufmann R.J. (1990) Methods Enzymol. 185, 537-566. Gene amplification of the construct was induced by increasing concentrations of methotrexate (MTX) to a final concentration of up to 20 nM MTX.

33.3 Generation of IGF-1R and CD3 cross-species specific bispecific single chain molecules

Cloning of cross-species specific binding molecules

Generally, bispecific single chain antibody molecules, each comprising a domain with a binding specificity cross-species specific for human and non-chimpanzee primate CD3epsilon as well as a domain with a binding specificity cross-species specific for human and non-chimpanzee primate IGF-1R, were designed as set out in the following Table 18:

Table 18: Formats of anti-CD3 and anti-IGF-1R cross-species specific bispecific single chain antibody molecules

SEQ ID (nucl/prot)	Formats of protein constructs (N → C)
2028/2027	IGF1R2HLxI2CHL
2042/2041	IGF1R7HLxI2CHL
2056/2055	IGF1R9HLxI2CHL
2070/2069	IGF1R10HLxI2CHL
2084/2083	IGF1R11HLxI2CHL
2098/2097	IGF1R12HLxI2CHL
2112/2111	IGF1R13HLxI2CHL
2126/2125	IGF1R15HLxI2CHL

2140/2139	IGF1R16HLxI2CHL
2154/2153	IGF1R17HLxI2CHL
2168/2167	IGF1R19HLxI2CHL
2182/2181	IGF1R20HLxI2CHL
2196/2195	IGF1R21HLxI2CHL
2210/2209	IGF1R23HLxI2CHL
2224/2223	IGF1R24HLxI2CHL

Generation, expression and purification of these cross-species specific bispecific single chain molecules was performed as described above.

The flow cytometric binding analysis of the IGF-1R and CD3 cross-species specific bispecific antibodies was performed as described above. The bispecific binding of the single chain molecules listed above, which are cross-species specific for IGF-1R and cross-species specific for human and non-chimpanzee primate CD3 was clearly detectable as shown in Figure 73. In the FACS analysis all constructs showed binding to CD3 and IGF-1R compared to the negative control. Cross-species specificity of the bispecific antibodies to human and macaque CD3 and IGF-1R antigens was demonstrated.

Bioactivity of the generated bispecific single chain antibodies was analyzed by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays as described above. All the cross-species specific bispecific single chain antibody constructs shown in Figure 74 demonstrated cytotoxic activity against human IGF-1R positive target cells elicited by stimulated human CD4/CD56 depleted PBMC and macaque IGF-1R positive target cells elicited by the macaque T cell line 4119LnPx.

Human/humanized equivalents of non-human scFvs cross-species specific for IGF-1R contained in the cross-species specific bispecific single chain molecules are generated as described herein. Cloning of cross-species specific binding molecules based on these human/humanized scFvs and expression and purification of these cross-species specific bispecific single chain molecules is performed as described above. Flow cytometric analysis of cross-species specific bispecific binding and analysis of bioactivity by chromium 51 (^{51}Cr) release in vitro cytotoxicity assays is performed as described above. Based on demonstrated cross-species specific bispecific binding and recruited cytotoxicity cross-species specific binding molecules are selected for further use.

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
1.	Human CD3 epsilon extracellular domain	human	aa	QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKE FSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMD
2.	Human CD3 epsilon 1-27	human	aa	QDGNEEMGGITQTPYKVSISGTTVILT
3.	*Callithrix jacchus* CD3 epsilon extracellular domain	*Callithrix jacchus*	aa	QDGNEEMGDTTQNPYKVSISGTTVTLTCPRYDGHEIKWLVNSQNKEGHEDHLLLEDFSEMEQSGY YACLSKETPAEEASHYLYLKARVCENCVEVD
4.	*Callithrix jacchus* CD3 epsilon 1-27	*Callithrix jacchus*	aa	QDGNEEMGDTTQNPYKVSISGTTVTLT
5.	*Saguinus oedipus* CD3 epsilon extracellular domain	*Saguinus oedipus*	aa	QDGNEEMGDTTQNPYKVSISGTTVTLTCPRYDGHEIKWLVNSQNKEGHEDHLLLEDFSEMEQSGY YACLSKETPAEEASHYLYLKARVCENCVEVD
6.	*Saguinus oedipus* CD3 epsilon 1-27	*Saguinus oedipus*	aa	QDGNEEMGDTTQNPYKVSISGTTVTLT
7.	*Saimiri sciureus* CD3 epsilon extracellular domain	*Saimiri sciureus*	aa	QDGNEEIGDTTQNPYKVSISGTTVTLTCPRYDGQEIKWLVNDQNKEGHEDHILLEDFSEMEQSGY YACLSKETPTEEASIIYLYLKARVCENCVEVD
8.	*Saimiri sciureus* CD3 epsilon 1-27	*Saimiri sciureus*	aa	QDGNEEIGDTTQNPYKVSISGTTVTLT
9.	CDR-L1 of F6A	artificial	aa	GSSTGAVTSGYYPN
10.	CDR-L2 of F6A	artificial	aa	GTKFLAP
11.	CDR-L3 of F6A	artificial	aa	ALWYSNRWV
12.	CDR-H1 of F6A	artificial	aa	IYAMN
13.	CDR-H2 of F6A	artificial	aa	RIRSKYNNYATYYADSVKS
14.	CDR-H3 of F6A	artificial	aa	HGNFGNSYVSFFAY
15.	VH of F6A	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSS
16.	VH of F6A	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATATCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGTAATGGGTTGCTCGCATAAGAAGTAATATAATAATGCAACATATTATGCCGATTCA GTGAAAAGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TATCCTTCTTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
17.	VL of F6A	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

18.	VL of F6A	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
19.	VH-P of F6A	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSS
20.	VH-P of F6A	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATATCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TATCCTTCTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
21.	VL-P of F6A	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
22.	VL-P of F6A	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
23.	VH-VL of F6A	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
24.	VH-VL of F6A	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATATCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TATCCTTCTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG

				TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
25.	VH-VL-P of F6A	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
26.	VH-VL-P of F6A	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATATCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGCAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TATCCTTCTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACACTCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAAATATTACTGTGTCTATGGTACAGCAACCCCCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
27.	CDR-L1 of H2C	artificial	aa	GSSTGAVTSGYYPN
28.	CDR-L2 of H2C	artificial	aa	GTKFLAP
29.	CDR-L3 of H2C	artificial	aa	ALWYSNRWV
30.	CDR-H1 of H2C	artificial	aa	KYAMN
31.	CDR-H2 of H2C	artificial	aa	RIRSKYNNYATYYADSVKD
32.	CDR-H3 of H2C	artificial	aa	HGNFGNSYTSYWAY
33.	VH of H2C	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
34.	VH of H2C	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA

35.	VL of H2C	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
36.	VL of H2C	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
37.	VH-P of H2C	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
38.	VH-P of H2C	artificial	nt	GAGGTGCAGCTGCTCGACTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
39.	VL-P of H2C	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
40.	VL-P of H2C	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
41.	VH-VL of H2C	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
42.	VH-VL of H2C	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC

				CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
43.	VH-VL-P of H2C	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
44.	VH-VL-P of H2C	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATTATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
45.	CDR-L1 of H1E	artificial	aa	GSSTGAVTSGYYPN
46.	CDR-L2 of H1E	artificial	aa	GTKFLAP
47.	CDR-L3 of H1E	artificial	aa	ALWYSNRWV
48.	CDR-H1 of H1E	artificial	aa	SYAMN
49.	CDR-H2 of H1E	artificial	aa	RIRSKYNNYATYYADSVKG
50.	CDR-H3 of H1E	artificial	aa	HGNFGNSYISFWAY
51.	VH of H1E	artificial	aa	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSS
52.	VH of H1E	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGAGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATTCGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATTATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACC TATCCTTCTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTC
53.	VL of H1E	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
54.	VL of H1E	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG

				TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATCGTACAGCAACCGCTGGGTGTTCGCTGGAGGAACCAAACTGACTGTCC TA
55.	VH-P of H1E	artificial	aa	EVQLLESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISFWAYWGQGTLVTVSS
56.	VH-P of H1E	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGAGGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATTCGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATTATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACC TATCCTTCTGGGCTTACTGGGGCCAAGGGACTCGTCACCGTCTCCTCA
57.	VL-P of H1E	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
58.	VL-P of H1E	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTAACTCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATCGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
59.	VH-VL of H1E	artificial	aa	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
60.	VH-VL of H1E	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGAGGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATTCGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATTATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACC TATCCTTCTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA

61.	VH-VL-P of H1E	artificial	aa	EVQLLESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
62.	VH-VL-P of H1E	artificial	nt	GAGGTGCAGCTGCTCGACTCTGGAGGAGGAGATTGGAGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATTCGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACC TATCCTTCTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
63.	CDR-L1 of G4H	artificial	aa	GSSTGAVTSGYYPN
64.	CDR-L2 of G4H	artificial	aa	GTKFLAP
65.	CDR-L3 of G4H	artificial	aa	ALWYSNRWV
66.	CDR-H1 of G4H	artificial	aa	RYAMN
67.	CDR-H2 of G4H	artificial	aa	RIRSKYNNYATYYADSVKG
68.	CDR-H3 of G4H	artificial	aa	HGNFGNSYLSYFAY
69.	VH of G4H	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSS
70.	VH of G4H	artificial	nt	GAGGTGCAGCTGGTCGACTCTGGAGGAGGAGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATCGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTACTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
71.	VL of G4H	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
72.	VL of G4H	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAAACTGGGTCCAACAAAAACCAGGTC ACGCACCCCGTCGTCTAATAGGTGGCACTAAGTTCCTCCCCCCGCTACTCCTGCCACATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA

				ATATTACTGTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
73.	VH-P of G4H	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSS
74.	VH-P of G4H	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATCGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTACTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
75.	VL-P of G4H	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
76.	VL-P of G4H	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGAGTGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
77.	VH-VL of G4H	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
78.	VH-VL of G4H	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATCGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTACTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
79.	VH-VL-P of G4H	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF

80.	VH-VL-P of G4H	artificial	nt	LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATCGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTACTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGCTGTTACATCTGGCTACT ACCCAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
81.	CDR-L1 of A2J	artificial	aa	RSSTGAVTSGYYPN
82.	CDR-L2 of A2J	artificial	aa	ATDMRPS
83.	CDR-L3 of A2J	artificial	aa	ALWYSNRWV
84.	CDR-H1 of A2J	artificial	aa	VYAMN
85.	CDR-H2 of A2J	artificial	aa	RIRSKYNNYATYYADSVKK
86.	CDR-H3 of A2J	artificial	aa	HGNFGNSYISWWAY
87.	VH of A2J	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSS
88.	VH of A2J	artificial	nt	GAGGTGCAGCTGGTCGACTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
89.	VL of A2J	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
90.	VL of A2J	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TCGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATCGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
91.	VH-P of A2J	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS

				VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSS
92.	VH-P of A2J	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
93.	VL-P of A2J	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
94.	VL-P of A2J	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TCGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAAACTGGGCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
95.	VH-VL of A2J	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDM RPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
96.	VH-VL of A2J	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGAITGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTCGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATG AGGCCCTCTGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
97.	VH-VL-P of A2J	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDM RPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
98.	VH-VL-P of A2J	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGAITGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG

				GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACT TATCCTGGTGGCCTTACTGGGCCCAAGCCACTCTGCTCACCCTCTCCTCAGCTGCTGCTGCTTCT GGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTCGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATG AGGCCCTCTGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
99.	CDR-L1 of E1L	artificial	aa	GSSTGAVTSGYYPN
100.	CDR-L2 of E1L	artificial	aa	GTKFLAP
101.	CDR-L3 of E1L	artificial	aa	ALWYSNRWV
102.	CDR-H1 of E1L	artificial	aa	KYAMN
103.	CDR-H2 of E1L	artificial	aa	RIRSKYNNYATYYADSVKS
104.	CDR-H3 of E1L	artificial	aa	HGNFGNSYTSYYAY
105.	VH of E1L	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSS
106.	VH of E1L	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAATCGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA CATCCTACTACGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
107.	VL of E1L	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
108.	VL of E1L	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
109.	VH-P of E1L	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSS
110.	VH-P of E1L	artificial	nt	GAGGTGCAGCTGCTCGACTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG

				GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAATCGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA CATCCTACTACCCTTACTGGGGCCCAAGGCACTCTGCTCACCCTCTCCTCA
111.	VL-P of E1L	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
112.	VL-P of E1L	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAAACTGGGTCCAACACAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
113.	VH-VL of E1L	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
114.	VH-VL of E1L	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAATCGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA CATCCTACTACGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
115.	VH-VL-P of E1L	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
116.	VH-VL-P of E1L	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAATCGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA

				CATCCTACTACGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGCCTCCAACAAAAACCAGGTCAGCCACCCCCTGCTCTAATAGCTGCGCACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
117.	CDR-L1 of E2M	artificial	aa	RSSTGAVTSGYYPN
118.	CDR-L2 of E2M	artificial	aa	ATDMRPS
119.	CDR-L3 of E2M	artificial	aa	ALWYSNRWV
120.	CDR-H1 of E2M	artificial	aa	GYAMN
121.	CDR-H2 of E2M	artificial	aa	RIRSKYNNYATYYADSVKF
122.	CDR-H3 of E2M	artificial	aa	HRNFGNSYISWFAY
123.	VH of E2M	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYISWFAYWGQGTLVTVSS
124.	VH of E2M	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAGGAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATAGGAACTTCGGTAATAGCTACT TATCCTGGTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
125.	VL of E2M	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
126.	VL of E2M	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TCGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAACTGGGTCCAACAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
127.	VH-P of E2M	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYISWFAYWGQGTLVTVSS
128.	VH-P of E2M	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATAGGAACTTCGGTAATAGCTACT

				TATCCTGGTTCGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
129.	VL-P of E2M	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
130.	VL-P of E2M	artificial	nt	GAGCTCGTTGTGACTCACGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TCGCTCCTCGACTGGGGCTGTTACATCTGGCTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
131.	VH-VL of E2M	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDM RPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
132.	VH-VL of E2M	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTTGGAATGGGTTGCTCGCATAAGAAGTAAATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATAGGAACTTCGGTAATAGCTACT TATCCTGGTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTCGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATG AGGCCCTCTGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
133.	VH-VL-P of E2M	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDM RPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
134.	VH-VL-P of E2M	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATAGGAACTTCGGTAATAGCTACT TATCCTGGTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTCGCTCCTCGACTGGGGCTGTTACATCTGGCTACT

				ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATG AGGCCCTCTGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTGCTATGGTACAGCAACCGCTGGG TCTTCGGTCGACGAACCAAACTGACTGTCCTA
135.	CDR-L1 of F7O	artificial	aa	GSSTGAVTSGYYPN
136.	CDR-L2 of F7O	artificial	aa	GTKFLAP
137.	CDR-L3 of F7O	artificial	aa	ALWYSNRWV
138.	CDR-H1 of F7O	artificial	aa	VYAMN
139.	CDR-H2 of F7O	artificial	aa	RIRSKYNNYATYYADSVKK
140.	CDR-H3 of F7O	artificial	aa	HGNFGNSYISWWAY
141.	VH of F7O	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSS
142.	VH of F7O	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
143.	VL of F7O	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
144.	VL of F7O	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
145.	VH-P of F7O	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSS
146.	VH-P of F7O	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
147.	VL-P of F7O	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

148.	VL-P of F7O	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GCCTCCCTCCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGCTACAGCCACAGCATCAGCCAGA ATATTACTGTGCTCTATCGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
149.	VH-VL of F7O	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
150.	VH-VL of F7O	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCACGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
151.	VH-VL-P of F7O	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLICGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
152.	VH-VL-P of F7O	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATGTGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCACGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG

				TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
153.	CDR-L1 of F12Q	artificial	aa	GSSTGAVTSGNYPN
154.	CDR-L2 of F12Q	artificial	aa	GTKFLAP
155.	CDR-L3 of F12Q	artificial	aa	VLWYSNRWV
156.	CDR-H1 of F12Q	artificial	aa	SYAMN
157.	CDR-H2 of F12Q	artificial	aa	RIRSKYNNYATYYADSVKG
158.	CDR-H3 of F12Q	artificial	aa	HGNFGNSYVSWWAY
159.	VH of F12Q	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSS
160.	VH of F12Q	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGCATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
161.	VL of F12Q	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
162.	VL of F12Q	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATCGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
163.	VH-P of F12Q	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSS
164.	VH-P of F12Q	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGCATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
165.	VL-P of F12Q	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
166.	VL-P of F12Q	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA

				GGCTCCCTGCCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
167.	VH-VL of F12Q	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLICGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
168.	VH-VL of F12Q	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
169.	VH-VL-P of F12Q	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTTSRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLICGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
170.	VH-VL-P of F12Q	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
171.	CDR-L1 of I2C	artificial	aa	GSSTGAVTSGNYPN
172.	CDR-L2 of I2C	artificial	aa	GTKFLAP

173.	CDR-L3 of I2C	artificial	aa	VLWYSNRWV
174.	CDR-H1 of I2C	artificial	aa	KYAMN
175.	CDR-H2 of I2C	artificial	aa	RIRSKYNNYATYYADSVKD
176.	CDR-H3 of I2C	artificial	aa	HGNFGNSYISYWAY
177.	VH of I2C	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
178.	VH of I2C	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATTAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
179.	VL of I2C	artificial	aa	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
180.	VL of I2C	artificial	nt	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
181.	VH-P of I2C	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
182.	VH-P of I2C	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATTAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
183.	VL-P of I2C	artificial	aa	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
184.	VL-P of I2C	artificial	nt	GAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTCTGTTCTATCGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA

185.	VH-VL of I2C	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
186.	VH-VL of I2C	artificial	nt	GAGGTGCAGCTGGTCGACTCTGGAGGAGGCATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
187.	VH-VL-P of I2C	artificial	aa	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGS GGGGSGGGGSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
188.	VH-VL-P of I2C	artificial	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACT ACCCAAACTGAGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTA
189.	MCSP-G4 VH-VL x H2C VH-VL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR

				DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
190.	MCSP-G4 VH-VL x H2C VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGATATCGTTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCACATATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACCGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAAIAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGCTGGACAGTCACACTCAC TTGTGGCTCCTCGACTGGCGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
191.	MCSP-G4 VH-VL x F12Q VH-VL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
192.	MCSP-G4 VH-VL x F12Q VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG

				GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGCTCACCCTCTCCTCAGGTGCTGCTTCTGGCGGCGGCCGCCTCCGCTGCT GGTTCTGATATCGTGATCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAG CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCCTGGGTGTTCGGTGGAGGAACCCAAACTGACTG TCCTA
193.	MCSP-G4 VH-VL x I2C VH-VL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRES G VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
194.	MCSP-G4 VH-VL x I2C VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGATATCGTGATCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC

				CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GCCTGAAGATCTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
195.	MCSP-G4 VH-VL-P x F6A VH-VL-P	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGSGGGGSGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
196.	MCSP-G4 VH-VL-P x F6A VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA

				GGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAT CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCCACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTCAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTATCCTTCTTCGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
197.	MCSP-G4 VH-VL-P x H2C VH-VL-P	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSISTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
198.	MCSP-G4 VH-VL-P x H2C VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCCATTGAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCCACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTCAGGACACTGCCGTGTA CTACTGTGTGAGACATGCGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG

				GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGCGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGCTCTAATAGCTGCCACTAAGTTCCTCGCCCCCGCTACTCCTGCCACATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
199.	MCSP-G4 VH-VL-P x H1E VH-VL-P	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNKNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLLESGG GLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
200.	MCSP-G4 VH-VL-P x H1E VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACGATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGAGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATTC GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAGGGAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACCTATCCTTCTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTGTTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC

				AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
201.	MCSP-G4 VH-VL-P x G4H VH-VL-P	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
202.	MCSP-G4 VH-VL-P x G4H VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACGATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATCG CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGGAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACTTATCCTACTTCGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCTACTACCCAAACTGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
203.	MCSP-G4 VH-VL-P x A2J VH-VL-P	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG

				VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
204.	MCSP-G4 VH-VL-P x A2J VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATGT CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAAAGAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACTTATCCTGGTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTCGCTCCTCGACTGGCGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
205.	MCSP-G4 VH-VL-P x E1L VH-VL-P	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSISTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGSGGGGSGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

206.	MCSP-G4 VH-VL-P x E1L VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GCCAGAGTCACCATGACCAGGGACACGTCCACCAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAATCGAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACACATCCTACTACTGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT TCTGAGCTCGTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
207.	MCSP-G4 VH-VL-P x E2M VH-VL-P	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKERFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHKNFGNSYISWFAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVVTQEPSLTVSPGGTVTLTCRSSTGAVISGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
208.	MCSP-G4 VH-VL-P x E2M VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG

				AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGCGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATGG CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATAGGAACTTCGGTAATACGTACTTATCCTGGTCGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTCGCTCCTCGACTGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
209.	MCSP-G4 VH-VL-P x F7O VH-VL-P	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGSGGGGSGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
210.	MCSP-G4 VH-VL-P x F7O VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGCGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA

				GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATGT GTACGCCATGAACTGGCTCCGCCAGGCTCCAGCAAAGCGTTTGGAATGGCTTGCTCGCATAAGAA GTAAATATAATAATTATCCAACATATTATGCCGATTCAGTGAAAAGAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAGCCTGAGAGCACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAAIAGCTACATATCCTGGTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
211.	MCSP-G4 VH-VL-P x F12Q VH-VL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSISTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSFVQLVESGG GLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
212.	MCSP-G4 VH-VL-P x F12Q VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACGCTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAG CTACGCCATGAACTGGCTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGCTTGCTCGCATAAGAA GTAAATATAATAATTATCCAACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATCTCCAGA

				GATGATTCAAAAAACACTGCCTATCTACAAATGAACACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGCTCGAACACTCACACTCAC TTGTGGCTCCTCGACTGCGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
213.	MCSP-G4 VH-VL-P x I2C VH-VL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYLHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
214.	MCSP-G4 VH-VL-P x I2C VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACCCTAACAGTGGTGCCACACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACCGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCCACATATTATGCCGATTCAGTGAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCAC TTGTGGCTCCTCGACTGCGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG

				GTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
215.	MCSP-D2 VH-VL x H2C VH-VL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTSYAQKFQ GRVTMTRDTSISTVYMELSNLRSDDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
216.	MCSP-D2 VH-VL x H2C VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACACCTTCACCGGCTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAG GGCTTGAGTGGATGGGAIGGATCAACCCTAACAGTGGTGGCACAAGCTTACGCCACAGAAGTTCCAG GGCAGAGTCACCATGACTAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAACCTGAG ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGATATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTTCACTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAGGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGTGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
217.	MCSP-D2 VH-VL x	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTSYAQKFQ

	F12Q VH-VL			GRVTMTRDTSTSTVYMELSNLRSDDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
218.	MCSP-D2 VH-VL x F12Q VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACACCTTCACCGGCTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAG GGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAGCTTACGCACAGAAGTTCCAG GGCAGAGTCACCATGACTAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAACCTGAG ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGATATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTTCACTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAG CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCCACAGATTATGCCGATTCAGTGAAGGGCAGGTTCACCATCTCCAGA GATGATTCAAAAACACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGCGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
219.	MCSP-D2 VH-VL x I2C VH-VL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTSYAQKFQ GRVTMTRDTSTSTVYMELSNLRSDDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG

				SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
220.	MCSP-D2 VH-VL x I2C VH-VL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACACCTTCACCGGCTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAG GGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACACAGCTACGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAACCTGAG ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGATATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
221.	MCSP-D2 VH-VL-P x H2C VH-VL-P	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTSYAQKFQ GRVTMTRDTSTSTVYMELSNLRSDDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLNSSNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
222.	MCSP-D2 VH-VL-P x H2C VH-VL-P	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACACCTTCACCGGCTACTATATGCACTGGGTGCGACAGGCCCCCTGGACAAG GGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACACAGCTACGCACAGAAGTTCCAG

				GGCAGAGTCACCATGACTAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAACCTGAG ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCCTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GCTTCTGACGTCGTGATCACCCAGTCTCCAGACTCCCTGCCTCTGTCTCTGGGCGAGAGGCCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCTCCAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGAGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACCGAGGACACTGCCGTGTA CTACTGTGTGAGACATGCGAACTTCGGTAATATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGCGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
223.	MCSP-F9 VH-VL x H2C VH-VL	artificial	aa	QVQLQESGPGLVKPSETLSLTCVVSGGSISSSNWWSWVRQPPGKGLEWLGTIYYNGNTYYNPSLK SRVTISVDTSKNQFSLRLSSVTAADTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSVPFTFGPGTKVDIKGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
224.	MCSP-F9 VH-VL x H2C VH-VL	artificial	nt	CAGGTGCAGCTGCAAGAGTCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTG CGTTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGCTGGGTCCGCCAGCCCCCAGGGA AGGGACTGGAGTGGCTTGGACTATCTATTATAATGGGAATACCTACTACAACCCGTCCCTCAAG AGTCGAGTCACCATCTCCGTAGACACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGAC CGCCGCAGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT GGTTCTGATATCGTGATGACACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACAATAAGAACTACTTAAATTGGT

				ACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGACAGATTTCACTCTCACCATCAGCAGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTGTTCCATTCACTTTCGGCCCTG GCACCAAACTGCATATCAAAGCAGCTGCTGCTCCCAGGTGCAGCTGGTCCAGTCTGGACAGCA TTGGTGCAGCCTGGAGGCTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTA CGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTA AATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT GATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGA CTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCT CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTG TGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTC AGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCA GGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCC TA
225.	MCSP-F9 VH-VL-P x H2C VH-VL-P	artificial	aa	EVQLQESGPGLVKPSETLSLTCVVSGGSISSSNWWSWVRQPPGKGLEWLGTIYYNGNTYYNPSLK SRVTISVDTSKNQFSLRLSSVTAADTAVYYCARSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSVPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
226.	MCSP-F9 VH-VL-P x H2C VH-VL-P	artificial	nt	GAGGTGCAGCTGCAAGAGTCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTG CGTTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGCTGGGTCCGCCAGCCCCCAGGGA AGGGACTGGAGTGGCTTGGGACTATCTATTATAATGGGAATACCTACAACCCGTCCCTCAAG AGTCGAGTCACCATCTCCGTAGACACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGAC CGCCGCAGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT GGTTCTGAGCTCGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACAATAAGAACTACTTAAATTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGACAGATTTCACTCTCACCATCAGCAGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTGTTCCATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA

				GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATATGCCAACATATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACCGAGGACACTGCCGTGTA CTACTGTGTGACACATGCGAACTTCGGTAATACCTACATATCCTACTGCGCTTACTGCGCCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGCGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGCGGCTGTTACATCTGGCTACCCAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
227.	MCSP-F9 VH-VL-P x G4H VH-VL-P	artificial	aa	EVQLQESGPGLVKPSETLSLTCVVSGGSISSSNWWSWVRQPPGKGLEWLGTIYYNGNTYYNPSLK SRVTISVDTSKNQFSLRLSSVTAADTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSELVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSVPFTFGPGTKVDIKSGGGGSEVQLLESGG GLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGGG SETVVTQFPSITVSPGGTVTITCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
228.	MCSP-F9 VH-VL-P x G4H VH-VL-P	artificial	nt	GAGGTGCAGCTGCAAGAGTCTGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTG CGTTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGCTGGGTCCGCCAGCCCCCAGGGA AGGGACTGGAGTGGCTTGGGACTATCTATTATAATGGGAATACCTACTACAACCCGTCCCTCAAG AGTCGAGTCACCATCTCCGTAGACACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGAC CGCCGCAGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGAGCTCGTGATCACACAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACACAATAAGAACTACTTAAATTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTGTTCCATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGCTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATCG CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATATGCCAACATATTATGCCGATTCAGTGAAAGGGAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACCGAGGACACTGCCGTGTA CTACTGTGTGAGACATGCGAACTTCGGTAATACTACTTATCCTACTTCGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT

				TCTGAGCTCGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTCCTTCGAGCCAAGCTCCCCTCACCCTCTCAGGGTACAGCCCAGACAGGATGAGCC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
229.	1-27 CD3 epsilon-Fc	artificial	aa	QDGNEEMGGITQTPYKVSISGTTVILTSGEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG KHHHHHH
230.	1-27 CD3 epsilon-Fc	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCAAGATGG TAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCACTCTGGAACCACAGTAA TATTGACATCCGGAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCT GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC CCGGACCCCTGAGGTCACATGCGTGGTGGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAG GGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAACATCA TCACCATCATCAT
231.	human 1-27 CD3 epsilon -EpCAM	artificial	aa	QDGNEEMGGITQTPYKVSISGTTVILTDYKDDDDKTASFAAAQKECVCENYKLAVNCFLNDNGQC QCTSIGAQNTVLCSKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCN GTSTCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALEEAIKTRYQL DPKFITNILYEDNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLRVNGEQLD LDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMG EMHRELNA
232.	human 1-27 CD3 epsilon -EpCAM	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCAAGATGG TAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCACTCTGGAACCACAGTAA TATTGACACAGATTACAAGGACGACGATGACAAGACTGCGAGTTTTGCCGCAGCTCAGAAAGAATGT GTCTGTGAAAACTACAAGCTGGCCGTAAACTGCTTTTTGAATGACAACTGGTCAATGCCAGTGTAC TTCGATTGGTGCACAAAATACTGTCCTTTGCTCAAAGCTGGCTGCCAAATGTTTGGTGATGAAGG CAGAAATGAACGGCTCAAAACTTGGGAGAAGAGCGAAACCTGAAGGGGCTCTCCAGAACAATGAT

				GGCCTTTACGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCAACGGCACCTC CACGTGCTGGTGTGTGAACACTGCTGGGGTCAGAAGAACTGACAAGGACACTGAAATAACCTGCT CTGAGCGAGTGAGAACCTACTGGATCATCATTGAATTAAAACACAAAGCAAGAGAAAAACCTTAT GATGTTCAAACTTTGCCCACTGCCACTTCAGCGACGGCCATCAAAACGCCTTATCAACTGCATCCAAA ATTTATCACAAATATTTTGTATGAGGATAATGTTATCACTATTGATCTGGTTCAAAATTCTTCTC AGAAAACTCAGAATGATGTTGGACATAGCTGATGTGGCTTATTATTTGAAAAAGATGTTAAAGGT GAATCCTTGTTTCATTCTAAGAAAATGGACCTGAGAGTAAATGGGGAACAACTGGATCTGGATCC TGGTCAAACTTTAATTATTATGTCGATGAAAAAGCACCTGAATTCTCAATGCAGGGTCTAAAAG CTGGTGTTATTGCTGTTATTGTGGTTGTGGTGATAGCAATTGTTGCTGCAATTGTTGTGCTGGTT ATTTCCAGAAAGAAGAGAATGGCAAAGTATGAGAAGGCTGAGATAAAGGAGATGGGTGAGATGCA TAGGGAACTCAATGCA
233.	marmoset 1-27 CD3 epsilon -EpCAM	artificial	aa	QDGNEEMGDTTQNPYKVSISGTTVTLTDYKDDDDKTASFAAAQKECVCENYKLAVNCFLNDNGQC QCTSIGAQNTVLCSKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCN GTSTCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALEEAIKTRYQL DPKFITNILYEDNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLRVNGEQLD LDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMG EMHRELNA
234.	marmoset 1-27 CD3 epsilon -EpCAM	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCAGGACGGG TAATGAAGAAATGGGTGATACTACACAGAACCCATATAAAGTTTCCATCTCAGGAACCACAGTAA CACTGACAGATTACAAGGACGACGATGACAAGACTGCGAGTTTGCCGCAGCTCAGAAAGAATGT GTCTGTGAAAACTACAAGCTGGCCGTAAACTGCTTTTGAATGACAACTGGTCAATGCCAGTGTAC TTCGATTGGTGCACAAAATACTGTCCTTGCTCAAGCTGGCTGCCAAATGTTTGGTGATGAAGG CAGAAATGAACGGCTCAAAACTTGGGAGAAGAGCGAAACCTGAAGGGGCTCTCCAGAACAATGAT GGCCTTTACGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCAACGGCACCTC CACGTGCTGGTGTGTGAACACTGCTGGGGTCAGAAGAACTGACAAGGACACTGAAATAACCTGCT CTGAGCGAGTGAGAACCTACTGGATCATCATTGAATTAAAACACAAAGCAAGAGAAAAACCTTAT GATGTTCAAAGTTTGCGGCACTTGCAGTGAGGAGGCGATCAAAACGCCGTATCAACTGGATCCAAA ATTTATCACAAATATTTTGTATGAGGATAATGTTATCACTATTGATCTGGTTCAAAATTCTTCTC AGAAAACTCAGAATGATGTTGGACATAGCTGATGTGGCTTATTATTTGAAAAAGATGTTAAAGGT GAATCCTTGTTTCATTCTAAGAAAATGGACCTGAGAGTAAATGGGGAACAACTGGATCTGGATCC TGGTCAAACTTTAATTATTATGTCGATGAAAAAGCACCTGAATTCTCAATGCAGGGTCTAAAAG CTGGTGTTATTGCTGTTATTGTGGTTGTGGTGATAGCAATTGTTGCTGCAATTGTTGTGCTGGTT ATTTCCAGAAAGAAGAGAATGGCAAAGTATGAGAAGGCTGAGATAAAGGAGATGGGTGAGATGCA TAGGGAACTCAATGCA
235.	tamarin 1-27 CD3 epsilon -EpCAM	artificial	aa	QDGNEEMGDTTQNPYKVSISGTTVTLTDYKDDDDKTASFAAAQKECVCENYKLAVNCFLNDNGQC QCTSIGAQNTVLCSKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCN GTSTCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALEEAIKTRYQL

				DPKFITNILYEDNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLRVNGEQLD LDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMG EMHRELNA
236.	tamarin 1-27 CD3 epsilon -EpCAM	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCAGGACGG TAATGAAGAAATGGGTGATACTACACAGAACCCATATAAAGTTTCCATCTCAGGAACCACAGTAA CACTGACAGATTACAAGCACGACGATGACAAGACTGCGAGTTTGCCGCAGCTCAGAAAGAATGT GTCTGTGAAAACTACAAGCCGGCCGTAACTGCTTTTTGAATGACAATGGTCAATGCCAGTGTAC TTCGATTGGTGCACAAAATACTGTGTCCTTTGCTCAAAGCTGGCTGCCAAATGTTTGGTGATGAAGG CAGAAATGAACGGCTCAAAACTTGGGAGAAGAGCGAAACCTGAAGGGGCTCTCCAGAACAATGAT GGCCTTTACGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCAACGGCACCTTC CACGTGCTGGTGTGTGAACACTGCTGGGGTCAGAAGAACTGACAAGGACACTGAAATAACCTGCT CTGAGCGAGTGAGAACCTACTGGATCATCATTGAATTAAAACACAAAGCAAGAGAAAAACCTTAT GATGTTCAAAGTTTGCGGACTGCACTTGAGGAGGCGATCAAAACGCGTTATCAACTGGATCCAAA ATTTATCACAAATATTTTGTATGAGGATAAIGTTATCACTATTGATCTGGTTCAAAATTCTTCTC AGAAAACTCAGAATGATGTGGACATAGCTGATGTGGCTTATTATTTTGAAAAAGATGTTAAAGGT GAATCCTTGTTTCATTCTAAGAAAATGGACCTGAGAGTAAATGGGGAACAACTGGATCTGGATCC TGGTCAAACTTTAATTTATTATGTCGATGAAAAAGCACCTGAATTCTCAATGCAGGGTCTAAAAG CTGGTGTTATTGCTGTTATTGTGGTTGTGATAGCAATTGTTGCTGGAATTGTTGTGCTGGTT ATTTCCAGAAAGAGAGAATGGCAAAGTATGAGAAGGCTGAGATAAAGGAGATGGGTGAGATGCA TAGGGAACTCAATGCA
237.	squirrel monkey 1-27 CD3 epsilon - EpCAM	artificial	aa	QDGNEEIGDTTQNPYKVSISGTTVTLTDYKDDDDKTASFAAAQKECVCSNYKLAVNCFLNDNGQC QCTSIGAQNTVLCSKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCN GTSTCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALEEAIKTRYQL DPKFITNILYEDNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLRVNGEQLD LDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMG EMHRELNA
238.	squirrel monkey 1-27 CD3 epsilon - EpCAM	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCAGGACGG TAATGAAGAGATTGGTGATACTACCCAGAACCCATATAAAGTTTCCATCTCAGGAACCACAGTAA CACTGACAGATTACAAGCACGACGATGACAAGACTGCGAGTTTGCCGCAGCTCAGAAAGAATGT GTCTGTGAAAACTACAAGCCGGCCGTAAACTGCTTTTTGAATGACAATGGTCAATGCCAGTGTAC TTCGATTGGTGCACAAAATACTGTGTCCTTTGCTCAAAGCTGGCTGCCAAATGTTTGGTGATGAAGG CAGAAATGAACGGCTCAAAACTTGGGAGAAGAGCGAAACCTGAAGGGGCTCTCCAGAACAATGAT GGCCTTTACGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCAACGGCACCTTC CACGTGCTGGTGTGTGAACACTGCTGGGGTCAGAAGAACTGACAAGGACACTGAAATAACCTGCT CTGAGCGAGTGAGAACCTACTGGATCATCATTGAATTAAAACACAAAGCAAGAGAAAAACCTTAT GATGTTCAAAGTTTGCGGACTGCACTTGAGGAGGCGATCAAAACGCGTTATCAACTGGATCCAAA ATTTATCACAAATATTTTGTATGAGGATAAIGTTATCACTATTGATCTGGTTCAAAATTCTTCTC

				AGAAAACTCAGAATGATGTGGACATAGCTGATGGCTTATTATTTGAAAAAGATGTTAAAGGT GAATCCTTGTTTCATTCTAAGAAAATGGACCTGAGAGTAAATGGGGAACAACTGGATCTGGATCC TGGTCAAACTTTAATTATTATGTCGATGAAAAAGCACCTGAATTCTCAATGCAGGGTCTAAAAG CTGGTGTTATTCCTGTTATTGTGCTTCTCGTCATACCAATTCTTGCTGCAATTGTTCTGCTGGTT ATTTCCAGAAAGAAGAGAATGGCAAAGTATGAGAAGGCTGAGATAAAGGAGATGGGTGAGATGCA TAGGGAACTCAATGCA
239.	swine 1-27 CD3 epsilon -EpCAM	artificial	aa	QEDIERPDEDTQKTFKVSISGDKVELTDYKDDDDKTASFAANQKECVCENYKLAVNCFLNDNGQC QCTSIGAQNTVLCSKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCN GTSTCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALEEAIKTRYQL DPKFITNLLYEDNVLTLDLVQNSSQKTQNDVDLADVAYYFEKDVKGESLFHSKKMDLEVNGEQLD LDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMG EMHRELNA
240.	swine 1-27 CD3 epsilon -EpCAM	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCAAGAAGA CATTGAAAGACCAGATGAAGATACACAGAAAACATTTAAAGTCTCCATCTCTGGAGACAAAGTAG AGCTGACAGATTACAAGGACGACGATGACAAGACTGCGAGTTTGCCGCAGCTCAGAAAGAATGT GTCTGTGAAAACTACAAGCTGGCCGTAAACTGCTTTTTGAATGACAACTGGTCAATGCCAGTGTAC TTCGATTGGTGCACAAAATACTGTCCTTGCTCAAGCTGGCTGCCAAATGTTTGGTGATGAAGG CAGAAATGAACGGCTCAAAACTTGGGAGAAGAGCGAAACCTGAAGGGGCTCTCCAGAACAATGAT GGCCTTTACGATCCTGACTGCGATGAGAGCGGCTCTTTAAGGCCAAGCAGTGCAACGGCACCTC CACGTGCTGGTGTGTGAACACTGCTGGGGTCAGAAGAACTGACAAGGACACTGAAATAACCTGCT CTGAGCGAGTGAGAACCTACTGGATCATCAATTGAATTAAAACACAAAGCAAGAGAAAAACCTTAT GATGTTCAAAGTTTGCGGACTGCACTTGAGGAGGCGATCAAAACGCGTTATCAACTGGATCCAAA ATTTATCACAAATATTTGTATGAGGATAAIGTTATCACTATTGATCTGGTTCAAAATTCTTCTC AGAAAACTCAGAATGATGTGGACATAGCTGATGTGGCTTATTATTTGAAAAAGATGTTAAAGGT GAATCCTTGTTTCATTCTAAGAAAATGGACCTGAGAGTAAATGGGGAACAACTGGATCTGGATCC TGGTCAAACTTTAATTATTATGTCGATGAAAAAGCACCTGAATTCTCAATGCAGGGTCTAAAAG CTGGTGTTATTGCTGTTATTGTGGTTGTGGTGATAGCAATTGTTGCTGGAATTGTTGTGCTGGTT ATTTCCAGAAAGAAGAGAATGGCAAAGTATGAGAAGGCTGAGATAAAGGAGATGGGTGAGATGCA TAGGGAACTCAATGCA
241.	human CD3 epsilon chain	human	aa	QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKE FSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDVMSVATIVIVDICITGGLLLLVYYW SKNRKAKAKPVTRGAGAGGRQRGQNKERPPPVPNPDYEPIRKGQRDLYSGLNQRRI
242.	human CD3 epsilon chain	human	nt	ATGCAGTCGGGCACTCACTGGAGATGTTCTGGGCCTCTGCCTCTTATCAGTTGGCGTTTGGGGCA AGATGGTAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCATCTCTGGAACCA CAGTAATATTGACATGCCCTCAGTATCCTGGATCTGAAATACTATGGCAACACAATGATAAAAAC ATAGGCGGTGATGAGGATGATAAAAACATAGGCAGTGATGAGGATCACCTGTCACTGAAGGAATT TTCAGAATTGGAGCAAAGTGGTTATATGTCTGCTACCCCAGAGGAAGCAAACCAGAAGATGCGA

				ACTTTATCTCTACCTGAGGGCACGCGTGTGAGAACTGCATGGAGATGGATGTCGGTG GCCACAATTGTCATAGTGGACATCTGCATCACTGGGGGCTTGCTGCTGGTTACTACTGGAG CAAGAATAGAAAGGCCAAGGCCAAGCCTGTGACACGAGGAGCGGGTGCTGGCGGCAGGCAAAGGG GACAAAACAAGCAGACGCCACCACCTGTTCCCAACCCACACTATGACCCCATCCCGCAAACGCCCAG CGGGACCTGTATTCTGGCCTGAATCAGAGACGCATC
243.	19 amino acid immunoglobulin leader peptide	artificial	aa	MGWSCIILFLVATATGVHS
244.	19 amino acid immunoglobulin leader peptide	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCC
245.	murine IgG1 heavy chain constant region	murine	aa	AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLS SSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQW NGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK
246.	murine IgG1 heavy chain constant region	murine	nt	GCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCAT GGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTG GATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGC AGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGAGACCGTCACCTGCAACGTTGCCCACCC GGCCAGCAGCACCAAGGTGGACAAGAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATAT GTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATT ACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTT CAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAG TTCAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAACCATCTCCAAAACCAA AGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGG AATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTT CGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTG TGTTACATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA
247.	human lambda light chain constant region	human	aa	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
248.	human lambda light chain constant region	human	nt	GGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAA CAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGG CAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAG

				TACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTG CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCA
249.	c-terminal domain construct of human MCSP	human	aa	DYKDDDDKSRTRSGSQLDGGLVLFSHRGTLDGGFRFRLSDGEHTSPGHFFRVTAQKQVLLSLKGS QTLTVCPGSVQPLSSQTLRASSSAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVY AGNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFEAACPQRPSHLWKNKGLWVPE GQRARITVAALDASNLLASVPSPQRSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAG QLVYAHGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVNEPPQFQASVPLRLTRGS RAPISRAQLSVVDPDSAPGEIEYEVQRAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSS VAGIFQLSMSDGASPPLFMSLAVDILPSAIEVQLRAPLEVPQALGRSSLSQQQLRVVSDREEPEA AYRLIQGPQYGHLLVGGRPTSAFSQFQLDQGEVVFAFTNSSSSHDHFKVLALARGVNASAVVNVI VRALLHVWAGGPWPQGATLRLDPTVLDAGELANRTCSVPRFRLLEGPRHGRVVRVPRARTEPGGS QLVEQFTQQDLEDGRLGLEVGRPEGRAPGPAGDSLTLELWAQGVPPAVASLDFATEPYNAARPYS VALLSVPEAARTEAGKPFSSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSVIIPMCLVLLLLA LILPLLFYLRKRNKTGKHDVQVLTAKPRNGLAGDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDP ELLQFCRTPNPALKNGQYWV
250.	c-terminal domain construct of human MCSP	human	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGACTACAA AGACGATGACGACAAGTCCCGTACGAGATCTGGATCCCAATTGGACGGCGGGCTCGTGGTTCT CACACAGAGGAACCCTGGATGGAGGCTTCCGCTTCCGCCTCTCTGACGGCGAGCACACTTCCCCC GGACACTTCTTCCGAGTGACGGCCCAGAAGCAAGTGCTCCTCTCGCTGAAGGGCAGCCAGACACT GACTGTCTGCCCAGGGTCCGTCCAGCCACTCAGCAGTCAGACCCTCAGGGCCAGCTCCAGCGCAG GCACTGACCCCCCAGCTCCTGCTCTACCGTGTGGTGCGGGGCCCCCAGCTAGGCCGGCTGTTCCAC GCCCAGCAGGACAGCACAGGGGAGGCCCTGGTGAACTTCACTCAGGCAGAGGTCTACGCTGGGAA TATTCTGTATGAGCATGAGATGCCCCCCCGAGCCCTTTGGGAGGCCCATGATACCCTAGAGCTCC AGCTGTCCTCGCCGCCTGCCCGGGACGTGGCCGCCACCCTTGCTGTGGCTGTGTCTTTGAGGCT GCCTGTCCCCAGCGCCCCAGCCACCTCTGGAAGAACAAAGGTCTCTGGGTCCCCGAGGGCCAGCG GGCCAGGATCACCGTGGCTGCTCTGGATGCCTCCAATCTCTTGGCCAGCGTTCCATCACCCCAGC GCTCAGAGCATGATGTGCTCTTCCAGGTCACACAGTTCCCCAGCCGCGGCCAGCTGTTGGTGTCC GAGGAGCCCCTCCATGCTGGGCAGCCCCACTTCCTGCAGTCCCAGCTGGCTGCAGGGCAGCTAGT GTATGCCCACGGCGGTGGGGCACCCAGCAGATGGCTTCCACTTTCGTGCCCACCTCCAGGGGC CAGCAGGGGCCTCCGTGGCTGGACCCCAAACCTCAGAGGCCTTGCCATCACGGTGAGGGATGTA AATGAGCGGCCCCCTCAGCCACAGGCCTCTGTCCCACTCCGGCTCACCCGAGGCTCTCGTGCCCC CATCTCCCGGGCCCAGCTGAGTGTGGTGGACCCAGACTCAGCTCCTGGGGAGATTGAGTACGAGG TCCAGCGGGCACCCCACAACGGCTTCCTCAGCCTGGTGGGTGGTGGCCTGGGGCCCGTGACCCGC TTCACGCAAGCCGATGTGGATTCAGGGCGGCTGGCCTTCGTGGCCAACGGGAGCAGCGTGGCAGG CATCTTCCAGCTGAGCATGTCTGATGGGGCCAGCCCACCCCTGCCCATGTCCCTGGCTGTGGGCGC TCCTACCATCCGCCATCGAGGTGCAGCTGCGGCACCCCTGGAGGTGCCCCCAAGCTTTGGGGCGC TCCTCACTGAGCCAGCACGCTCCGGGTGGTTTCAGATCGGGAGGAGCCAGAGGCAGCATACCG

				GTTGATCCAGGGACCCCAGTATGGCATCTCCTGGTGGGCGGGCGGCCCACCTCGGCCTTCAGCC AATTCCAGATAGACCAGGGCGAGGTGGTCTTTGCCTTCACCAACTCCTCCTCCTCATGACCAC TTCAGAGTCCTGGCACTCGCTAGGGGTGTCAATGCATCAGCCGTAGTGAACGTCACTGTGAGGGC TCTGCTGCATCTGTGCGCACGTGGCCCATGCCCCCAGCGTGCCACCCTCGCCCTCGACCCCACCG TCCTAGATGCTGGCGAGCTGGCCAACCGCACAGACAGTGTGCCGCGCTCCGCCTCCTGGAGGGA CCCCGGCATGGCCGCGTCGTCCGCGTGCCCCGAGCCAGGACGGAGCCCGGGGGCAGCCAGCTGGT GGAGCAGTTCACTCAGCAGGACCTTGAGGACGGGAGGCTGGGGCTGGAGGTGGGCAGGCCAGAGG GGAGGGCCCCCCGGCCCCCGGCAGGTGACAGTCICACTCTGGAGCTGTGGGCACAGGGCGTCCCGCCT GCTGTGGCCTCCCTGGACTTTGCCACTGAGCCTTACAATGCTGCCCGGCCCTACAGCGTGGCCCT GCTCAGTGTCCCCGAGGCCGCCCGGACGGAAGCAGGGAAGCCAGAGAGCAGCACCCCCACAGGCG AGCCAGGCCCCATGGCATCCAGCCCTGAGCCCGCTGTGGCCAAGGGAGGCTTCCTGAGCTTCTA GAGGCCAACATGTTCAGCGTCATCATCCCCATGTGCCTGGTACTTCTGCTCCTGGCGCTCATCCT GCCCCTGCTCTTCTACCICCGAAAACGCAACAAGAGCGGCAAGCATGACGTCCAGGTCCTGACTG CCAAGCCCCGCAACGGCCTGGCTGGTGACACCGAGACCTTTCGCAAGGTGGAGCCAGGCCAGGCC ATCCCGCTCACAGCTGTGCCTGGCCAGGGGCCCCCTCCAGGAGGCCAGCCTGACCCAGAGCTGCT GCAGTTCTGCCGGACACCCAACCCTGCCCTTAAGAATGGCCAGTACTGGGTG	
251.	partial sequence of cynomolgus MCSP	Macaque (Cynomolgus)	aa	PSNGRVVLRAAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFRFGLSDGEHTSSGHFFRVTAQKQV TLSLEGSRTLTVCPGSVQPLSSQTLRASSSAGTDPQLLTYRVVRGPQTGRLFHAQQDSTGFAIVN FTQAEVYAGNILYEHEMPTEPFWEAHDTLELQLSSPPARDVAATLAVAVSFEAACPQRPSHLWKN KGLWVPEGQRAKITMAALDASNLLASVPSSQRLEHCVLFQVTQFPSRGQLLVSEEPLHAGQPHFL QSQLAAGQLVYAFGGGGTQQDGFHFRAHLQGPAGATVAGFQTSEAFAITVRDVNERPPQFQASVP LRITRGSRAPISFAQLSVVDPDSAPGEIEYEVQRAPHNGFLSLVGGGPGPVNRFTQADVDSGRLA FVANGSSVAGVFQLSMSDGASPPLPMSLAVDILPSAIEVQLQAPLEVPQALGRSSLSQQQLRVVS DREEPEAAYRLIQGPKYGILLVGGQPASAFSQLQIDQGEVVFAFTNFSSSIIDLFRVLALARGVNA SAVVNITVRALLHVWAGGPWPQGATLRLDPTILDAGELANRTGSVPRFRLLEGPRHGRVVRVPRA RMEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPSPTGDSLTLELWAQGVPPAVASLDFATEPY NAARPYSVALLSVPEATRTEAGKPESSTPTGEPGPMASSPVPAVAKGGFLGFLEAMMFSVIIPXC LVLLLLALIILPLLFYLLRKRNKTGKHDVQVLTAKPRNGLAGDTETFRKVEPGQGPP PGGQPDPELLQFCRTPNPALKNGQYWV	
252.	partial sequence of cynomolgus MCSP	Macaque (Cynomolgus)	nt	CCCAGCAACGGACGGGTAGTGCTGCGGGCGGCCGGGGCACCGAGGTGCGCAGCTTCACGCAGGC CCAGCTGGATGGCGGACICGTGCTGTTCTCACACAGAGGAACCCTGGATGGAGGCTTCCGCTTCG GCCTCTCCGATGGCGAGCACACTTCCTCTGGACACTTCTTCCGAGTGACGGCCCAGAAGCAAGTG CTCCTCTCGCTGGAGGGCAGCCGGACACTGACTGTCTGCCCAGGGTCCGTGCAGCCACTCAGCAG TCAGACCCTCAGAGCCAGCTCCAGCGCAGGCACCGACCCCCAGCTCCTGCTCTACCGTGTGGTGC GGGGCCCCCAGCTAGGCCGGCTGTTCCATGCCCAGCAGGACAGCACAGGGGAGGCCCTGGTGAAC TTCACTCAGGCAGAGGTCTATGCTGGGAATATTCTGTATGAGCATGAGATGCCCACCGAGCCCTT CTGGGAGGCCCATGATACCCTAGAGCTCCAGCTGTCCTCACCACCTGCCCGGGACGTGGCTGCCA	

				CCCTTGCTGTGGCTGTCTTTGAGGCTGCCTGTCCCCAGCGCCCCAGCCACCTCTGGAAGAAC AAAGGTCTCTGGGTCCCCGAGGGCCAGCGGGCCAAGATCACCATGGCTGCCCTGGATGCCTCCAA CCTCTTGGCCAGCGTTCCATCATCCCAGCGCCTAGAGCATGATGTGCTCTTCCAGGTCACGCAGT TCCCAGCCGCGCCCAGCTATTGGTCTCTGAGCAGCCCCTCCACGCTGCGCAGCCCCACTTCCTG CAGTCCCAGCTGGCTGCAGGGCAGCTAGTGTATGCCCACGGCGGTGGGGGTACCCAACAGGATGG CTTCCACTTTCGTGCCCACCTCCAGGGGCCAGCAGGGGCCACCGTGGCTGGACCCCAAACCTCAG AGGCTTTTGCCATCACGGTGCGGGATGTAAATGAGCGCCCCCCTCAGCCACAGGCCTCTGTCCCA CTCCGGATCACCCGAGGCTCTCGAGCCCCCATCTCCCGGGCCCAGCTGAGTGTCGTGGACCCAGA CTCAGCTCCTGGGGAGATTGAGTATGAGGTCCAGCGGGCACCCCACAACGGCTTCCTCAGCCTGG TGGGTGGTGGCCCGGGGCCCGTGAACCGCTTCACGCAAGCCGATGTGGATTCGGGCGGCTGGCC TTCGTGGCCAACGGGAGCAGCGTAGCAGGCGTCTTCCAGCTGAGCATGTCTGATGGGGCCAGCCC ACCGCTGCCCATGTCCCTGGCCGTGGACATCCTACCATCCGCCATCGAGGTGCAGCTGCAGGCAC CCCTGGAGGTGCCCCCAACGCTTTGGGGCGCTCCTCACTGAGCCAGCAGCTCCGGGTGGTTTCA GATAGGGAGGAGCCAGACGCAGCATACCGCCTCATCCAGGGACCAAAGTACGGGCATCTCCTGGT GGGTGGGCAGCCCGCCTCGGCCTTCAGCCAACTCCAGATAGACCAGGGCGAGGTGGTCTTTGCCT TCACCAACTTCTCCTCCTCTCATGACCACTTCAGAGTCCTGGCACTGGCTAGGGGTGTCAACGCA TCAGCCGTAGTGAACATCACTGTGAGGGCTCTGCTGCACGTGTGGGCAGGTGGGCCATGGCCCCA GGGTGCTACCCTGCGCCTGGACCCAACCATCCTAGATGCTGGCGAGCTGGCCAACCGCACAGGCA GTGTGCCCCGCTTCCGCCTCCTGGAGGGACCCCGGCATGGCCCGCGTGGTCCGTGTGCCCCGAGCC AGGATGGAGCCTGGGGGCAGCCAGCTGGTGGAGCAGTTCACTCAGCAGGACCTTGAGGATGGGAG GCTGGGGCTGGAGGTGGCCAGGCCAGAGGGAAGGGCCCCCCAGCCCCACAGGCGACAGTCTCACTC TGGAGCTGTGGGCACAGCGCGTCCCACCTGCTGTGGCCTCCCCTGGACTTTGCCACTGAGCCTTAC AATGCTGCCCGGCCCTACAGCGTGTGGCCCTGCTCAGTGTCCCCGAGGCCACCCCGGACGGAAGCAGG GAAGCCAGAGACCACACCCCCACAGGCCAGCCAGGCCCCCATGGCATCTACGCCCTCTGCCCTGCTG TGGCCAAGGGAGGCTTCCTGGGCTTCCTTGAGGCCAACATGTTCAGTGTCATCATCCCCRTGTGC CTGGTCCTTCTGCTCCTGGCGCTCATCTTGCCCCTGCTCTTCTACCTCCGAAAACGCAACAAGAC GGGCAAGCATGACGTCCAGGTCCTGACTGCCAAGCCCCGCAATGGTCTGGCTGGTGACACTGAGA CCTTTCGCAAGGTGGAGCCAGGCCAGGCCAICCCGCTCACAGCTGTGCCTGGCCAGGGGCCCCCT CCGGGAGGCCAGCCTGACCCAGAGCTGCTGCAGTTCTGCCGGACACCCAACCCTGCCCTTAAGAA TGGCCAGTACTGGGTG
253.	PCR primer for CD3 epsilon chain - forward primer	artificial	nt	AGAGTTCTGGGCCTCTGC
254.	PCR primer for CD3 epsilon chain - reverse primer	artificial	nt	CGGATGGGCTCATAGTCTG
255.	His6-human CD3	artificial	aa	HHHHHHQDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDED

	epsilon			HLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDVMSVATIVIVDICITGGLL
				LLVYYWSKNRKAKAKPVTRGAGAGGRQRGQNKERPPPVPNPDYEPIRKGQRDLYSGLNQRRI
256.	His6-human CD3 epsilon	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCCATCATCA CCATCATCATCAAGATGCTAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCA TCTCTGGAACCACAGTAATATTGACATGCCCTCAGTATCCTGGATCTGAAATACTATGGCAACAC AATGATAAAAACATAGGCGGTGATGAGGATGATAAAAACATAGGCAGTGATGAGGATCACCTGTC ACTGAAGGAATTTCAGAATGGAGCAAGTGGTTATATGTCTGCTACCCCAGAGGAAGCAAAC CAGAAGATGCGAACTTTTATCTCTACCTGAGGGCACGCGTGTGTGAGAACTGCATGGAGATGGAT GTGATGTCGGTGGCCACAATTGTCATAGTGGACATCTGCATCACTGGGGGCTTGCTGCTGGT TTACTACTGGAGCAAGAATAGAAAGGCCAAGCCTGTGACACGAGGAGGGGTGCTGGCG GCAGGCAAAGGGGACAAAACAAGGAGAGGCCACCACCTGTTCCCAACCCAGACTATGAGCCCATC CGGAAAGGCCAGCGGGACCTGTATTCTGGCCTGAATCAGAGACGCATC
257.	CD33 AH3 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFK GRVTMSSDTSTSTAYLEINSLRSDDTAIYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
258.	CD33 AH3 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAAAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAGGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGTCTTCGGATACCTCTACCAGCACTGCCTATTTGGAAATCAACAGCCTCAG AAGTGATGACACGGCTATATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACCGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG

				CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACAAAAACCAGCTCAGGCACCCCCTGTCTCTAATAGCGTGGCACTAAGTTCCTCGCCCCCGCT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
259.	CD33 AH3 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFK GRVTMSSDTSTSTAYLEINSLRSDDTAIYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggggg ggggggsDIVMTQSPDSLTVSLGERATINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
260.	CD33 AH3 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAAAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAGGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGTCTTCGGATACCTCTACCAGCACTGCCTATTTGGAAATCAACAGCCTCAG AAGTGATGACACGGCTATATATTACTGTGCGCGCTGGAGTTGGAGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACCGTCACCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGSTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGGCAAGGCTGCCCTCACCCTCAGGGGTACA

				GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
261.	CD33 AH3 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFK GRVTMSSDTSTSTAYLEINSLRSDDTAIYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
262.	CD33 AH3 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAAAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAGGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGTCTTCGGATACCTCTACCAGCACTGCCTATTTGGAAATCAACAGCCTCAG AAGTGATGACACGGCTATATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACACTGTCTGCCCACTTCCCGA TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACTCCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
263.	CD33 AF5 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTSDTSTSTAYLELHNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS

				TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
264.	CD33 AF5 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTTCGGATACCTCTACCAGCACTGCCTATTTGGAACTCCACAACCTCAG AAGTGATGACAGGGCTGTATATTACTGTGCGCGCTTGGAGTTGATGGTTACTACGTTTACGT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
265.	CD33 AF5 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTSDTSISTAYLELHNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

266.	CD33 AF5 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GCACGGGTTACCATGACTTCGGATACCTCTACCAGCACTGCCTATTTGCAACTCCACACAACCTCAG AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAACCAGGTCAGGCACCCCGTGGTCTATAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
267.	CD33 AF5 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTSDTSTSTAYLELHNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
268.	CD33 AF5 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTTCGGATACCTCTACCAGCACTGCCTATTTGCAACTCCACAACCTCAG AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGATGGTTACTACGTTTACT

				TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGCCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGAITAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCICAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACIGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
269.	CD33 AC8 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTTDTSTSTAYMEIRNLRNDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
270.	CD33 AC8 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCACTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCAG AAATGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC

				TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAACTACCCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGAACTTCGGTAATAGCTACATACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGICTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
271.	CD33 AC8 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTTDTSTSTAYMEIRNLRNDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGTPDRFSGSGSGTDFTLTTDSLQPEDSATYYCQQSAHFPTTFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
272.	CD33 AC8 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCAG AAATGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACCGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACCCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG

				TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTCTTCTGACTCACGCAACCTTCACTCACCGTATCACCTGGTCG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCAGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
273.	CD33 AC8 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTTDTSTSTAYMEIRNLRNDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsgggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
274.	CD33 AC8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCAG AAATGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAACAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTCCCACTTCCCGA TCACCTTTGGCCAAGGGACACCACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTCTTCTGACTCACGCAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG

				TCCAACAAAAACCAGGTCAGGCACCCCGTGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTCACTGTCCTA
275.	CD33 AH11 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTSDTSTSTAYMEISSLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
276.	CD33 AH11 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTTCGGATACCTCTACCAGCACTGCCTATATGGAAATCAGCAGCCTCAG AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGACAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACIGGGGCTGTTACATCTGGCTACTACCCAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAAATATTACTGTGCICTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
277.	CD33 AH11 HL x	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK

	F12Q HL			GRVTMTSDTSTSTAYMEISSLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
278.	CD33 AH11 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTTCGGATACCTCTACCAGCACTGCCTATATGGAAATCAGCAGCCTCAG AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACACAAAAACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GTCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
279.	CD33 AH11 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFK GRVTMTSDTSTSTAYMEISSLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGG

				SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
280.	CD33 AH11 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCACTCTGGAGCTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAG GGACGGGTTACCATGACTTCGGATACCTCTACCAGCACTGCCTATATGGAAATCAGCAGCCTCAG AAGTGATGACACGGCTGTATATTACTGTGCGCGCGCTGGAGTTGGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACTGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
281.	CD33 B3 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGETNYADKFQ GRVTFTSDTSTSTAYMELRNLKSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSMTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLDIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
282.	CD33 B3 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCACTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGACAAACTATGCTGATAAGTTCCAG

				GGACGCGTTACCTTCACTTCGGATACCTCTACCAGCACTGCCTATATGGAACTCCGCAACCTCAA AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAACGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GCCTCCGGTGGTGGTCGTTCTCACATCCTGATCACACACTCTCCAGACTCCATGACTCTCTCT GGGCGAGGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTACACAGCTCCACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGACATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGICTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
283.	CD33 B3 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGETNYADKFQ GRVTFTSDTSTSTAYMELRNLKSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggggg gsggggsDIVMTQSPDSMTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLDIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
284.	CD33 B3 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCIGGATAAACACCTACACTGGAGAGACAAACTATGCTGATAAGTTCCAG GGACGCGTTACCTTCACTTCGGATACCTCTACCAGCACTGCCTATATGGAACTCCGCAACCTCAA AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCATGACTCTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTACACAGCTCCACGAATAAGA

				ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACACAGTCTGCCCACTTCCCGA TCACCTTTCGCCAAGCGCACACCACTGCACATTAAATCCCGCAGCTGGTGCTCCGACGCTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACIGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
285.	CD33 B3 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGETNYADKFQ GRVTFTSDTSTSTAYMELRNLKSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSMTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLDIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
286.	CD33 B3 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCCTACACTGGAGAGACAAACCATATGCTGATAAGTTCCAG GGACGCGTTACCTTCACTTCGGATACCTCTACCAGCACTGCCTATATGGAACTCCGCAACCTCAA AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACCGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCATGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGACATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG

				ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GCACACTGCCCTGTACTACTGTGTGACACATCGGAACTTCGCTAATAGCTACATATCCTACTGCG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCCTGCTTGAGAGGCAAGGCTGCCCCTCACCCTCTCAGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
287.	CD33 F2 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGETNYADKFQ GRVTFTSDTSTSTAYMELRNLKSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSLSVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFIAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
288.	CD33 F2 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGACAAACTATGCTGATAAGTTCCAG GGACGCGTTACCTTCACTTCGGATACCTCTACCAGCACTGCCTATATGGAACTCCGCAACCTCAA AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGTCTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGAITAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC

				TCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCACATTCTCAGGCTCCCTGCTTGCAGGCAAGCGCTGCCCTCACCCTCACAGGCTACA GCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
289.	CD33 F2 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGETNYADKFQ GRVTFTSDTSTSTAYMELRNLKSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggsggg gsggggsDIVMTQSPDSLSVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGVPDRFSGSGSGTDFTLTISSLQPEDSATYYCQQSAHFPLTFGQGTRLEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
290.	CD33 F2 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGACAAACTATGCTGATAAGTTCCAG GGACGCGTTACCTTCACTTCGGATACCTCTACCAGCACTGCCTATATGGAACTCCGCAACCTCAA AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGTCTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGCAGGCAAGCGCTGCCCTCACCCTCACAGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG

				GAACCAAACTGACTGTCCTA
291.	CD33 F2 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGETNYADKFQ GRVTFTSDTSTSTAYMELRNLKSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSLSVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
292.	CD33 F2 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCACTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGACAAACTATGCTGATAAGTTCCAG GGACGCGTTACCTTCACTTCGGATACCTCTACCAGCACTGCCTATATGGAACTCCGCAACCTCAA AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGATGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGTCTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGTCTTAATAGGTGGGACTAAGTTCCTCGCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
293.	CD33 B10 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQ GRVTMTTDTSTSTAYMEIRNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSNNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDGLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGSEVQL

				VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
294.	CD33 B10 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACCTATGCTGATAAGTTCCAG GGACGCGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCAG AAGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTACT TTGACTACTGGGGCCAAGGCACCACTCGTCTCCTCAGGTGGTGGTTCTTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAACAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGTTCTGGGACAGATTTCACTCTCAC TATTGACGGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
295.	CD33 B10 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQ GRVTMTTDTSTSTAYMEIRNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSNNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDGLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
296.	CD33 B10 HL x	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGTGAGTCAAGGTCTCCTG

	F12Q HL			CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCIGGATAAACACCTACACTGGAGAGCCAACCTATGCTGATAAGTTCCAG GGACGCGTTACCATGACIACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCAG AACTGATGACACGGCTGIATATTACTGTGCCGCCTGCACTTGCAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAACGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCAICAACTGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCAACAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGTTCTGGGACAGATTTCACTCTCAC TATTGACGGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
297.	CD33 B10 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQ GRVTMTTDTSTSTAYMEIRNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSgggggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSNNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDGLQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQIVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
298.	CD33 B10 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCIGGATAAACACCCTACACTGGAGAGCCAACCTATGCTGATAAGTTCCAG GGACGCGTTACCATGACIACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCAG AAGTGATGACACGGCTGIATATTACTGTGCCGCCTGCACTTGCAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAACGCACTACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC

				GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAACAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGTTCTGGCACACATTTCACTCTCAC TATTGACGGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGAITAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGICTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACIGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
299.	CD33 E11 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQ GRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSgggggsggg gsgggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
300.	CD33 E11 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTGCACTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCIGGATAAACACCTACACTGGAGAGCCAACCTATGCTGATAAGTTCCAG GGACGCGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCTGG AGGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCCGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA

				TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAACTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAACACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACAIGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGICTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCICAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCGACIGGGGCTGTTACATCTGGCTACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTSGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGCICTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
301.	CD33 E11 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQ GRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSgggsggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARTRSKYNNYATYYADSVKGR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
302.	CD33 E11 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTAIGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCIGGATAAACACCTACACTGGAGAGCCAACCTATGCTGATAAGTTCCAG GGACGCGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCGG AGGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTTCGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCCGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA

				GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCCACTGCGGCTCTTACATCTGGCAACTACCCAAACTGCG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACA GCCAGAGGATGAGGCAGAAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
303.	CD33 E11 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQ GRVTMTTDTSTSTAYMELRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSgggggggg gsggggsDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
304.	CD33 E11 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGAGTCAGTCAAGGTCTCCTG CAAGGCTAGCGGGTATACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGG GTTTAGAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACCCTATGCTGATAAGTTCCAG GGACGCGTTACCATGACTACGGATACCTCTACCAGCACTGCCTATATGGAAATCCGCAACCTCGG AGGTGATGACACGGCTGTATATTACTGTGCGCGCTGGAGTTGGAGTGATGGTTACTACGTTTACT TTGACTACTGGGGCCAAGGCACTTCGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCT GGGCGAGAGGACCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCACGAATAAGA ACTCCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTCCTGGGCATCT ACGCGGGAATCCGGGATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC TATTGACAGCCCGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACACAGTCTGCCCACTTCCCGA TCACCTTTGGCCAAGGGACACGACTGGAGATTAAATCCGGAGGTGGTGGCTCCGAGGTGCAGCTG GTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGA GGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGG CTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGG AACAGTCACACTCACTTCTGGCTCCTCCACTGCGGCTCTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGT

				ACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGTACA GCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAG GAACCAAACTGACTGTCCTA
305.	CD33	human	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGATCCAAA TTTCTGGCTGCAAGTGCAGGAGTCAGTGACCGTACAGGAGGGTTTGTGCGTCCTCGTGCCCTGCA CTTTCTTCCATCCCATACCCTACTACGACAAGAACTCCCCAGTTCATGGTTACTGGTTCCGGGAA GGAGCCATTATATCCGGGGACTCTCCAGTGGCCACAACAAGCTAGATCAAGAAGTACAGGAGA GACTCAGGGCAGATTCCCCCCTCCTTGGGGAICCCCAGTAGGAACACAACTGCTCCCTGAGCATCGTAG ACGCCAGGAGGAGGGATAATGGTTCATACTTCTTTCGGATGGAGAGGAAGTACCAAATACAGT TACAAATCTCCCCAGCTCTCTGTGCATGTGACAGACTTGACCCACAGGCCCCAAAATCCTCATCCC TGGCACTCTAGAACCCGGCCACTCCAAAAACCTGACCTGCTCTGTGTCCTGGGCCTGTGAGCAGG GAACACCCCCGATCTTCTCCTGGTTGTCAGCTGCCCCCACCTCCCTGGGCCCCAGGACTACTCAC TCCTCGGTGCTCATAATCACCCCACGGCCCCAGGACCACGGCACCAACCTGACCTGTCAGGTGAA GTTCGCTGGAGCTGGTGTGACTACGGAGAGAACCATCCAGCTCAACGTCACCTATGTTCCACAGA ACCCAACAACTGGTATCTTTCCAGGAGATGGCTCAGGGAAACAAGAGACCAGAGCAGGAGTGGTT CATGGGGCCATTGGAGGAGCTGGTGTTACAGCCCTGCTCGCTCTTTGTCTCTGCCTCATCTTCTT CATAGTGAAGACCCACAGGAGGAAAGCAGCCAGGACAGCAGTGGGCAGGAATGACACCCACCCTA CCACAGGGTCAGCCTCCCCGAAACACCAGAAGAAGTCCAAGTTACATGGCCCCACTGAAACCTCA AGCTGTTCAGGTGCCGCCCCTACTGTGGAGATGGATGAGGAGCTGCACTTATGCTTCCCTCAACTT TCATGGGATGAATCCTTCCAAGGACACCTCCACCGAATACTCAGAGGTCAGGACCCAGTCCGGGC ATCATCACCATCATCATTGA
306.	CD33	human	aa	MGWSCIILFLVATATGVHSDPNFWLQVQESVTVQEGLCVLVPCTFFHPIPYYDKNSPVHGYWFRE GAIISGDSPVATNKLDQEVQETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYS YKSPQLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSWLSAAPTSLGPRTTH SSVLIITPRPQDHGTNLTCQVKFAGAGVTTERTIQLNVTYVPQNPTTGIFPGDGSGKQETRAGVV HGAIGGAGVTALLALCLCLIFFIVKTHRRKAARTAVGRNDTHPTTGSASPKHQKKSKLHGPTETS SCSGAAPTVEMDEELHYASLNFHGMNPSKDTSTEYSEVRTQSGHHHHH
307.	CD33	macaque	nt	ATGCCGCTGCTGCTACTGCTGCCCCTGCTGTGGGCAGGGGCCCTGGCTATGGATCCAAGAGTCAG GCTGGAAGTGCAGGAGTCAGTGACAGTACAGGAGGGTTTGTGCGTCCTTGTGCCCTGCACTTTCT TCCATCCCGTACCCTACCACACACCAGGAATTCCCCAGTTCATGGTTACTGGTTCCGGGAAGGAGCC ATTGTATCCTTGGACTCTCCAGTGGCCACAAACAAGCTAGATCAAGAAGTACAGGAGAGGACCCA GGGCCGATTCCGCCTCCTTGGGGATCCCAGTAGGAACAACTGCTCCCTGAGCATCGTAGATGCCA GGAGGAGGGATAACGGTTCATACTTCTTTCGGATGGAGAAAGGAAGTACCAAATACAGTTACAAA TCTACCCAGCTCTCTGTGCATGTGACAGACTTGACCCACAGGCCCCAAATCCTCATCCCTGGAGC CCTAGACCCTGACCACTCCAAAAACCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGAACAC CTCCAATCTTCTCCTGGATGTCAGCTGCCCCCACCTCCCTGGGCCTCAGGACCACTCACTCCTCG GTGCTCATAATCACCCCACGGCCCCAGGACCACGGCACCAACCTCACCTGTCAGGTGAAGTTCCC

				TGGAGCTGGCGTGACCACGGAGAGAACCATCCAGCTCAATGTCTCCTATGCTTCACAGAACCCAA GAACTGATATCTTCTTCTAGGAGACGGCTCAGGAAACAAGGAGTGGTTCAGGGACCATCGGGGGA GCTGGTGTCACAGTCCTCGCTCTTTGTCTCTGCCTCATCTTCTTCACAGTGAAGACTCACAG GAGGAAAGCAGCCAGCACACCAGTGGCAGCATCGACACCCACCCCGCCACAGGCCCAACATCCT CGAAACACCAGAAGAAGTCCAAGTTACATGGCGCCACTGAAACCTCAGGCTGTTCAGGTACCACC CTTACTGTGGAGATGGATGAGGAGCTGCACTACGCTTCCCTCAACTTCCATGGGATGAATCCTTC TGAGGACACCTCCACCGAATACTCAGAGGTCAGGACCCAGTGA
308.	CD33	macaque	aa	MPLLLLPLLWAGALAMDPRVRLEVQESVTVQEGLCVLVPCTFFHPVPYYHTRNSPVHGYWFREGA IVSLDSPVATNKLDQEVQETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRMEKGSTKYSYK SPQLSVHVTDLTHRPQLLTPGALDPDHSKNLTCSVPWACEQGTPPTFSWMSAAPTSLGLRTTHSS VLITPRPQDHGTNLTCQVKFPGAGVTTERTIQLNVSYASQNPRTDIFLGDGSGKQGVVQGAIGG AGVTVLALCLCLIFFTVKTHRRKAARTAVGRIDTHPATGPTSSKHQKSKLHGATETSGCSGTT LTVEMDEELHYASLNFHGMNPSEDTSTEYSEVRTQ
309.	1-27 CD3-Fc + Leader	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGGTGTACACTCCCAAGATGG TAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCACACTCTTGGAACCACAGTAA TATTGACATCCGGAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCT GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTC CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAG GGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAATAG
310.	1-27 CD3-Fc + Leader	artificial	aa	MGWSCIILFLVATATGVHSQDGNEEMGGITQTPYKVSISGTTVILTSGEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
311.	CD33 UD H2C HL x AF5 HL	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVLSGGGGSQVQLV QSGAEVKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFKGRVTM TSDTSTSTAYLELHNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSGGGGSGGGGSGGG

				GSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWASTRESG IPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIK
312.	CD33 UD H2C HL x AF5 HL	artificial	nt	GAGGTGCAGCTGGTCGACTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTTGTTGAACAGTCACACTCACTTTGTGGCTCCTCGACTTGGGCCTGTTACATCTGGCTACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAAATATTACTGTGCTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTATCCGGAGGTGGTGGCTCCCAGGTGCAGCTGGTC CAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCGTCAGTCAAGGTCTCCTGCAAGGCTAGCGGGTA TACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGGGTTTAAAGTGGATGG GCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAGGGACGGGTTACCATG ACTTCGGATACCTCTACCAGCACTGCCTATTTGGAACTCCACAACCTCAGAAGTGATGACACGGC TGTATATTACTGTGCGCGCCTGGAGTTGGATGGTTACTACGTTTACTTTGACTACTGGGGCCC AAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCTGGGCGAGAGGACCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGAACTCCTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAATTACTCCTTTCCTGGGCATCTACGCGGGAATCCGGG ATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACTATTGACAGCCTGCA GCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGATCACCTTTGGCCAAG GGACACGACTGGAGATTAAA
313.	CD33 UD F12Q HL x AF5 HL	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLICGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLSGGGGSQVQLV QSGAEVKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFKGRVTM TSDTSTSTAYLELHNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWASTRESG IPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIK
314.	CD33 UD F12Q HL x AF5 HL	artificial	nt	GAGGTGCAGCTGGTCGACTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA

				GTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACG TTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GCCGGCGGCGGCTCCCGTGGTGGTCTCTCACACTCTTGTGACTCAGCAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACT ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGG TGTTCGGTGGAGGAACCAAACTGACTGTCCTATCCGGAGGTGGTGGCTCCCAGGTGCAGCTGGTC CAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCGTCAGTCAAGGTCTCCTGCAAGGCTAGCGGGTA ACCTTCACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGACAGGGTTAAAGTGGATGG GCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAGGGACGGGTTACCATG ACTTCGGATACCTCTACCAGCACTGCCTATTTGGAACTCCACAACCTCAGAAGTGATGACACGGC TGTATATTACTGTGCGCCCTGGAGTTGGAGTGATGGTTACTACGTTTACTTTGACTACTGGGGCC AAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCTGGGCGAGAGGACCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAGACAGCTCCAAGAATAAGAACTCCTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTCCTAAATTACTCCTTTCCTGGGCATCTACGCGGGAATCCGGG ATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACTATTGACAGCCTGCA GCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGATCACCTTTGGCCAAG GGACACGACTGGAGATTAAA
315.	CD33 UD I2C HL x AF5 HL	artificial	aa	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGS GGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKF LAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLSGGGGSQVQLV QSGAEVKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYADDFKGRVTM TSDTSTSTAYLELHNLRSDDTAVYYCARWSWSDGYYVYFDYWGQGTTVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSKNKNSLAWYQQKPGQPPKLLLSWASTRESG IPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQSAHFPITFGQGTRLEIK
316.	CD33 UD I2C HL x AF5 HL	artificial	nt	GAGGTGCAGCTGGTGGAGTCTGGAGGAGGAITGGTGCAGCCTGGAGGGTCATTGAAACTCTCATG TGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGG GTTTGGAATGGGTTGCTCGCATAAGAAGTAAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAA CTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACA TATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGT ATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACT

				ACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGG TCTTCGGTCGAGGAACCAAACTGACTGTCCTATCCCGCAGGTGGCTCCCAGGTGCAGCTGGTC CAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCGTCAGTCAAGGTCTCCTGCAAGGCTAGCGGGTA TACCTTCACAAACTATGCAATGAACTGGGTGAAGCAGGCTCCAGGACAGGGTTTAAAGTGGATGG GCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAGGGACGGTTACCATG ACTTCGGATACCTCTACCAGCACTGCCTATTTGGAACTCCCACAACCTCAGAAGTGATGACACGGC TGTATATTACTGTGCGCGCTGGAGTTGGACTACTTTACTTGACTACTGGGGCC AAGGCACTACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGACTGTGTCTCTGGGCGAGAGGACCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCAAGAATAAGAACTCCTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTCAAATTACTCCTTTCCTGGGCATCTACGCGGGAATCCGGG ATCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACTATTGACAGCCTGCA GCCTGAAGATTCTGCAACTTACTATTGTCAACAGTCTGCCCACTTCCCGATCACCTTTGGCCAAG GGACACGACTGGAGATTAAA
317.	MCSP-A9 HL x H2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYPFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARSWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHFNTPFAFGQGTKLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
318.	MCSP-A9 HL x H2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGCTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACCCCTTCACCGGCTACTACATGCACTGGGTGCGACAGGCCCCTGGACAAG GGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAG GGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAG ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACAATAAGAACTACTTAAATTGGT ACCAGCAGAAACCAGGACAGCCTCCTCAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCCTGCA GGCTGAAGATGTGGCGGTTTATTACTGTCAACACAACATTTTAATACTCCGTTCGCTTTTGGCCAGG GGACCAAGCTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA

				GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATATGCCAACATATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGACACATGCGAACTTCGGTAATAGCTACATATCCTACTGCTGCGCTTACTGGCCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
319.	MCSP-A9 HL x F12Q HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYPFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTITADESTSTAYMELSRLRSDDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHFNTPFAFGQGTKLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
320.	MCSP-A9 HL x F12Q HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACCCCTTCACCGGCTACTACATGCACTGGGTGCGACAGGCCCCTGGACAAG GGCTTGAGTGGATGGGATGGATCAACCCTAACCCTCAGTGGTGGCCACAAACTATGCACAGAAGTTTCAG GGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGGCTGAG ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATCACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACAATAAGAACTACTTAAATTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAACAACATTTTAATACTCCGTTCGCTTTTGGCCAGG GGACCAAGCTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAG CTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATATGCCAACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGCGAACTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT

				TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTCCTTCGAGCCAAGCCTCCCCTCACCCTCTCAGGGTACAGCCACAGCATCAGCC AGAATATTACTGTGTTCTATGGTACAGCAACCGCCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
321.	MCSP-A9 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYPFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTITADESTSTAYMELSRLRSDDTAVYYCARSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHFNTPFAFGQGTKLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
322.	MCSP-A9 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTG CAAGGCTTCTGGATACCCCTTCACCGGCTACTACATGCACTGGGTGCGACAGGCCCCTGGACAAG GGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAG GGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGGCTGAGA ATCTGACGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACACAATAAGAACTACTTAAATTGGT ACCAGCAGAAACCAGGACAGCCTCCTCAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA GGCTGAAGATGTGGCGGTTATTACTGTCAACAACATTTTAATACTCCGTTCGCTTTTGGCCAGG GGACCAAGCTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCCTGGGTGTTCGGTGGAGGAACCAAACTGACTG

				TCCTA
323.	MCSP-C8 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISGLQAEDVAVYYCQQHYSTPFTFGPGTKVDIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
324.	MCSP-C8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAACAGCAAGAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGTGGCCTGCA GGCTGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCCTG GGACCAAAGTGGATATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGCTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
325.	MCSP-B8 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLTVSPGERATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQHYSTPFTFGQGTRLEIKSGGGGSEVQLVESGG

				GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
326.	MCSP-B8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCTTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTGGT GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGACTGTGTCTCCGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCAAGAACACATTAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCGATTCCCTGCA GCCTGAAGATAGTGCAACTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCAGG GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
327.	MCSP-B7 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLTVSLGERTTINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTIDSLQPEDIATYYCQQHYSTPFTFGQGTRLEIKSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
328.	MCSP-B7 HL x I2C	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG

	HL			CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTIGGATCAACCCTAACAGTGGTGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTCGGTCTCCTCGCTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGACTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCAAGAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCGATTCCCTGCA GCCTGAAGATATTGCAACTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTGGCCAGG GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
329.	MCSP-G8 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLTVSLGERATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRES VPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQHYSTPFTFGQGTRLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
330.	MCSP-G8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTIGGATCAACCCTAACAGTGGTGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTCGGTCTCCTCGCTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT

				GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGACTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAACAGCAAGAACACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCCGATTCCCTGCA GCCTGAAGATAGTGCAACTTATTACTGTCAGCAACATTATAGTACTCCCATTCACTTTTGGCCAGG GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGCGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
331.	MCSP-D5 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTIDSLQAEDSATYYCQQHYSTPFTFGQGTRLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
332.	MCSP-D5 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTAACAGCAAGAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCGATTCCCTGCA GGCTGAAGATAGTGCAACTTATTACTGTCAGCAACATTATAGTACTCCCATTCACTTTTGGCCAGG

			GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATATCCAACATATTATGCCGATTCACTGAAAGACAGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGCGCTGTTACATCTGGCAACTACCCAACAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
333.	MCSP-F7 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSISTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGERATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTIDVLQPEDIATYYCQQHYSTPFTFGQGTRLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
334.	MCSP-F7 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCAAGAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCGATGTCCTGCA GCCTGAAGATATTGCAACTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTGGCCAGG GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA

				CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGCGGCTGTTACATCTCGCCAACTACCCAAACTGCGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
335.	MCSP-G5 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSISTVYMELSSLRSEDTAVYYCARSWYASWGQGTLVTVSSGGGGSGGGGSGGG GSDIVMTQSPDSLAVSLGDRATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTIDSLQPEDSATYYCQQHYSTPFTFGQGTRLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVISGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
336.	MCSP-G5 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGACAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCAACAAGAACACTATAGCTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCGATTCCCTGCA GCCTGAGGATAGTGCAACTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCAGG GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAGGACAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGCGGCTGTTACATCTCGCCAACTACCCAAACTGCGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC

				TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
337.	MCSP-F8 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGG GSDIVMTQSPDSLTVSLGERATINCKSSQSVLNSKNNRNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTIDSLQAEDSAIYYCQQHYSTPFTFGQGTRLEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
338.	MCSP-F8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCACTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACCCAGTCTCCAGACTCCCTGACTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTTTTAAACAGCAAGAACAATAGGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCGATTCCCTGCA GGCTGAAGATAGTGCAATTTATTACTGTCAGCAACATTATAGTACTCCATTCACTTTTGGCCAGG GGACCAGACTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGCGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
339.	MCSP-G10 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASMKVSCKASGYTFTNYYIHWVRQAPGQGLEWMGWINPNSGATNYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAKSWVSWFASWGQGTLVTVSSGGGGSGGGSGGG

					GSDIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLNWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHFNTPFAFGQGTKLEIKSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARF SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
340.	MCSP-G10 HL x I2C HL	artificial	nt		CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAGGCCTGGGGCCTCAATGAAGGTCTCCTG CAAGGCTTCTGGGTACACCTTCACCAACTACTATATACACTGGGTGCGACAGGCCCCTGGACAAG GTCTTGAGTGGATGGGTTGGATCAACCCTAACAGTGGTGCCACAAACTATGCACAGAAGTTCCAG GGCAGAGTCACCATGACCAGGGACACGTTCACAGACACAGTCTACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTACTGTGCGAAATCCTGGGTCTCCTGGTTTGCTTCCTGGGGTC AAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC CATCAACTGCAAGTCCAGCCAGAGTGTCTTATCCAGCTCCAACAATAAGAACTACTTAAATTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA GGCTGAAGATGTGGCGGTTTATTACTGTCAACAACATTTTAATACTCCGTTCGCTTTTGGCCAGG GGACCAAGCTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGA GGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAA GTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTTGGAATGGGTTGCTCGCATAAGAA GTAAATATAATTATGCCACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGA GATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTA CTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAG GGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGT TCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAG GTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTC TCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGC AGAATATTACTGTGTTCTATGGTACAGCCACCCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTG TCCTA
341.	Human CD3 epsilon 1-8 (N-terminus)	human	aa		QDGNEEMG
342.	*Saimiri sciureus* CD3 epsilon 1-8 (N-terminus)	*Saimiri sciureus*	aa		QDGNEEIG
343.	Thioate-modified CpG-Oligonucleotide	artificial	nt		TCCATGACGTTCCTGATGCT

344.	MVH1	artificial	nt	(GC)AGGTGCAGCTCGAGGAGTCAGGACCT
345.	MVH2	artificial	nt	GAGGTCCAGCTCGAGCACTCTGGACCT
346.	MVH3	artificial	nt	CAGGTCCAACTCGAGCACCCTGGGGCT
347.	MVH4	artificial	nt	GAGGTTCAGCTCGAGCAGTCTGGGGCA
348.	MVH5	artificial	nt	GA(AG)GTGAAGCTCGAGGAGTCTGGAGGA
349.	MVH6	artificial	nt	GAGGTGAAGCTTCTCGAGTCTGGAGGT
350.	MVH7	artificial	nt	GAAGTGAAGCTCGAGGAGACTCTGGGGGA
351.	MVH8	artificial	nt	GAGGTTCAGCTCGAGCAGTCTGGAGCT
352.	MuVHBstEII	artificial	nt	TGAGGAGACGGTGACCGTGGTCCCTTGGCCCCAG
353.	MUVK1	artificial	nt	CCAGTTCCGAGCTCGTTGTGACTCAGGAATCT
354.	MUVK2	artificial	nt	CCAGTTCCGAGCTCGTGTTGACGCAGCCGCCC
355.	MUVK3	artificial	nt	CCAGTTCCGAGCTCGTGCTCACCCAGTCTCCA
356.	MUVK4	artificial	nt	CCAGTTCCGAGCTCCAGATGACCCAGTCTCCA
357.	MUVK5	artificial	nt	CCAGATGTGAGCTCGTGATGACCCAGACTCCA
358.	MUVK6	artificial	nt	CCAGATGTTGAGCTCGTCATGACCCAGTCTCCA
359.	MUVK7	artificial	nt	CCAGTTCCGAGCTCGTGATGACACAGTCTCCA
360.	MuVkHindIII/BsiW1	artificial	nt	TGGTGCACTAGTCGTACGTTTGATCTCCAAGCTTGGTCCC
361.	forward primer	artificial	nt	GATCTGGTCTACACCATCGAGC
362.	reverse primer	artificial	nt	GGAGCTGCTGCTGGCTCAGTGAGG
363.	forward primer	artificial	nt	TTCCAGCTGAGCATGTCTGATGG
364.	reverse primer	artificial	nt	CGATCAGCATCTGGGCCCAGG
365.	forward primer	artificial	nt	GTGGAGCAGTTCACTCAGCAGGACC
366.	reverse primer	artificial	nt	GCCTTCACACCCAGTACTGGCC
367.	forward primer	artificial	nt	TCCCGTACGAGATCTGGATCCCAATTGGATGGCGGACTCGTGCTGTTCTCACACAGAGG
368.	reverse primer	artificial	nt	AGTGGGTCGACTCACACCCAGTACTGGCCAITCTTAAGGGCAGGG
369.	forward primer	artificial	nt	GAGGAATTCACCATGCCCCTGCTGCTACTGCTGCCCCTGCTGTGGGCAGGGGCCCTGGCTATGG
370.	reverse primer	artificial	nt	GATTTGTAACTGTATTTCGTACTTCC
371.	forward primer	artificial	nt	ATTCCGCCTCCTTGGGGATCC
372.	reverse primer	artificial	nt	GCATAGGAGACATTGAGCTGGATGG
373.	forward primer	artificial	nt	GCACCAACCTGACCTGTCAGG
374.	reverse primer	artificial	nt	AGTGGGTCGACTCACTGCGTCCTGACCTCTGAGTATTCG
375.	PSCA-1 VL	artificial	aa	DIQLTQSPSSLSASVGDRVTITCSASSSVRFIHWYQQKPGKAPKRLIYDTSKLASGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQWSSSPFTFGQGTKVEIK
376.	PSCA-1 VL	artificial	nt	GACATCCAGCTGACCCAGAGCCCATCCAGCCTGTCTGCTAGCGTGGGCGACAGAGTGACCATCAC CTGCAGCGCCAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGCCCGGCAAGGCCCCA

				AGAGGCTGATCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAAGCAGATTCAGCGGCAGCGGC TCCGGCACCGACTTCACCCTGACCATCAGCAGCCTGCAGCCAGAGGACTTCGCTACCTATTACTG CCAGCAGTGGAGCAGCACCCCCTTCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAG
377.	PSCA-1 LCDR1	artificial	aa	SASSSVRFIH
378.	PSCA-1 LCDR2	artificial	aa	DTSKLAS
379.	PSCA-1 LCDR3	artificial	aa	QQWSSSPFT
380.	PSCA-1 H	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDYYIHWVRQAPGKGLEWVAWIDPENGDTEFVPKFQ GRATISADTSKNTAYLQMNSLRAEDTAVYYCKTGGFWGQGTLVTVSS
381.	PSCA-1 H	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGCGGAGGACTGGTGCAGCCAGGCGGCTCCCTGAGACTGAGCTG CGCCGCCAGCGGCTTCAACATCAAGGACTACTACATCCACTGGGTCCGGCAGGCTCCAGGCAAGG GACTGGAATGGGTGGCCTGGATCGACCCAGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAG GGCAGAGCCACCATCAGCGCCGACACCTCCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAG GGCCGAGGACACCGCCGTGTACTACTGCAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCA CCGTGTCCTCC
382.	PSCA-1 HCDR1	artificial	aa	DYYIH
383.	PSCA-1 HCDR2	artificial	aa	WIDPENGDTEFVPKFQG
384.	PSCA-1 HCDR3	artificial	aa	GGF
385.	PSCA-1 HL	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDYYIHWVRQAPGKGLEWVAWIDPENGDTEFVPKFQ GRATISADTSKNTAYLQMNSLRAEDTAVYYCKTGGFWGQGTLVTVSSGGGGSGGGGSGGGGSDIQ LTQSPSSLSASVGDRVTITCSASSSVRFIHWYQQKPGKAPKRLIYDTSKLASGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQWSSSPFTFGQGTKVEIK
386.	PSCA-1 HL	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGCGGAGGACTGGTGCAGCCAGGCGGCTCCCTGAGACTGAGCTG CGCCGCCAGCGGCTTCAACATCAAGGACTACTACATCCACTGGGTCCGGCAGGCTCCAGGCAAGG GACTGGAATGGGTGGCCTGGATCGACCCAGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAG GGCAGAGCCACCATCAGCGCCGACACCTCCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAG GGCCGAGGACACCGCCGTGTACTACTGCAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCA CCGTGTCCTCCGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTGACATCCAG CTGACCCAGAGCCCCATCAGCCTGTCTGCTAGCGTGGGCGACAGAGTGACCATCACCTGCAGCGC CAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGAGGCTGA TCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAAGCAGATTCAGCGGCAGCGGCTCCGGCACC GACTTCACCCTGACCATCAGCAGCCTGCAGCCAGAGGACTTCGCTACCTATTACTGCCAGCAGTG GAGCAGCACCCCCTTCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAG
387.	PSCA-1 LH	artificial	aa	DIQLTQSPSSLSASVGDRVTITCSASSSVRFIHWYQQKPGKAPKRLIYDTSKLASGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQWSSSPFTFGQGTKVEIKGGGGSGGGGSGGGGSEVQLVESGG GLVQPGGSLRLSCAASGFNIKDYYIHWVRQAPGKGLEWVAWIDPENGDTEFVPKFQGRATISADT SKNTAYLQMNSLRAEDTAVYYCKTGGFWGQGTLVTVSS

388.	PSCA-1 LH	artificial	nt	GACATCCAGCTGACCCAGAGCCCATCCAGCCTGTCTGCTAGCGTGGGCGACAGAGTGACCATCAC CTGCAGCGCCAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGCCCGGCAAGGCCCCCA AGAGGCTGATCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAAGCAGATTCAGCGGCAGCGGC TCCGGCACCGACTTCACCCTGACCATCAGCCCTCCAGCCACAGGACTTCGCTACCTATTACTG CCAGCAGTGGAGCAGCACCCCCTTCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGGGTGGTG GTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGGTGCAGCTGGTCGAGTCTGGCGGA GGACTGGTGCAGCCAGGCGGCTCCCTGAGACTGAGCTGCGCCGCCAGCGGCTTCAACATCAAGGA CTACTACATCCACTGGGTCCGGCAGGCTCCAGGCAAGGGACTGGAATGGGTGGCCTGGATCGACC CAGAGAACGGCGACACCCAGTTCGTGCCCAAGTTCCAGGGCAGAGCCACCATCAGCGCCGACACC TCCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGGGCCGAGGACACCGCCGTGTACTACTG CAAGACCGGCGGCGGCTTCTGGGGACAGGGCACCCTGGTCACCGTGTCCTCC
389.	PSCA-1 HL x I2C HL	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDYYIHWVRQAPGKGLEWVAWIDPENGDTEFVPKFQ GRATISADTSKNTAYLQMNSLRAEDTAVYYCKTGGFWGQGTLVTVSSGGGGSGGGGSDIQ LTQSPSSLSASVGDRVTITCSASSSVRFIHWYQQKPGKAPKRLIYDTSXLASGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQWSSSPFTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
390.	PSCA-1 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGCGGAGGACTGGTGCAGCCAGGCGGCTCCCTGAGACTGAGCTG CGCCGCCAGCGGCTTCAACATCAAGGACTACTACATCCACTGGGTCCGGCAGGCTCCAGGCAAGG GACTGGAATGGGTGGCCTGGATCGACCCAGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAG GGCAGAGCCACCATCAGCGCCGACACCTCCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAG GGCCGAGGACACCGCCGTGTACTACTGCAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCA CCGTGTCCTCCGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTGACATCCAG CTGACCCAGAGCCCATCCAGCCTGTCTGCTAGCGTGGGCGACAGAGTGACCATCACCTGCAGCGC CAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGAGGCTGA TCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAAGCAGATTCAGCGGCAGCGGCTCCGGCACC GACTTCACCCTGACCATCAGCAGCCTGCAGCCAGAGGACTTCGCTACCTATTACTGCCAGCAGTG GAGCAGCAGCCCCTTCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGGTCCGGAGGTGGTGGAT CCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAA GGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATT CAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAAC AACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTA CATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTT CTGGCGGCGGCGGCTCCGGTGGTGGTTCTGACTGTTGTGACTCAGGAACCTTCACTCACC

				GTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAA CTACCCAAACTGGGTCCAACACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGT TCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACC CTCTCAGGCGTACAGCCAGAGGATGAGGCAGAATATTACTGTCTTCTATGGTACAGCAACCGCTG GGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
391.	PSCA-1 LH x I2C HL	artificial	aa	DIQLTQSPSSLSASVGDRVTITCSASSSVRFIHWYQQKPGKAPKRLIYDTSKLASGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQWSSSPFTFGQGTKVEIKGGGSGGGGSGGGGSEVQLVESGG GLVQPGGSLRLSCAASGFNIKDYYIHWVRQAPGKGLEWVAWIDPENGDTEFVPKFQGRATISADT SKNTAYLQMNSLRAEDTAVYYCKTGGFWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSC AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVISGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
392.	PSCA-1 LH x I2C HL	artificial	nt	GACATCCAGCTGACCCAGAGCCCATCCAGCCTGTCTGCTAGCGTGGGCGACAGAGTGACCATCAC CTGCAGCGCCAGCAGCAGGCGTGCGGTTCATCCACTGGTATCAGCAGAAGCCCGGCAAGGCCCCCA AGAGGCTGATCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAGCAGATTCAGCGGCAGCGGC TCCGGCACCGACTTCACCCTGACCATCAGCAGCCTGCAGCCAGAGGACTTCGCTACCTATTACTG CCAGCAGTGGAGCAGCACCCCTTCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGGGTGGTG GTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGGTGCAGCTGGTCGAGTCTGGCGGA GGACTGGTGCAGCCAGGCGGCTCCCTGAGACTGAGCTGCGCCGCCAGCGGCTTCAACATCAAGGA CTACTACATCCACTGGGTCCGGCAGGCTCCAGGGCAAGGAACTGGAATGGGTGGCCTGGATCGACCC CAGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAGGGCCAGAGCCACCATCAGCGCCGACACC TCCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGGGCCGAGGACACCGCCGTGTACTACTG CAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCACCGTGTCCTCCGGAGGTGGTGGATCCG AGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGCTCATTGAAACTCTCATGT GCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGG TTTGGAATGGGTTGCTCCCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAG TGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAAC TTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACAT ATCCTACTGGGCTTACTGGGCCAAGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTG GCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTA TCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGT GTTCGGTGGAGGAACCAAACTGACTGTCCTA
393.	PSCA-2 VL	artificial	aa	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQSPQLLIYRMSNLASGVPD

				RFSGSGSGTAFTLRISRVEAEDVGVYYCLQHLEYPYTFGGGTKLELK
394.	PSCA-2 VL	artificial	nt	GACATCGTGATGACCCAGGCCGCTCCAAGCGTGCCAGTGACCCCAGGCGAGAGCGTGTCCATCAG CTGCAGGTCCAGCAAGAGCCCTGCTGCACAGCAACGGCAACACCTACCTGTACTGGTTTCTGCAGA GGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGAC AGATTCAGCGGCAGCGGCTCTGGAACCGCCTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGA CGTGGGCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCGGAGGGACCAAGC TGGAACTGAAC
395.	PSCA-2 LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
396.	PSCA-2 LCDR2	artificial	aa	RMSNLAS
397.	PSCA-2 LCDR3	artificial	aa	LQHLEYPYT
398.	PSCA-2 H	artificial	aa	QVQVQQPGAELVKPGAPVKLSCKASGYTFTNYWLNWVKQRPGRGLEWIGRIDPSDSEIHYDQKFK DKATLTVDKSSSTAYTQLSSLTSEDSAVYYCATLTGTYAMAYWGQGTSVTVSS
399.	PSCA-2 H	artificial	nt	CAGGTGCAGGTGCAGCAGCCCAGGCGCCGAACTGGTCAAGCCTGGCGCCCCAGTGAAGCTGTCCTG CAAGGCCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTGAAACAGAGGCCCGGCAGGG GCCTGGAATGGATCGGCAGGATCGACCCCAGCGACAGCGAGATCCACCTACGACCAGAAGTTCAAG GACAAGGCCACCCTGACCGTGGACAAGAGCAGCAGCACCGCCTACATCCAGCTGTCCAGCCTGAC CAGCGAGGACAGCGCCGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCC AGGGCACCAGCGTGACCGTGTCTTCC
400.	PSCA-2 HCDR1	artificial	aa	NYWLN
401.	PSCA-2 HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
402.	PSCA-2 HCDR3	artificial	aa	TGIYAMAY
403.	PSCA-2 LH	artificial	aa	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQSPQLLIYRMSNLASGVPD RFSGSGSGTAFTLRISRVEAEDVGVYYCLQHLEYPYTFGGGTKLELKGGGSGGGGSGGGSQVQ VQQPGAELVKPGAPVKLSCKASGYTFTNYWLNWVKQRPGRGLEWIGRIDPSDSEIHYDQKFKDKA TLTVDKSSSTAYIQLSSLTSEDSAVYYCALIGIYAMAYWGQGTSVTVSS
404.	PSCA-2 LH	artificial	nt	GACATCGTGATGACCCAGGCCGCTCCAAGCGTGCCAGTGACCCCAGGCGAGAGCGTGTCCATCAG CTGCAGGTCCAGCAAGAGCCCTGCTGCACAGCAACGGCAACACCTACCTGTACTGGTTTCTGCAGA GGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGAC AGATTCAGCGGCAGCGGCTCTGGAACCGCCTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGA CGTGGGCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCGGAGGGACCAAGC TGGAACTGAAGGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG GTGCAGCAGCCAGGCGCCGAACTGGTCAAGCCTGGCGCCCCAGTGAAGCTGTCCTGCAAGGCCAG CGGCTACACCTTCACCAACTACTGGCTGAACTGGGTGAAACAGAGGCCCGGCAGGGCCTGGAAT GGATCGGCAGGATCGACCCCAGCGACAGCGAGATCCACTACGACCAGAAGTTCAAGGACAAGGCC ACCCTGACCGTGGACAAGAGCAGCAGCACCGCCTACATCCAGCTGTCCAGCCTGACCAGCGAGGA CAGCGCCGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCACCA

				GCGTGACCGTGTCTTCC
405.	PSCA-2 LH x I2C HL	artificial	aa	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQSPQLLIYRMSNLASGVPD RFSGSGSGTAFTLRISRVEAEDVGVYYCLQHLEYPYTFGGGTKLELKGGGGSGGGGSGGGGSQVQ VQQPGAELVKPGAPVKLSCKASGYTFTNYWLNWVKQRPGRGLEWIGRIDPSDSEIHYDQKFKDKA TLTVDKSSSTAYIQLSSLTSEDSAVYYCALIGIYAMAYWGQGTSVTVSSGGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQ TVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
406.	PSCA-2 LH x I2C HL	artificial	nt	GACATCGTGATGACCCAGGCCGCTCCAAGCGTGCCAGTGACCCCAGGCGAGAGCGTGTCCATCAG CTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTACCTGTACTGGTTTCTGCAGA GGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGAC AGATTCAGCGGCAGCGGCTCTGGAACCGCCTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGA CGTGGGCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCGGAGGGACCAAGC TGGAACTGAAGGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG GTGCAGCAGCCAGGCGCCGAACTGGTCAAGCCTGGCGCCCCAGTGAAGCTGTCCTGCAAGGCCAG CGGCTACACCTTCACCAACTACTACGGCTGAACTGGGTGAAACAGAGGCCCGGCAGGGCCTGGAAT GGATCGGCAGGATCGACCCCAGCGACAGCGAGATCCACTACGACCAGAAGTTCAAGGACAAGGCC ACCCTGACCGTGGACAAGAGCAGCACAGCGCCTACATCCAGCTGTCCAGCCTGACCAGCGAGGA CAGCGCCGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCACCA GCGTGACCGTGTCTTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTTCGAGTCTGGAGGAGGATTG GTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGC CATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAT ATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGAT TCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTG TGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTC TGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAG ACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGG CACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGC TCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATA TTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
407.	PSCA-3 VL	artificial	aa	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSTLDSGVPD RETGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK
408.	PSCA-3 VL	artificial	nt	GACGTGGTCATGACCCAGACCCCCCTGACCCTGAGCGTGACCATCGGCCAGCCAGCCAGCATCTC TTGCAAGTCCAGCCAGTCCCTGCTGGACAGCGACGGCAAGACCTACCTGAACTGGCTGCTGCAGA GGCCAGGCCAGAGCCCCAAGAGGCTGATCTACCTGGTGTCCAAGCTGGACAGCGGCGTGCCAGAC

				AGATTCACCGGCAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGA CCTGGGCGTGTACTACTGCTGGCAGGGCACCCACTTCCCAAGGACCTTCGGCGGAGGGACCAAGC TGGAAATCAAG
409.	PSCA-3 LCDR1	artificial	aa	KSSQSLLDSDGKTYLN
410.	PSCA-3 LCDR2	artificial	aa	LVSTLDS
411.	PSCA-3 LCDR3	artificial	aa	WQGTHFPRT
412.	PSCA-3 H	artificial	aa	EVQLQQSGPDLEKPGASVKISCKPSGNSFTGYYIHWVKQSHGKSLEWIGRVDPNNGFTSYNQKFK GKAILTVDKSSSTAYMELRSLTSEDSAVYYCVGNFFDSWGQGTTLTVSS
413.	PSCA-3 H	artificial	nt	GAAGTGCAGCTGCAGCAGAGCGGCCCCAGACCTGGAAAAGCCCAGGCGCCAGCGTGAAGATTTCCTG CAAGCCCAGCGGCAACACGCTTCACCGGCTACTACATCCACTGGGTGAAACAGTCCCACGGGAAGA GCCTGGAATGGATCGGCAGAGTGGACCCCAACAACGGCTTCACCTCCTACACCAGAAGTTCAAG GGCAAGGCCATCCTGACCGTGGACAAGAGCAGCAGCACCGCCTACATGGAACTGAGAAGCCTGAC CAGCGAGGACAGCGCCGTGTACTATTGCGTGGGCAACTTCTTCGACAGCTGGGGCCAGGGAACCA CACTGACCGTGTCCTCC
414.	PSCA-3 HCDR1	artificial	aa	GYYIH
415.	PSCA-3 HCDR2	artificial	aa	RVDPNNGFTSYNQKFKG
416.	PSCA-3 HCDR3	artificial	aa	NFFDS
417.	PSCA-3 HL	artificial	aa	EVQLQQSGPDLEKPGASVKISCKPSGNSFTGYYIHWVKQSHGKSLEWIGRVDPNNGFTSYNQKFK GKAILTVDKSSSTAYMELRSLTSEDSAVYYCVGNFFDSWGQGTTLTVSSGGGGSGGGGSGGGGSD VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSTLDSGVPDR FTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK
418.	PSCA-3 HL	artificial	nt	GAAGTGCAGCTGCAGCAGAGCGGCCCCAGACCTGGAAAAGCCCAGGCGCCAGCGTGAAGATTTCCTG CAAGCCCAGCGGCAACACGCTTCACCGGCTACTACATCCACTGGGTGAAACAGTCCCACGGGAAGA GCCTGGAATGGATCGGCAGAGTGGACCCCAACAACGGCTTCACCTCCTACACCAGAAGTTCAAG GGCAAGGCCATCCTGACCGTGGACAAGAGCAGCACCGCCTACATGGAACTGAGAAGCCTGAC CAGCGAGGACAGCGCCGTGTACTATTGCGTGGGCAACTTCTTCGACAGCTGGGGCCAGGGAACCA CACTGACCGTGTCCTCCGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGACATCCTG GTGGTCATGACCCAGACCCCCCTGAGCCTGAGCGTGACCATCGGCCAGCCAGCCATCTCTTG CAAGTCCAGCCAGTCCCTGCTGGACAGCGACGGCAAGACCTACCTGAACTGGCTGCTGCAGAGGC CAGGCCAGAGCCCCAAGAGGCTGATCTACCTGGTGTCCAAGCTGGACAGCGGCGTGCCAGACAGA TTCACCGGCAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACCT GGCGTGTACTACTGCTCCAGCGGCACCCACTTCCCAAGGACCTTCGGCGGAGGGACCAAGCTGG AAATCAAG
419.	PSCA-3 LH	artificial	aa	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSTLDSGVPD RFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIKGGGSGGGGSGGGGSEVQ LQQSGPDLEKPGASVKISCKPSGNSFTGYYIHWVKQSHGKSLEWIGRVDPNNGFTSYNQKFKGKA

				ILTVDKSSSTAYMELRSLTSEDSAVYYCVGNFFDSWGQGTTLTVSS
420.	PSCA-3 LH	artificial	nt	GACGTGGTCATGACCCAGACCCCCCTGACCCTGAGCGTGACCATCGGCCAGCCAGCCATCTC TTGCAAGTCCAGCCAGTCCCTGCTGGACAGCGACGGCAAGACCTACCTGAACTGGCTGCTGCAGA GGCCAGGCCAGAGCCCCAAGAGGCTGATCTACCTGGTGTCCAACCCTGGACAGCGGCGTGCCAGAC AGATTCACCGGCAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGA CCTGGGCGTGTACTACTGCTGGCAGGGCACCCACTTCCCAAGGACCTTCGGCGGAGGGACCAAGC TGGAAATCAAGGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTGAAGTGCAG CTGCAGCAGAGCGGCCCCAGACCTGGAAAGCCAGGCGCCAGCGTGAAGATTTCCTGCAAGCCCAG CGGCAACAGCTTCACCGGCTACTACATCCACTGGGTGAAACAGTCCCACGGGAAGAGCCTGGAAT GGATCGGCAGATTGGACCCCAACAACGGCTTCACCTCCTACAACCAGAAGTTCAAGGGCAAGGCC ATCCTGACCGTGGACAAGAGCAGCAGCACCGCCTACATGGAACTGAGAAGCCTGACCAGCGAGGA CAGCGCCGTGTACTATTGCGTGGGCAACTCTCTTCGACAGCTGGGGCCAGGGAACCACACTGACCG TGTCCTCC
421.	PSCA-3 HL x I2C HL	artificial	aa	EVQLQQSGPDLEKPGASVKISCKPSGNSFTGYYIHWVKQSHGKSLEWIGRVDPNNGFTSYNQKFK GKAILTVDKSSSTAYMELRSLTSEDSAVYYCVGNFFDSWGQGTTLTVSSGGGGSGGGGSGGGGSD VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSTLDSGVPDR FTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIKSGGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLICGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
422.	PSCA-3 HL x I2C HL	artificial	nt	GAAGTGCAGCTGCAGCAGAGCGGCCCAGACCTGGAAAAGCCAGGCGCCAGCGTGAAGATTTCCTG CAAGCCCAGCGGCAACAGCTTCACCGGCTACTACATCCACTGGGTGAAACAGTCCCACGGGAAGA GCCTGGAATGGATCGGCAGAGTGGACCCCAACAACGGCTTCACCTCCTACAACCAGAAGTTCAAG GGCAAGGCCATCCTGACCGTGGACAAGAGCAGCACCGCCTACATGGAACTGAGAAGCCTGACC CAGCGAGGACAGCGCCGTGTACTATTGCGTGGGCAACTTCTTCGACAGCTGGGGCCAGGGAACCA CACTGACCGTGTCCTCCGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAC GTGGTCATGACCCAGACCCCCCTGACCCTGAGCGTGACCATCGGCCAGCCAGCCATCTCTTG CAAGTCCAGCCAGTCCCTGCTGGACAGCGACGGCAAGACCTACCTGAACTGGCTGCTGCAGAGGC CAGGCCAGAGCCCCAAGAGGCTGATCTACCTGGTGTCCAACCCTGGACAGCGGCGTGCCAGACAGA TTCACCGGCAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACCT GGGCGTGTACTACTGCTGGCAGGGCACCCACTTCCCAAGGACCTTCGGCGGAGGGACCAAGCTGG AAATCAAGGGTGGTGGTGGTTCTGGAGGTGGCAGCTGGTCGAGTCTGGAGGAGGATTTGGTGCAG CCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAA CTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATA ATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAA AACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAG

				ACATGGGAACTTCGGTAATAGCTACATATCCTACTGGCTTACTGGGCCAAGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTT GTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGGCTCCTC GACTGGGGCTCTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCACGCACCCC GTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTG CTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGTACAGCCAGAGGACTGAGGCAGAATATTACTG TGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
423.	PSCA-3 LH x I2C HL	artificial	aa	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSTLDSGVPD RFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIKGGGSGGGGSGGGGSEVQ LQQSGPDLEKPGASVKLSCKPSGNSFTGYYLHWVKQSHGKSLEWIGRVDPNNGNTSYNQKFKGKA ILTVDKSSSTAYMELRSLTSEDSAVYYCVGNFFDSWGQGTTLTVSSGGGGSEVQLVESGGGLVQP GGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKN TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
424.	PSCA-3 LH x I2C HL	artificial	nt	GACGTGGTCATGACCCAGACCCCCCCTGACCCTGAGCGTGACCATCGGCCAGCCAGCCATCTC TTGCAAGTCCAGCCAGTCCCTGCTGGACAGCGACGGCAAGACCTACCTGAACTGGCTGCTGCAGA GGCCAGGCCAGAGCCCCAAGAGGCTGATCTACCTGGTGTCCAAGCTGGACAGCGGCGTGCCAGAC AGATTCACCGGCAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGA CCTGGGCGTGTACTACTGCTGGCAGGGCACCCACTTCCCCAAGGACCTTCGGCGGAGGGACCAAGC TGGAAATCAAGGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTGAAGTGCAG CTGCAGCAGAGCGGCCCCAGACCTGGAAAGCCCAGGCGCCAGCGGTGAAGATTTCCTGCAAGCCCAG CGGCAACAGCTTCACCGGCTACTACATCCACTGGGTGAAACAGTCCCACGGGAAGAGCCTGGAAT GGATCGGCAGAGTGGACCCCAACAACGGCTTCACCTCCTACAACCAGAAGTTCAAGGGCAAGGCC ATCCTGACCGTGGACAAGAGCAGCAGCACCGCCTACATGGAACTGAGAAGCCTGACCAGCGAGGA CAGCGCCGTGTACTATTGCGTGGGCAACTTCTTCGACAGCTGGGGCCAGGGAACCACACTGACCG TGTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCT GGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAACTAAGTACGCCATGAACTG GGTCCGCCAGGCTCCAGGCAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTAT ATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAAC ACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACA TGGGAACTTCGGTAATACGCTACATATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCG TCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTG GTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTT GGAGGCAAGGCTGCCCTCACCCTCTCAGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGT

				TCTATGGTACAGCAACCGCCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
425.	PSCA-4 VL	artificial	aa	QVVLTQSPAIMSASPGEKVTMACSASSVRFIHWYQQKSGTSPKRWIYDTSKLASGVPTRFSGSG SGTSYSLTISTMEAEDAATYYCQQWSSSPFTFGSGTKLEIK
426.	PSCA-4 VL	artificial	nt	CAGGTGGTGCTGACCCAGAGCCCAGCCATCATGAGCGCCAGCCCAGGCGAGAAGGTGACCATGCC CTGCAGCGCCAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGTCCGGCACCAGCCCCA AGAGATGGATCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAACCAGATTCAGCGGAAGCGGC TCCGGCACCTCCTACAGCCTGACCATCAGCACCATGGAAGCCGAGGACGCCGCCACCTACTACTG CCAGCAGTGGAGCAGCAGCCCCTTCACCTTCGGCAGCGGCACCAAGCTGGATCATCAAG
427.	PSCA-4 LCDR1	artificial	aa	SASSSVRFIH
428.	PSCA-4 LCDR2	artificial	aa	DTSKLAS
429.	PSCA-4 LCDR3	artificial	aa	QQWSSSPFT
430.	PSCA-4 H	artificial	aa	EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEFVPKFQ GKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGGFWGQGTLVTVSS
431.	PSCA-4 H	artificial	nt	GAAGTGCAGCTGCAGCAGTCTGGAGCCGAGCTGGTCAGATCTGGAGCCAGCGTGAAGCTGTCTTG CACCGCCAGCGGCTTCAACATCAAGGACTACTACATCCACTGGGTGAACCAGAGGCCCGACCAGG GCCTGGAATGGATCGGCTGGATCGACCCCGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAG GGCAAGGCCACCATGACCGCCGACACATCTTCAGCAACACCGCCTACCTGCACCTGAGCAGCCTGAC CTCTGAGGACACCGCCGTGTACTACTGCAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCA CCGTGTCCTCC
432.	PSCA-4 HCDR1	artificial	aa	DYYIH
433.	PSCA-4 HCDR2	artificial	aa	WIDPENGDTEFVPKFQG
434.	PSCA-4 HCDR3	artificial	aa	GGF
435.	PSCA-4 HL	artificial	aa	EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEFVPKFQ GKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGGFWGQGTLVTVSSGGGGSGGGGSGGGGSQVV LTQSPAIMSASPGEKVTMACSASSVRFIHWYQQKSGTSPKRWIYDTSKLASGVPTRFSGSGSGT SYSLTISTMEAEDAATYYCQQWSSSPFTFGSGTKLEIK
436.	PSCA-4 HL	artificial	nt	GAAGTGCAGCTGCAGCAGTCTGGAGCCGAGCTGGTCAGATCTGGAGCCAGCGTGAAGCTGTCTTG CACCGCCAGCGGCTTCAACATCAAGGACTACTACATCCACTGGGTGAACCAGAGGCCCGACCAGG GCCTGGAATGGATCGGCTGGATCGACCCCGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAG GGCAAGGCCACCATGACCGCCGACACATCTTCAGCAACACCGCCTACCTGCACCTGAGCAGCCTGAC CTCTGAGGACACCGCCGTGTACTACTGCAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCA CCGTGTCCTCCGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGGTG CTGACCCAGAGCCCAGCCATCATGAGCGCCAGCCCAGGCGAGAAGGTGACCATGGCCTGCAGCGC CAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGTCCGGCACCAGCCCCAAGAGATGGA TCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAACCAGATTCAGCGGAAGCGGCTCCGGCACC TCCTACAGCCTGACCATCAGCACCATGGAAGCCGAGGACGCCGCCACCTACTACTGCCAGCAGTG

				GAGCAGCAGCCCCCTTCACCTTCGGCAGCGGCACCAAGCTGATCATCAAG
437.	PSCA-4 LH	artificial	aa	QVVLTQSPAIMSASPGEKVTMACSASSSVRFIHWYQQKSGTSPKRWIYDTSKLASGVPTRFSGSG SGTSYSLTISTMEAEDAATYYCQQWSSSPFTFGSGTKLEIKGGGGSGGGGSGGGGSEVQLQQSGA ELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEFVPKFQGKATMTADI FSNTAYLHLSSLTSEDTAVYYCKTGFWGQGTLVTVSS
438.	PSCA-4 LH	artificial	nt	CAGGTGGTGCTGACCCAGAGCCCAGCCATCATGAGCGCCAGGCCAGGCGAGAAAGTGACCATGGC CTGCAGCGCCAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGTCCGGCACCAGCCCCA AGAGATGGATCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAACCAGATTCAGCGGAAGCGGC TCCGGCACCTCCTACAGCCTGACCATCAGCACCATGGAAGCCGAGGACGCCGCCACCTACTACTG CCAGCAGTGGAGCAGCACCCCCTTCACCTTCGGCAGCGGCACCAAGCTGATCATCAAGGGTGGTG GTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAAGTGCAGCTGCAGCAGTCTGGAGCC GAGCTGGTCAGATCTGGAGCCAGCGTGAAGCTGTCTTGCACCGCCAGCGGCTTCAACATCAAGGA CTACTACATCCACTGGGTGAACCAGAGGCCCGACCAGGGCCTGGAATGGATCGGCTGGATCGACC CCGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAGGGCAAGGCCACCATGACCGCCGACATC TTCAGCAACACCGCCTACCTGCACCTGAGCAGCCTGACCTCTGAGGACACCGCCGTGTACTACTG CAAGACCGGCGGCTTCTGGGACAGGGCACCCTGGTCACCGTGTCCTCC
439.	PSCA-4 HL x I2C HL	artificial	aa	EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEFVPKFQ GKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGFWGQGTLVTVSSGGGGSGGGGSGGGGSQVV LTQSPAIMSASPGEKVTMACSASSSVRFIHWYQQKSGTSPKRWIYDTSKLASGVPTRFSGSGSGT SYSLTISTMEAEDAATYYCQQWSSSPFTFGSGTKLEIKSGGGSGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
440.	PSCA-4 HL x I2C HL	artificial	nt	GAAGTGCAGCTGCAGCACTCTGGAGCCGAGCTGGTCAGATCTGGAGCCAGCGTGAAGCTGTCTTG CACCGCCAGCGGCTTCAACATCAAGGACTACTACATCCACTGGGTGAACCAGAGGCCCGACCAGG GCCTGGAATGGATCGGCTGGATCGACCCCGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAG GGCAAGGCCACCATGACCGCCGACATCTTCAGCAACACCGCCTACCTGCACCTGAGCAGCCTGAC CTCTGAGGACACCGCCGTGTACTACTGCAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCA CCGTGTCCTCCGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGGTG CTGACCCAGAGCCCAGCCATCATGAGCGCCAGGCGAGAAAGTGACCATGGCCTGCAGCGC CAGCAGCAGCGTGCGGTTCATCCACTGGTATCAGCAGAAGTCCGGCACCAGCCCCAAGAGATGGA TCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAACCAGATTCAGCGGCTCCGGCACC TCCTACAGCCTGACCATCAGCACCATGGAAGCCGAGGACGCCGCCACCTACTACTGCCAGCAGTG GAGCAGCACCCCCTTCACCTTCGGCAGCGGCACCAAGCTGATCATCAAGTCCGGAGGTGGTGAT CCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGIACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAA

				GGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAACTATGCAACATATTATGCCGATT CAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAAC AACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTA CATATCCTACTCGGCTTACTGGGCCAACGCACTCTGCTCACCGTCTCCTCAGGTGCTGGCTGGTT CTGGCGGCGGCGCTCCCGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACC GTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAA CTACCCAAACTGGGTCCAACAAAAACCAGGTCACGCCCCGTGGTCTCAATAGGTGGGACTAAGT TCCTCGCCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACC CTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTG GGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
441.	PSCA-4 LH x I2C HL	artificial	aa	QVVLTQSPAIMSASPGEKVTMACSASSSVRFIHWYQQKSGTSPKRWIYDTSKLASGVPTRFSGSG SGTSYSLTISTMEAEDAATYYCQQWSSSPFTFGSGTKLEIKGGGGSGGGGSGGGGSEVQLQQSGA ELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEFVPKFQGKATMTADI FSNTAYLHLSSLTSEDTAVYYCKTGGFWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSC AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
442.	PSCA-4 LH x I2C HL	artificial	nt	CAGGTGGTGCTGACCCAGAGCCCAGCCATCATGAGCGCCAGCCCAGGCGAGAAGGTGACCATGGC CTGCAGCCGCCAGCAGCAGCGTGCCGGTTCATCTCACTGGTATCAGCAGAAGTCCGGCACCAGCCCCA AGAGATGGATCTACGACACCAGCAAGCTGGCTAGCGGCGTGCCAACCAGATTCAGCGGCGAAGCGGC TCCGGCACCTCCTACAGCCTGACCATCAGCACCATGGAAGCCGAGGACGCCGCCACCTACTACTG CCAGCAGTGGAGCAGCACCCCTTCACCTTCGGCAGCGGCACCAAGCTGATCATCAAGGGTGGTG GTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAAGTGCAGCTGCAGCAGTCTGGAGCC GAGCTGGTCAGATCTGGAGCCAGCGTGAAGCTGTCTTGCACCGCCAGCGGCTTCAACATCAAGGA CTACTACATCCACTGGGTGAACCAGAGGCCCGACCAGGGCCTGGAATGGATCGGCTGGATCGACC CCGAGAACGGCGACACCGAGTTCGTGCCCAAGTTCCAGGGCAAGGCCACCATGACCGCCGACATC TTCAGCAACACCGCCTACCTGCACCTGAGCAGCCTGACCTCTGAGGACACCGCCGTGTACTACTG CAAGACCGGCGGCTTCTGGGGACAGGGCACCCTGGTCACCGTGTCCTCCGGAGGTGGTGGATCCG AGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGT GCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGG TTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAACTATGCAACATATTATGCCGATTCAG TGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTACTACAAATGAACAAC TTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACAT ATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTG GCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTA TCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA

					CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAA-AGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGACGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGT GTTCGGTGCAGGAACCAAACTGACTGTCCTA
443.	PSCA	human	aa		MGWSCIILFLVATATGVHSDYKDDDDKLLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGL LTVISKGCSLNCVDDSQDYYVGKKNITCCDIDLCNASGAHALQPAAA-LALLPALGLLLWGPGQL
444.	PSCA	human	nt		ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGATTACAA GGACGACGATGACAAGCTGCTGTGCTACTCCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGC AGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTC CTGACCGTCATCAGCAAAGGCTGCAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGG CAAGAAGAACATCACGTCCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGC CGGCTGCTGCCATCCTTCCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTC TAG
445.	PSCA	Macaque (Cynomolgus)	aa		MGWSCIILFLVATATGVHSDYKDDDDKLLCYSCKAQVSNEDCLNVENCTQPEEQCWTERIRAVGL LTVISKGCSSNCVDDSQDYYVGKKNITCCDIDLCNASGAHALQPAAA-LALLPALSLLLWGPRQL
446.	PSCA	Macaque (Cynomolgus)	nt		ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGATTACAA GGACGACGATGACAAGCTGCTGTGCTACTCCTGCAAGGCCCAGGTGAGCAACGAGGACTGCCTGA ATGTGGAGAACTGCACGCAGCCGGAGGAGCAGTGCTGGACCGAGCGCATCCGCGCCGTGGGCCTC CTGACCGTCATCAGCAAAGGCTGCAGCTCAAACTGCGTGGATGACTCACAGGACTACTACGTGGG CAAGAAGAACATCACCTCCTGTGACACCGACCTGTGCAACGCCAGCGGGGCCCATGCACTGCAGC CGGCTGCTGCCATCCTGGCACTGCTCCCTGCACTCAGCCTGCTGCTTTGGGGCCCCAGACAGCTG TAG
447.	forward primer	artificial	nt		CACCACAGCCCACCAGTGACC
448.	reverse primer	artificial	nt		GAGGCCTGGGGCACCACACCC
449.	P3-VH-A-XhoI	artificial	nt		CCTGATCTCGAGAGCGGCSCAGASSTGRAAAAGCCAGGCGCCACGGTGAAGATT
450.	P3-VH-B	artificial	nt		GGCGCCACGGTGAAGATTTCCTGCAAGSYCAGCGGCWACACGTTCACCGGCTACTACATCCACTG GGTG
451.	P3-VH-C	artificial	nt		GTAGGAGGTGAAGCCGTTGTTGGGGTCCACTCTGCCSATCCATTCCAGGCYCTTCCCGKGGGMCT GTTKCACCCAGTGGATGTAGTA
452.	P3-VH-D	artificial	nt		AACGGCTTCACCTCCTACAACCAGAAGTTCAAGGGCARGGYCAYAMTKACCGYGGACAMGAGCAC CRRCACCGCCTACATGGAACTC
453.	P3-VH-E	artificial	nt		GCTGTCGAAGAAGTTGCCCRCGCAATAGTACACGGCGGTGTCCTCGCTGSKCAGGCTKCTCAGTT CCATGTAGGCGGT
454.	P3-VH-F-BstEII	artificial	nt		CACGTCGGTGACCGTGGTTCCCTGGCCCCAGCTGTCGAAGAAGTTGCC
455.	PSCA2VH-A-XHO1	artificial	nt		CAGGTGCTCGAGYCAGGCGCCGAASTGRWGAAGCCTGGCGCCMCAGTGAAGMTATCCTGCAAGGY

				CAGCGGCTACACCTTCACCAAC
456.	PSCA2VH-B	artificial	nt	GCTGTCGCTGGGGGTCGATCCTGCCYATCCATTCCAGGCCCYTGCCGGGCSYCTGTTKCACCCAGT TCAGCCAGTAGTTGGTGAAGGTGTAGCC
457.	PSCA2VH-C	artificial	nt	AGGATCGACCCCAGCGACAGCGAGATCCACTACGACCAGAAGTTCAAGGACARAGYCACCMTAAC CGYGGACAMGAGCACCRRCACCGCCTAC
458.	PSCA2VH-D	artificial	nt	GGCCAGGGCGCAATAGTACACGGCGGTGTCCTCGCTTSTCAGGCTGGACAGCTSSATGTAGGCGG TGYYGGTGCTC
459.	PSCA2VH-E-BSTE2	artificial	nt	AGACACGGTGACCGTGGTGCCCTGGCCCCAGTAGGCCATGGCGTAGATGCCGGTCAGGGCGCAAT AGTACAC
460.	P3-VL-A-SacI	artificial	nt	CCTGTAGAGCTCGTCATCACCCAGTCCCCCCTGTCCCTGMSCGTGACCMTCGGCCAGCCAGCCAG CATC
461.	P3-VL-B	artificial	nt	CCAGTTCAGGTAGGTCTTGCCGTCGTGTCCAGCAGGGACTGGCTGGACTTGCAAGAGATGCTGG CTGGCTGGCC
462.	P3-VL-C	artificial	nt	AAGACCTACCTGAACTGGYTSCWGCAGAGGCCAGGCCAGAGCCCCARGAGGCTGATCTACCTGGT GTCCACCCTG
463.	P3-VL-D	artificial	nt	GGTGAAGTCGGTGCCGGAGCCGCTGCCGGAGAATCTGTCTGGCACGCCGCTGTCCAGGGTGGACA CCAGGTA
464.	P3-VL-E	artificial	nt	TCCGGCACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACSTGGGCGTGTACTACTG CTGGCAGGGCACC
465.	P3-VL-F-BsiWI/SpeI	artificial	nt	CCAGACACTAGTCGTACGCTTGATTTCCAGCTTGGTCCCTCCGCCGAAGGTCCTTGGGAAGTGGG TGCCCTGCCAGCAGTA
466.	PSCA2VL-a-SAC1	artificial	nt	CAGACAGAGCTCGTGATCACCCAGKCASCTCYAAGCSTGCCAGTGACCCCAGGCGAGYCAGYGTC CATCAGCTGCAGGTCCAGC
467.	PSCA2VL-b	artificial	nt	CTGGGGGCTCTGGCCTGGCYTCTGCAGAWACCAGTACAGGTAGGTGTCTGCCGTTGCTGTGCAGCA GGCTCTTGCTGGACCTGCAGCTGATG
468.	PSCA2VL-c	artificial	nt	CCAGGCCAGAGCCCCCAGCTGCTGATCTACAGGATGAGCAACCCTGGCTAGCGGCGTGCCAGACAG ATTCAGCGGCAGCGGCTCTGGAACC
469.	PSCA2VL-d	artificial	nt	CAGGCAGTAGTACACGCCCACGTCCTCGGCCTCCACCCTGCTGATCYCCAGGGTGAAGKCGGTTC CAGAGCCGCTGCC
470.	PSCA2VL-e-BsiW1-Spe1	artificial	nt	GTGCTGACTAGTCGTACGCTTGATTTCCAGCTTGGTCCCTTGGCCGAAGGTGTAGGGGTATTCCA GGTGCTGCAGGCAGTAGTACACGCC

471.	HD37 L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
472.	HD37 L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC

				CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TCCAACCTATCACTGTCAGCAAAGTACTCACGATCCCGTCGACCTTCGGTGCAGGCACCAAGCTCG AGATCAAA
473.	HD37 LCDR1	artificial	aa	KASQSVDYDGDSYLN
474.	HD37 LCDR2	artificial	aa	DASNLVS
475.	HD37 LCDR3	artificial	aa	QQSTEDPWT
476.	HD37 H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
477.	HD37 H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
478.	HD37 HCDR1	artificial	aa	SYWMN
479.	HD37 HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
480.	HD37 HCDR3	artificial	aa	RETTVGRYYYAMDY
481.	HD37 LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

482.	HD37 LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACACAGACTTCACCCTCAACATCCATCCTCCTGCAGAAGCTGCATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
483.	HD37 LH x H2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSIGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
484.	HD37 LH x H2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG

				TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGACCTGGTGAGGCCTGGCTCCTCAGTGAAGATTTCCTGCAAGGCTTCTCG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTCTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
485.	HD37 LH x F12Q HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
486.	HD37 LH x F12Q HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG

					CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTCGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTCACTGCAGACGAATCCTCCAGCACACCCTACATCCAACTCAGCAGCCTACGCATCTGACCACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTCGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGCCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
487.	hCD19 26-D6 L	artificial	aa		DIQMTQSPASLSASLGDRVTITCKASQSVDYDGDSYLNWYQQKPGKAPKLLIYDASNLVSGIPSR FSGSGSGTDFTLTISSLQQVDFATYYCQQSIEDPWTFGQGTKVEIK
488.	hCD19 26-D6 L	artificial	nt		GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGAAAC CAGGAAAGGCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCATCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCAGTTCTCTGCAGCAGGTGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG AGATCAAA
489.	hCD19 26-D6 LCDR1	artificial	aa		KASQSVDYDGDSYLN
490.	hCD19 26-D6 LCDR2	artificial	aa		DASNLVS

491.	hCD19 26-D6 LCDR3	artificial	aa	QQSTEDPWT
492.	hCD19 26-D6 H	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVKQGPGQGLEWMGQIWPGDGDTNYNGKFK GRVTMTADASTSTVYMELSSLRSEDTAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
493.	hCD19 26-D6 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTCCTG CAAGGCTTCTGGCTATACATTCACTAGCTACTGGATGAACTGGGTGAAGCAGGGCCCTGGACAGG GTCTTGAGTGGATGGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAGAGTCACTATGACTGCTGACGCATCCACCAGCACACAGTCTACATGGAACTCAGCAGCCTGCG ATCTGAGGACACTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
494.	hCD19 26-D6 HCDR1	artificial	aa	SYWMN
495.	hCD19 26-D6 HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
496.	hCD19 26-D6 HCDR3	artificial	aa	RETTVGRYYYAMDY
497.	hCD19 26-D6 LH x I2C HL	artificial	aa	DIQMTQSPASLSASLGDRVTITCKASQSVDYDGDSYLNWYQQKPGKAPKLLIYDASNLVSGIPSR FSGSGSGTDFTLTISSLQQVDFATYYCQQSTEDPWTFGQGTKVEIKGGGSGGGGSGGGGSQVQL VQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVKQGPGQGLEWMGQIWPGDGDTNYNGKFKGRVT MTADASTSTVYMELSSLRSEDTAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
498.	hCD19 26-D6 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCCCCAGCCTCTTTCTCTGCCCTCTCTAGGGCACAGAGTCACCATCAC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGAAAC CAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCATCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCAGTTCTCTGCAGCAGGTGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG

				AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCTTCTGG CTATACATTCACTAGCTACTGGATGAACTGGGTGAAGCAGGGCCCTGGACAGGGTCTTGAGTGGA TCGGACAGATTTGGCCTCGAGATGCTGATACTAACTACAATGCAAACTTCAAGGCTACACTCACT ATGACTGCTGACGCCATCCACCAGCACAGTCTACATGGAACTCAGCAGCCTGCGATCTGAGGACAC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
499.	hCD19 45-A10 L	artificial	aa	DIQMTQSPASLSVSVGERVTITCKASQSVDYDGDSYLNWYQQKPGKAPKLLIYDASNLVSGVPPR FSGSGSGTDFTLTISSVQPEDFATYYCQQSIEDPWTFGQGTKVEIK
500.	hCD19 45-A10 L	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGTCACCATCAC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGAAAC CAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGGTCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCAGTTCTTGTGCAGCCGGAGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG AGATCAAA
501.	hCD19 45-A10 LCDR1	artificial	aa	KASQSVDYDGDSYLN
502.	hCD19 45-A10 LCDR2	artificial	aa	DASNLVS

503.	hCD19 45-A10 LCDR3	artificial	aa	QQSTEDPWT
504.	hCD19 45-A10 H	artificial	aa	QVQLVQSGAELKKPGSSVKISCKASGYSFTSYWMNWVKQAPGQGLEWMGQIWPGDGDTNYNGKFK GKATMTADPSTSTAYMELSSLGSEDTAVYYCARRETTVGRYYYAMDYWGQGTTVTVSS
505.	hCD19 45-A10 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGCTGAAGAAGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATTCATTCACTAGCTACTGGATGAACTGGGTGAAGCAGGCCCCTGGACAGG GTCTTGAGTGGATGGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTATGACTGCTGACCCATCCACCAGCACACGCCTACATGGAACTCAGCAGCCTGGG ATCTGAGGACACTGCGGTCTATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
506.	hCD19 45-A10 HCDR1	artificial	aa	SYWMN
507.	hCD19 45-A10 HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
508.	hCD19 45-A10 HCDR3	artificial	aa	RETTVGRYYYAMDY
509.	hCD19 45-A10 LH x I2C HL	artificial	aa	DIQMTQSPASLSVSVGERVTITCKASQSVDYDGDSYLNWYQQKPGKAPKLLIYDASNLVSGVPPR FSGSGSGTDFTLTISSVQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSGGGGSGGGGSQVQL VQSGAELKKPGSSVKISCKASGYSFTSYWMNWVKQAPGQGLEWMGQIWPGDGDTNYNGKFKGKAT MTADPSTSTAYMELSSLGSEDTAVYYCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
510.	hCD19 45-A10 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGAAAC CAGGAAAGGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGGTCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCAGTTCTGTGCAGCCGGAGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG

				AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGCCTGAAGAAGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATTCATTCACTAGCTACTGGATGAACTGGGTGAAGCAGGCCCCTGGACAGGGTCTTGAGTGGA TCGGACAGATTTGGCCTCGAGATGCTGATACTAACTACAATGCAAACTTCAAGGCTAAACCCACT ATGACTGCTGACCCATCCACCAGCACAGCCTACATGGAACTCAGCAGCCTGGGATCTGAGGACAC TGCGGTCTATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
511.	hCD19 46-B11 L	artificial	aa	DIQMTQSPASLSASVGERVTITCKASQSVDYDGDSYLNWYQQIPGKPPKLLIYDASNLVSGIPSR FSGSGSGTDFTLTIHSLEQEDFATYYCQQSTEDPWTFGQGTKVEIK
512.	hCD19 46-B11 L	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGCGTCTGTAGGGGAAAGAGTCACCATCAC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATAC CAGGAAAGCCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCATCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCCATTCTCTGGAGCAGGAGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG AGATCAAA
513.	hCD19 46-B11 LCDR1	artificial	aa	KASQSVDYDGDSYLN
514.	hCD19 46-B11 LCDR2	artificial	aa	DASNLVS
515.	hCD19 46-B11 LCDR3	artificial	aa	QQSTEDPWT

516.	hCD19 46-B11 H	artificial	aa	QVQLVQSGAEVVRPGASVKVSCKASGYSFTSYWMNWVRQPPGQGLEWIGQIWPGDGDTNYNGKFK GRATMTADASTSTVYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYWGQGTTVTVSS
517.	hCD19 46-B11 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAGGCCTGGGGCCTCAGTGAAGGTTTCCTG CAAGGCTTCTGGCTATTCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCCCCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAGAGCCACTATGACTGCTGACGCATCCACCAGCACAGTCTACATGGAACTCAGCAGCCTGCG ATCTGAGGACACTGCGGTCTATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
518.	hCD19 46-B11 HCDR1	artificial	aa	SYWMN
519.	hCD19 46-B11 HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
520.	hCD19 46-B11 HCDR3	artificial	aa	RETTTVGRYYYAMDY
521.	hCD19 46-B11LH x I2C HL	artificial	aa	DIQMTQSPASLSASVGERVTITCKASQSVDYDGDSYLNWYQQIPGKPPKLLIYDASNLVSGIPSR FSGSGSGTDFTLTIHSLEQEDFATYYCQQSIEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQL VQSGAEVVRPGASVKVSCKASGYSFTSYWMNWVRQPPGQGLEWIGQIWPGDGDTNYNGKFKGRAT MTADASTSTVYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
522.	hCD19 46-B11LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGCGTCTGTAGGGGAAAGAGTCACCATCAC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATAC CAGGAAAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCATCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCCATTCTCTGGAGCAGGAGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAGGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCTTCTGG CTATTCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCCCCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAGAGCCACT ATGACTGCTGACGCATCCACCAGCACAGTCTACATGGAACTCAGCAGCCTGCGATCTGAGGACAC TGCGGTCTATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT

				ACTGGGGCCAAGGGACCACCGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
523.	hCD19 47-A3 L	artificial	aa	DIQMTQSPASLSASVGERVTITCKASQSVDYDGDSYLNWYQQIPGKAPKLLIYDASNLVSGVPSR FSGSGSGTDFTLTISSLQTEDFATYYCQQSTEDPWTFGQGTKVEIK
524.	hCD19 47-A3 L	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGTCACCATCAC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATAC CAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGGTCCCATCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCAGTTCTCTGCAGACGGAGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTTCGGACGTTCGGTCAAGGGACCAAGGTGG AGATCAAA
525.	hCD19 47-A3 LCDR1	artificial	aa	KASQSVDYDGDSYLN
526.	hCD19 47-A3 LCDR2	artificial	aa	DASNLVS
527.	hCD19 47-A3 LCDR3	artificial	aa	QQSTEDPWT
528.	hCD19 47-A3 H	artificial	aa	QVQLVQSGAEVKKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDGDTNYNGKFK GRVTMTADASTSTVYMELSSLGSEDTAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS

529.	hCD19 47-A3 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GCTAGAGTCACTATGACTGCTCACGCCATCCACCAGCACACAGTCTACATGCAACTCAGCAGCCTGCG ATCTGAGGACACTGCGGTCTATTTCTGTGCCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
530.	hCD19 47-A3 HCDR1	artificial	aa	SYWMN
531.	hCD19 47-A3 HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
532.	hCD19 47-A3 HCDR3	artificial	aa	RETTVGRYYYAMDY
533.	hCD19 47-A3 LH x I2C HL	artificial	aa	DIQMTQSPASLSASVGERVTITCKASQSVDYDGDSYLNWYQQIPGKAPKLLIYDASNLVSGVPSR FSGSGSGTDFTLTISSLQTEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSGGGSGGGSQVQL VQSGAEVKKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVT MTADASTSTVYMELSSLGSEDTAVYFCARETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
534.	hCD19 47-A3 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGTCACCATCAC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATAC CAGGAAAGGCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGGTCCCATCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATCAGTTCTCTGCAGACGGAGGATTT CGCAACCTATTACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGG AGATCAAAGGTGGTGGTCGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACT ATGACTGCTGACGCATCCACCAGCACAGTCTACATGGAACTCAGCAGCCTGAGGATCTGAGGACAC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC

				GAGTCTGGAGGAGGATTCGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
535.	HD37-DT L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDTYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
536.	HD37-DT L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATACTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
537.	HD37-DT LCDR1	artificial	aa	KASQSVDYDGDTYLN
538.	HD37-DT LCDR2	artificial	aa	DASNLVS
539.	HD37-DT LCDR3	artificial	aa	QQSTEDPWT
540.	HD37-DT H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSS
541.	HD37-DT H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC

				ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
542.	HD37-DT HCDR1	artificial	aa	SYWMN
543.	HD37-DT HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
544.	HD37-DT HCDR3	artificial	aa	RETTVGRYYYAMDY
545.	HD37-DT LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDTYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
546.	HD37-DT LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATACTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC

				AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC ACAGGATGAGCCAGAATATTACTGTGTCTTCTATGGTACACGCAACCGCTGGCTGTTCGCTGGCAGGAA CCAAACTGACTGTCCTA
547.	HD37-A L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGASYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
548.	HD37-A L	artificial	nt	GATATCCAGCTGACCCACTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGCTAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
549.	HD37-A LCDR1	artificial	aa	KASQSVDYDGASYLN
550.	HD37-A LCDR2	artificial	aa	DASNLVS
551.	HD37-A LCDR3	artificial	aa	QQSTEDPWT
552.	HD37-A H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
553.	HD37-A H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
554.	HD37-A HCDR1	artificial	aa	SYWMN
555.	HD37-A HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG

556.	HD37-A HCDR3	artificial	aa	RETTTVGRYYYAMDY
557.	HD37-A LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGASYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
558.	HD37-A LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGCTAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGCACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAACGACTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA

559.	HD37-G L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGGSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
560.	HD37-G L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTGGTAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
561.	HD37-G LCDR1	artificial	aa	KASQSVDYDGGSYLN
562.	HD37-G LCDR2	artificial	aa	DASNLVS
563.	HD37-G LCDR3	artificial	aa	QQSTEDPWT
564.	HD37-G H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
565.	HD37-G H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
566.	HD37-G HCDR1	artificial	aa	SYWMN
567.	HD37-G HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
568.	HD37-G HCDR3	artificial	aa	RETTVGRYYYAMDY
569.	HD37-G LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGGSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV

				ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
570.	HD37-G LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACCGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGAAC AGTCACACTCACTTGTGGCCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
571.	HD37-S L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGSSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
572.	HD37-S L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAAGGTGGATGC

				TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
573.	HD37-S LCDR1	artificial	aa	KASQSVDYDGSSYLN
574.	HD37-S LCDR2	artificial	aa	DASNLVS
575.	HD37-S LCDR3	artificial	aa	QQSTEDPWT
576.	HD37-S H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
577.	HD37-S H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
578.	HD37-S HCDR1	artificial	aa	SYWMN
579.	HD37-S HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
580.	HD37-S HCDR3	artificial	aa	RETTVGRYYYAMDY
581.	HD37-S LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGSSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSIGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
582.	HD37-S LH x I2C HL	artificial	nt	GATATCCAGCTGACCCACTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTTCTAGTTATTTGAACTGGTACCAACAGATTC

				CAGGACAGCCACCCAAACTCCTCATCTATGACATCCAATCTAGTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGTCGAGGGACCAAGCTCG ACATCAAACGTGGTGCTCGTTCTGCGGCGGCCGCTCCCGTGCTGGTGCTTCTCAGCTGCAGCTG CAGCAGTCTGGGGCCTGACCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
583.	HD37-T L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGTSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
584.	HD37-T L	artificial	nt	GATATCCAGCTGACCCACTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTACAAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGTCGAGGGACCAAGCTCG AGATCAAA
585.	HD37-T LCDR1	artificial	aa	KASQSVDYDGTSYLN
586.	HD37-T LCDR2	artificial	aa	DASNLVS

587.	HD37-T LCDR3	artificial	aa	QQSTEDPWT
588.	HD37-T H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSS
589.	HD37-T H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
590.	HD37-T HCDR1	artificial	aa	SYWMN
591.	HD37-T HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
592.	HD37-T HCDR3	artificial	aa	RETTTVGRYYYAMDY
593.	HD37-T LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGTSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
594.	HD37-T LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTCCAAGGCCAGCCAAAGTGTTGATTATGATGGTACAAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC

				TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACCGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTCGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAACTACGCCATGAACTGGCTCCGCCAGGCTCCAGGAAAGCGTTTGCAATGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
595.	HD37-I L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGISYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
596.	HD37-I L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTATCAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
597.	HD37-I LCDR1	artificial	aa	KASQSVDYDGISYLN
598.	HD37-I LCDR2	artificial	aa	DASNLVS
599.	HD37-I LCDR3	artificial	aa	QQSTEDPWT
600.	HD37-I H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
601.	HD37-I H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG

				GTCTTGAGTGGATTGGACACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACACAGCCTACATGCAACTCAGCAGCCTAG ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATACT ATGCTATGACTACTGGGGCCAAGGCACCACGGTCACCGTCTCCTCC
602.	HD37-I HCDR1	artificial	aa	SYWMN
603.	HD37-I HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
604.	HD37-I HCDR3	artificial	aa	RETTTVGRYYYAMDY
605.	HD37-I LH x I2C HL	artificial	aa	DTQITQSPASLAVSLGQRATISCKASQSVDYDGTSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGSGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
606.	HD37-I LH x I2C HL	artificial	nt	GATATCCAGCTGACCCACTCTCCATCCTCCCTGTCTATAGGCGATCAGGCCAGCATCTC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTATCAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTCGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTCGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT

				ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTCTGGCGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCCTGGCTCTAATACGTCGGACTAAGTTCCTCGCCCCCCGTACT CCTGCCAGATTCTCAGGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
607.	HD37-L L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGLSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
608.	HD37-L L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCTGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
609.	HD37-L LCDR1	artificial	aa	KASQSVDYDGLSYLN
610.	HD37-L LCDR2	artificial	aa	DASNLVS
611.	HD37-L LCDR3	artificial	aa	QQSTEDPWT
612.	HD37-L H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
613.	HD37-L H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
614.	HD37-L HCDR1	artificial	aa	SYWMN

615.	HD37-L HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
616.	HD37-L HCDR3	artificial	aa	RETTTVGRYYYAMDY
617.	HD37-L LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGLSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
618.	HD37-L LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTCTGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA

619.	HD37-V L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGVSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
620.	HD37-V L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGTCAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
621.	HD37-V LCDR1	artificial	aa	KASQSVDYDGVSYLN
622.	HD37-V LCDR2	artificial	aa	DASNLVS
623.	HD37-V LCDR3	artificial	aa	QQSTEDPWT
624.	HD37-V H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
625.	HD37-V H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
626.	HD37-V HCDR1	artificial	aa	SYWMN
627.	HD37-V HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
628.	HD37-V HCDR3	artificial	aa	RETTVGRYYYAMDY
629.	HD37-V LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGVSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGGSGGGGSGGGGSQVQL

				QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
630.	HD37-V LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGTCAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTACATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAATAAATAATATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTTACTTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
631.	HD37-E L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGESYLNWYQQIPGQPPXLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
632.	HD37-E L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGAGAGTTATTTGAACTGGTACCAACAGATTC

				CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG ACATCAAA
633.	HD37-E LCDR1	artificial	aa	KASQSVDYDGESYLN
634.	HD37-E LCDR2	artificial	aa	DASNLVS
635.	HD37-E LCDR3	artificial	aa	QQSTEDPWT
636.	HD37-E H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
637.	HD37-E H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
638.	HD37-E HCDR1	artificial	aa	SYWMN
639.	HD37-E HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
640.	HD37-E HCDR3	artificial	aa	RETTVGRYYYAMDY
641.	HD37-E LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGESYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIKGGGSGGGSGGGSGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

642.	HD37-E LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGAGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACACAGACTTCACCCTCAACATCCATCCTCCTGCAGAAGCTGCATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTCGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGCCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
643.	HD37-Q L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGQSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
644.	HD37-Q L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGAGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTTCGGTGGAGGGACCAAGCTCG AGATCAAA

645.	HD37-Q LCDR1	artificial	aa	KASQSVDYDGQSYLN
646.	HD37-Q LCDR2	artificial	aa	DASNLVS
647.	HD37-Q LCDR3	artificial	aa	QQSTEDPWT
648.	HD37-Q H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSS
649.	HD37-Q H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
650.	HD37-Q HCDR1	artificial	aa	SYWMN
651.	HD37-Q HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
652.	HD37-Q HCDR3	artificial	aa	RETTTVGRYYYAMDY
653.	HD37-Q LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGQSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
654.	HD37-Q LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCAGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG

				AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTCGAGATGCTCATACTAACTACAATGCAAAGTTCAAGGCTAAACCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
655.	HD37-N L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGNSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
656.	HD37-N L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTAACAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
657.	HD37-N LCDR1	artificial	aa	KASQSVDYDGNSYLN
658.	HD37-N LCDR2	artificial	aa	DASNLVS
659.	HD37-N LCDR3	artificial	aa	QQSTEDPWT

660.	HD37-N H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
661.	HD37-N H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
662.	HD37-N HCDR1	artificial	aa	SYWMN
663.	HD37-N HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
664.	HD37-N HCDR3	artificial	aa	RETTVGRYYYAMDY
665.	HD37-N LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGNSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGSGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
666.	HD37-N LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTAACAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTCGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC

				GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATTCATTCAAAAAACACTCCCTATCTACAAATGAACAACTTGAAAACTCAGCA CACTGCCGTGTACTACTCTGTGAGACATGGCAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
667.	HD37-K L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGKSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
668.	HD37-K L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTAAGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
669.	HD37-K LCDR1	artificial	aa	KASQSVDYDGKSYLN
670.	HD37-K LCDR2	artificial	aa	DASNLVS
671.	HD37-K LCDR3	artificial	aa	QQSTEDPWT
672.	HD37-K H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
673.	HD37-K H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTACTAACAATGGAAAGTTCAAG GGTAAAGCCACACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT

				ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
674.	HD37-K HCDR1	artificial	aa	SYWMN
675.	HD37-K HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
676.	HD37-K HCDR3	artificial	aa	RETTTVGRYYYAMDY
677.	HD37-K LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGKSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADKSSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
678.	HD37-K LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTAAGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAAGGTGCATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC

				AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTCTCCTA
679.	HD37-R L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGRSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
680.	HD37-R L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTCGTAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
681.	HD37-R LCDR1	artificial	aa	KASQSVDYDGRSYLN
682.	HD37-R LCDR2	artificial	aa	DASNLVS
683.	HD37-R LCDR3	artificial	aa	QQSTEDPWT
684.	HD37-R H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
685.	HD37-R H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACACTCTGACTGCAGACGAATCCTCCAGCACACAGCCTACATGCAACTCAGCAGCCTAG ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
686.	HD37-R HCDR1	artificial	aa	SYWMN
687.	HD37-R HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
688.	HD37-R HCDR3	artificial	aa	RETTVGRYYYAMDY

689.	HD37-R LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGRSYLNWYQQIPGQPPXLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
690.	HD37-R LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTCGTAGTTATTTGAACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCTTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
691.	HD37-H L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGHSYLNWYQQIPGQPPXLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK

692.	HD37-H L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCACAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
693.	HD37-H LCDR1	artificial	aa	KASQSVDYDGHSYLN
694.	HD37-H LCDR2	artificial	aa	DASNLVS
695.	HD37-H LCDR3	artificial	aa	QQSTEDPWT
696.	HD37-H H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
697.	HD37-H H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
698.	HD37-H HCDR1	artificial	aa	SYWMN
699.	HD37-H HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
700.	HD37-H HCDR3	artificial	aa	RETTVGRYYYAMDY
701.	HD37-H LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGHSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGSGGGSGGVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS

				GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
702.	HD37-H LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGAIGGTCACAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCCTGTGGAGAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGGCACCCCGTGGTCTATAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
703.	HD37-Y L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGYSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
704.	HD37-Y L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTTACAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA

705.	HD37-Y LCDR1	artificial	aa	KASQSVDYDGYSYLN
706.	HD37-Y LCDR2	artificial	aa	DASNLVS
707.	HD37-Y LCDR3	artificial	aa	QQSTEDPWT
708.	HD37-Y H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSS
709.	HD37-Y H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
710.	HD37-Y HCDR1	artificial	aa	SYWMN
711.	HD37-Y HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
712.	HD37-Y HCDR3	artificial	aa	RETTTVGRYYYAMDY
713.	HD37-Y LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGYSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
714.	HD37-Y LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTACAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC

				TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGACCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCACTAGCTACTGCATCAACTGGCGTGAACCAGAGGCCTGGACACAGGGCTCTTGACTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTTACACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCCACCCCGTGGTCTATAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
715.	HD37-P L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGPSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
716.	HD37-P L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTCCAAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
717.	HD37-P LCDR1	artificial	aa	KASQSVDYDGPSYLN
718.	HD37-P LCDR2	artificial	aa	DASNLVS
719.	HD37-P LCDR3	artificial	aa	QQSTEDPWT

720.	HD37-P H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
721.	HD37-P H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
722.	HD37-P HCDR1	artificial	aa	SYWMN
723.	HD37-P HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
724.	HD37-P HCDR3	artificial	aa	RETTVGRYYYAMDY
725.	HD37-P LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGPSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGSGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
726.	HD37-P LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCCAAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTCGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC

				GAGTCTGGAGGAGGATTCGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
727.	HD37-F L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGFSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK
728.	HD37-F L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTTCAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
729.	HD37-F LCDR1	artificial	aa	KASQSVDYDGFSYLN
730.	HD37-F LCDR2	artificial	aa	DASNLVS
731.	HD37-F LCDR3	artificial	aa	QQSTEDPWT
732.	HD37-F H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSS
733.	HD37-F H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT

				ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
734.	HD37-F HCDR1	artificial	aa	SYWMN
735.	HD37-F HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
736.	HD37-F HCDR3	artificial	aa	RETTTVGRYYYAMDY
737.	HD37-F LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGFSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADKSSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
738.	HD37-F LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTTCAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAAGGTGCATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCACACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC

				AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTCTCCTA
739.	HD37-W L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGWSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
740.	HD37-W L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTTGGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
741.	HD37-W LCDR1	artificial	aa	KASQSVDYDGWSYLN
742.	HD37-W LCDR2	artificial	aa	DASNLVS
743.	HD37-W LCDR3	artificial	aa	QQSTEDPWT
744.	HD37-W H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
745.	HD37-W H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACACTCTGACTGCAGACGAATCCTCCAGCACACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
746.	HD37-W HCDR1	artificial	aa	SYWMN
747.	HD37-W HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
748.	HD37-W HCDR3	artificial	aa	RETTVGRYYYAMDY

749.	HD37-W LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGWSYLNWYQQIPGQPPXLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIKGGGGSGGGGSGGGGSQVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
750.	HD37-W LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATCTC CTGCAAGGCCAGCCAAACTGTTGATTATGATGGTTGGAGTTATTTGAACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTGGAATGGGTTG CTCGCATAAGAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTCTCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTCTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCTTCAGGTGGTGGTGGTTCTGGCGGCGGCTCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
751.	HD37-M L	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGMSYLNWYQQIPGQPPXLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSIEDPWTFGGGTKLEIK

752.	HD37-M L	artificial	nt	GATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTC CTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTATGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAA
753.	HD37-M LCDR1	artificial	aa	KASQSVDYDGMSYLN
754.	HD37-M LCDR2	artificial	aa	DASNLVS
755.	HD37-M LCDR3	artificial	aa	QQSTEDPWT
756.	HD37-M H	artificial	aa	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFK GKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSS
757.	HD37-M H	artificial	nt	CAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTG CAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGG GTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAG GGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACT ATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
758.	HD37-M HCDR1	artificial	aa	SYWMN
759.	HD37-M HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
760.	HD37-M HCDR3	artificial	aa	RETTVGRYYYAMDY
761.	HD37-M LH x I2C HL	artificial	aa	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGMSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGSGGGSGGVQL QQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKAT LTADESSSTAYMQLSSLASEDSAVYFCARRETTVGRYYYAMDYWGQGTTVTVSSGGGGSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS

				GGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
762.	HD37-M LH x I2C HL	artificial	nt	GATATCCAGCTGACCCAGTCTCCACTCTCCCTGCCTGTCACTCTTGGCCAGCCGGCCTCCATCTCC CTGCAAGGCCAGCCAAACGTGTTGATTATGATGGTATGAGTTATTTGAACTGGTACCAACAGATTC CAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGG TTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCCGTGGAGAAGGTGGATGC TGCAACCTATCACTGTCAGCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCG AGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG CAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGG CTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGA TTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACT CTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTC TGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG CTCGCATAAGAGTAAATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTC ACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTT ACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCC GGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTGTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAA CCAAACTGACTGTCCTA
763.	37VH-aXho1	artificial	nt	CAGCTGCTCGAGTCTGGGGCTGAGGTGRWGARGCCTGGGKCCTCAGTGAAGRTTTCCTGCAAGGC TTCTGGC
764.	37VH-b	artificial	nt	CCACTCAAGACCCTGTCCAGGGSSCTGCYTCACCCAGTTCATCCAGTAGCTAGWGAATGYATAGC CAGAAGCCTTTGCAGGA
765.	37VH-c	artificial	nt	GGACAGGGTCTTGAGTGGATKGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAA GTTCAAG

766.	37VH-d	artificial	nt	CAGGCTGCTGAGTTSCATGTAGRCTGTGCTGGTGGATKYGTCASSAGTCAKAGTGRCTYTACCCT TGAACTTTCCATTGTAG
767.	37VH-e	artificial	nt	CATGSAACTCAGCAGCCTGSSATCTGAGGACACTGCGGTCTATTWCTGTGCAAGACGGGAGACTA CGACGG
768.	37VH-fBstE2	artificial	nt	GGAGACGGTGACCGTGGTCCCTTGGCCCCAGTAGTCCATAGCATAGTAATAACGGCCTACCGTCG TAGTCTCCCGTCTTGC
769.	37VL-A-SacI	artificial	nt	CAGCTGGAGCTCCAGATGACCCAGTCTCCAKCTTCTTTGKCTGYGTCTSTAGGGSASAGAGYCAC CATCWCCTGCAAGGCCAGC
770.	37VL-B	artificial	nt	CTGTTGGTACCAGTTCAAATAASTSNNACCATCATAATCAACACTTTGGCTGGCCTTGCAGGTGA TGGT
771.	37VL-C	artificial	nt	TTGAACTGGTACCAACAGAWACCAGGAMAGSCACCCAAACTCCTCATCTATGATGCATCCAATCT AGTTTCT
772.	37VL-D	artificial	nt	GAGGGTGAAGTCTGTCCCAGACCCACTGCCACTAAACCTGGRTGGGAYCCCAGAAACTAGATTGG ATGC
773.	37VL-E	artificial	nt	GGGACAGACTTCACCCTCAMCATCMRTYCTSTGSAGMMGGWGGATKYCGCAACCTATYACTGTCA GCAAAGTACTGAG
774.	37VL-F-BsiW1Spe1	artificial	nt	ACTCAGACTAGTCGTACGTTTGATCTCCACCTTGGTCCCTTGACCGAACGTCCACGGATCCTCAG TACTTTGCTGACAG
775.	Flag-tag	artificial	aa	DYKDDDDK
776.	human cMET construct	artificial	nt	ATGAAGGCCCCCGCTGTGCTTGCACCTGGCATCCTCGTGCTCCTGTTTACCTTGGTGCAGAGGAG CAATGGGGAGTGTAAAGAGGCACTAGCAAAGTCCGAGATGAATGTGAATATGAAGTATCAGCTTC CCAACTTCACCGCGGAAACACCCATCCAGAATGTCATTCTACATGAGCATCACATTTTCCTTGGT GCCACTAACTACATTTATGTTTTAAATGAGGAAGACCTTCAGAAGGTTGCTGAGTACAAGACTGG GCCTGTGCTGGAACACCCAGATTGTTTCCCATGTCAGGACTGCAGCAGCAAAGCCAATTTATCAG GAGGTGTTTGGAAAGATAACATCAACATGGCTCTAGTTGTGGACACCTACTATGATGATCAACTC ATTAGCTGTGGCAGCGTCAACAGAGGGACCTGCCAGCGACATGTCTTTCCCCACAATCATACTGC TGACATACAGTCGGAGGTTCACTGCATATTCTCCCCACAGATAGAAGAGCCCAGCCAGTGTCCTG

ACTGTGTGGTGAGCGCCCTGGGAGCCAAAGTCCTTTCATCTGTAAAGGACCGGTTCATCAACTTC
TTTGTAGGCAATACCATAAATTCTTCTTATTTCCCAGATCATCCATTGCATTCGATATCAGTGAG
AAGGCTAAAGGAAACGAAAGATGGTTTTATGTTTTTGACGGACCAGTCCTACATTGATGTTTTAC
CTCAGTTCAGAGATTCTTACCCCATTAACTATCTCCATGCCTTTGAAAGCAACAATTTATTTAC
TTCTTGACGGTCCAAAGGCAAACTCTAGATGCTCAGACTTTCACACAAGAATAATCAGGTTCTG
TTCCATAAACTCTGGATTCCATTCCTACATGGAAATGCCTCTGGAGTGTATTCTCACAGAAAAGA
GAAAAAAGAGATCCACAAAGAAGGAAGTGTTTAATATACTTCAGGCTGCGTATGTCAGCAAGCCT
GGGGCCCAGCTTGCTAGACAAATAGGAGCCAGCCTGAATGATGACATTCTTTTCGGGGTGTTCGC
ACAAAGCAAGCCAGATTCTGCCGAACCAATGGATCGATCTGCCATGTGTGCATTCCCTATCAAAT
ATGTCAACGACTTCTTCAACAAGATCGTCACACAAAAACAATGTGAGATGTCTCCAGCATTTTAC
GGACCCAATCATGAGCACTGCTTAATAGGACACTTCTGAGAAATTCACTCAGGCTGTGAAGCGCG
CCGTGATGAATATCGAACAGAGTTTACCACAGCGCGTTGACTTATTCATGGGTCAAT
TCAGCGAAGTCCTCTTAACATCTATATCCACCTTCATTAAAGGAGACCTCACCATAGCTAATCTT
GGGACATCAGAGGGTCGCTTCATGCAGGTTGTGGTTTCTCGATCAGGACCATCAACCCCTCATGT
GAATTTTCTCCTGGACTCCCATCCAGTGTCTCCAGAAGTGATTGTGGAGCATACATTAAACCAAA
ATGGCTACACACTGGTTATCACTGGGAAGAAGATCACGAAGATCCCATTGAATGGCTTGGGCTGC
AGACATTTCCAGTCCTGCAGTCAATGCCTCTCTCTGCCCCACCCTTTGTTCAGTGTGGCTGGTGCCA
CGACAAATGTGTGCGATCCGAGGAATGCCTGAGCGGGACATGGACTCAACAGATCTGTCTGCCTG
CAATCTACAAGGTTTCCCAAATAGTGCACCCCTTGAAGGAGGGACAAGGCTGACCATATGTGGC
TGGGACTTTGGATTCGGAGGAATAATAAATTTGATTTAAAGAAAACTAGAGTTCTCCTTGGAAA
TGAGAGCTGCACCTTGACTTTAAGTGAGAGCACGATGAATACATTGAAATGCACAGTTGGTCCTG
CCATGAATAAGCATTTCAATATGTCCATAATTATTTCAAATGGCCACGGGACAACACAATACAGT
ACATTCTCCTATGTGGATCCTGTAATAACAAGTATTTCGCCGAAATACGGTCCTATGGCTGGTGG
CACTTTACTTACTTTAACTGGAAATTACCTAAACACGTGGCAATAGCACACACATTTCAATTCGTC
GAAAAACATGTACTTTAAAAAGTGTGTCAAACAGTATTCTTGAATGTTATACCCCAGCCCCAAACC
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CAATAACAGGTGTTGGGAAAAACCTGAACTCAGTTAGTGTCCCGAGAACGGTCATAAATGTGCAT
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CACTCCTTCCCCTGCAACACGCTGAATCTGCAACTCCCCCTGAAAACCAAAGCCTTTTCATGTTAG
ATGGGATCCTTTCCAAATACTTTGATCTCATTTATGTACATAATCCTGTGTTTAAGCCTTTTGAA
AAGCCAGTGATGATCTCAATGGGCAATGAAAATGTACTGGAAATTAAGGGAAATGATATTGACCC
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CTGAAGCCGTTTTATGCACGGTCCCCAATGACCTGCTGAAATTGAACAGCGAGCTAAATATAGAG
TGGAAGCAAGCAATTTCTTCAACCGTCCTTGGAAAAGTAATAGTTCAACCAGATCAGAATTTCAC
AGGATTGATTGCTGGTGTTGTCTCAATATCAACAGCACTGTTATTACTACTTGGGTTTTTCCTGT
GGCTGAAAAAGAGAAAGCAAATTAAAGATCTGGGCAGTGAATTAGTTCGCTACGATGCAAGAGTA

				CACACTCCTCATTTGGATAGGCTTGTAAGTGCCCGAAGTGTAAGCCCAACTACAGAAATGGTTC AAATGAATCTGTAGACTACCGAGCTACTTTTCCAGAAGATCAGTTTCCTAATTCATCTCAGAACG GTTCATGCCGACAAGTGCAGTATCCTCTGACAGACATGTCCCCCATCCTAACTAGTGGGACTCT CATATATCCAGTCCATTACTGCAAAATACTGTCCACATTGACCTCACTGCTCTAAATCCACAGCT GGTCCAGGCAGTGCAGCATGTAGTGATTGGGCCCAGTAGCCTGATTTGTGCATTTCAATGAAGTCA TAGGAAGAGGGCATTTTGCTTGTGTATATCATGGGACTTTGTTGGACAATGATGGCAAGAAAATT CACTGTGCTGTGAAATCCTTGAACAGAATCACTGACATAGGAGAAGTTTCCCAATTCTGACCGA GGGAATCATCATGAAAGATTTAGTCATCCCAATGTCCTCTCGCTCCTGGGAATCTGCCTGCGAA GTGAAGGGTCTCCGCTGGTGGTCCTACCATACATGAAACATGGAGATCTTCGAAATTTCATTCGA AATGAGACTCATAATCCAACTGTAAAAGATCTTATTGGCTTTGGTCTTCAAGTAGCCAAAGGCAT GAAAATATCTTGCAAGCAAAAAGTTTGTCCACAGAGACTTGGCTGCAAGAAACTGTATGCTGGATG AAAAATTCACAGTCAAGGTTGCTGATTTTGGTCTTGCCAGAGACATGTATGATAAAGAATACTAT AGTGTACACAACAAACACAGTGCAAAGCTGCCAGTGAAGTGGATGGCTCTGGAAAGTCTGCAAAC TCAAAAGTTTACCACCAACTCAGATGTGTGGTCCTTTGGCGTGCTCCTCTGGGAGCTGATGACAA GAGGAGCCCCACCTTATCCTGACGTAAACACCTTTGATATAACTGTTTACTTGTTGCAAGGGAGA AGACTCCTACAACCCGAATACTGCCCAGACCCCTTATATGAAGTAATGCTAAAATGCTGGCACCC TAAAGCCGAAATGCGCCCATCCTTTTCTGAACTGGTGTCCCGGATATCAGCGATCTTCTCTACTT TCATTGGGGAGCACTATGTCCATGTGAACGCTACTTATGTGAACGTAAAATGTGTCGCTCCGTAT CCTTCTCTGTTTGTCATCACAAGATAACGCTGATGATGAGGTGGACACACGACCAGCCTCCTTCTG GGAGACATCATAG
777.	human cMET construct	artificial	aa	MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHEHHIFLG ATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPCQDCSSKANLSGGVWKDNINMALVVDTYYDDQL ISCGSVNRGTCQRHVFPHNHTADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINF FVGNTINSSYIFPDHPLHISISVRRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYVHAFESNNFIY FLTVQRETLDAQTFHTRIIRFCSINSGLHSYMEMPLECILTEKRKKRSTKKEVFNILQAAYVSKP GAQLARQIGASLNDDILFGVFAQSKPDSAEPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFY GPNHEHCFNRTLLRNSSGCEARRDEYRTEFTTALQRVDLFMGQFSEVLLTSISTFIKGDLTIANL GTSEGRFMQVVVSRSGPSTPHVNFLLDSHPVSPEVIVEHTLNQNGYTLVITGKKITKIPLNGLGC RHFQSCSQCLSAPPFVQCGWCHDKCVRSEECLSGTWTQQICLPAIYKVFPNSAPLEGGTRLTICG WDFGFKKNNKFDLKKTRVLLGNESCTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTTQYS TFSYVDPVITSISPKYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLKSVSNSILECYTPAQT ISTEFAVKLKIDLANRETSIFSYREDPIVYEIHPTKSFISGGSTITGVGKNLNSVSVPRMVINVH EAGRNFTVACQHRSNSEIICCTTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPFE KPVMISMGNENVLEIKGNDIDPEAVKGEVLKVGNKSCENIHLHSEAVLCTVPNDLLKLNSELNIE WKQAISSTVLGKVIVQPDQNFTGLIAGVVSISTALLLLLGFFLWLKKRKQIKDLGSELVRYDARV HTPHLDRLVSARSVSPTTEMVSNESVDYRATFPEDQFPNSSQNGSCRQVQYPLTDMSPILTSGDS DISSPLLQNTVHIDLSALNPELVQAVQHVVIGPSSLIVHFNEVIGRGHFGCVYHGTLLDNDGKKI

				HCAVKSLNRITDIGEVSQFLTEGIIMKDFSHPNVLSLLGICLRSEGSPLVVLPYMKHGDLRNFIR NETHNPTVKDLIGFGLQVAKGMKYLASKKFVHRDLAARNCMLDEKFTVKVADFGLARDMYDKEYY SVHNKTGAKLPVKWMALESLQTQKFTTKSDVWSFGVLLWELMTRGAPPYPDVNTFDITVYLLQGR RLLQPEYCPDPLYEVMLKCWHPKAEMRPSFSELVSRISAIFSTFIGEHYVHVNATYVNVKCVAPY PSLLSSEDNADDEVDTRPASFWETS
778.	forward primer	artificial	nt	AGGAATTCACCATGAAGGCCCCCGCTGTGCTTGCACC
779.	reverse primer	artificial	nt	CTCCAGAGGCATTTCCATCTAGG
780.	forward primer	artificial	nt	GTCCAAAGGGAAACTCTACATGC
781.	reverse primer	artificial	nt	GGAGACACTGGATGGGAGTCCAGG
782.	forward primer	artificial	nt	CATCAGACGCTCCCTTCATCCAGC
783.	reverse primer	artificial	nt	GCTTTGGTTTTCAGGGGGAGTTGC
784.	forward primer	artificial	nt	ATCCAACCAAATCTTTATTAGTGGTGG
785.	reverse primer	artificial	nt	GACTTCATTGAAATGCACAATCAGG
786.	forward primer	artificial	nt	TGCTCTAAATCCAGAGCTCGTCC
787.	reverse primer	artificial	nt	CTCAGATAAGAAATTCCTTAGAATCC
788.	macaque cMET construct	artificial	nt	ATGAAGGCCCCCGCTGTGCTTGCACCTGGCATCCTCGTGCTCCTGTTTACCTTGGTGCAGAGGAG CAATGGCCAGTGTAAACACGCCACTAGCAAAGTCCCGACATGAATGTCAATATGAAGTATCACCTTC CCAACTTCACCGCGCGGAAACAGCCATCCAGAATGTCATTCTACATGAGCATCACATTTTCCTCGGT GCCACCAACTACATTTATATGTTTTAAATGAGGAAGACCTTCAGAAGGTTGCTGAGTACAAGACCGG GCCTGTGCTGGAACACCCAGATTGTTTCCCGTGTCAGGACTGCAGCAGCAAAGCCAATTTATCAG GAGGCGTTTGGAAAGATAACATCAACATGGCTCTGGTTGTGGACACCTACTATGATGATCAACTC ATTAGCTGTGGCAGCGTCAACAGAGGGACCTGCCAGCGACATGTCTTTCCCCATAATCATACTGC TGACATACAGTCGGAGGTTCACTGCATATTCTCCCCACAGATAGAAGAGCCCAACCAGTGCCCTG ACTGTGTGGTGAGCGCCCTGGGAGCCAAAGTCCTTTCATCTGTAAAGGACCGGTTCATCAACTTC TTTGTAGGCAATACCATAAATTCTTCTTATTTCCCACATCATCCGTTGCATTCGATATCAGTGAG AAGGCTAAAGGAACGAAAGATGGTTTTATGTTTTTGACAGACCAGTCCTACATTGATGTTTTAC CTGAGTTCAGAGATTCTTACCCCATTAAGTACATCCACGCTTTTGAAAGCAACAATTTATTTAC TTCTTGACGGTCCAAAGGCAAACTCTAAATGCTCAGACTTTTCACACAAGAATAATCAGGTTCTG TTCCTTAAACTCTGGATTGCACTCCTACATGGAAATGCCTCTAGAGTGTATTCTCACAGAAAAGA GAAAAAAGAGATCCACAAAGAAGGAAGTGTTTAATATCCTTCAGGCTGCATATGTCAGCAAGCCC

GGGGCCCAGCTTGCTAGACAAATAGGAGCCAGCCTGAATGATGACATTCTCTTTGGGGTGTTCGC
ACAAAGCAAGCCAGATTCTGCCGAACCAATGGATCGATCTGCAATGTGTGCATTTCCTATCAAAT
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CGACCCAATCATCAGCACTCTTTTAATACGCACACTTCTGACAAAATTCATCAGCCTGTGAACGCC
CCGTGATGAATATCGAGCAGAGTTTACCACAGCTTTGCAGCGGGTTGACTTATTCATGGGTCAAT
TCAGCGAAGTCCTCTTAACATCTATATCCACCTTCGTGAAAGGAGACCTCACCATCGCTAATCTT
GGGACATCAGAGGGTCGCTTCATGCAGGTTGTGGTTTCTCGATCAGGACCATCAACCCTCATGT
GAATTTTCTCCTGGACTCTCACCCGGTGTCTCCAGAAGTGATTGTGGAGCATCCATTAAACCAGA
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AGACATTTCCAGTCCTGCAGTCAGTGCTCTCTGCCCCACCCTTTGTGCAGTGTGGCTGGTGCCA
CGACAAATGTGTGCGATCGGAGGAATGCCCCAGTGGGACATGGACTCAACAGATCTGTCTGCCTG
CAATCTACAAGGTTTCCCAACTAGTGCACCCCTTGAAGGAGGGACAAGGCTGACCATATGTGGC
TGGGACTTTGGATTTCGGAGGAATAATAAATTTGATTTAAAGAAAACTAGAGTTCTCCTTGGAAA
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ACATTTTCCTATGTGGATCCTATAATAACAAGTATTTCGCCAAAATATGGCCCTATGGCTGGTGG
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GAAAACATGTACTTTAAAAAGTGTGTCAAACAGTATTCTCGAATGTTATACCCCAGCCCAAACC
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CAATAACAGGTGTTGGGAAAAACCTGCATTCAGTTAGTGTCCCGAGGATGGTCATAAATGTGCAT
GAAGCAGGAAGGAACTTTACAGTGGCATGTCAGCATCGCTCTAATTCAGAGATAATCTGCTGTAC
CACTCCTTCCCTGCAACACAGCTGAATCTGCAACTCCCCCTGAAAACCAAAGCCTTTTTCATGTTAG
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TGAAGCAGTTAAAGGTGAAGTGTTAAAAGTTGGAAATAAGAGCTGTGAGAATATACACTTACATT
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TGGAAGCAAGCAATTTCTTCAACCGTCCTTGGAAAAGTAATAGTTCAACCAGATCAGAATTTCAC
CGGATTGATTGCTGGTGTTGTCTCAATATCAATAGCACTCTTACTACTACTTGGGCTTTTCCTGT
GGCTGAAAAAGAGAAAGCAAATTAAAGATCTGGGCAGTGAATTAGTTCGCTATGATGCAAGAGTA
CACACTCCTCATTTGGATAGGCTTGTAAGTGCCCGAAGTGTAAGCCCAACAACAGAAATGGTTTC
AAATGAATCTGTAGACTACCGAGCTACTTTTCCAGAAGATCAGTTTCCTAATTCATCTCAGAACG
GTTCATGCCGACAAGTGCAGTATCCTCTGACAGACATGTCCCCCATCCTGACTAGTGGGGACTCT
GATATATCCAGTCCATTACTGCAAAACACTGTCCACATTGACCTCAGCGCTCTAAATCCAGAGCT
GGTCCAGGCAGTGCAGCATGTAGTGATTGGGCCCAGTAGCCTGATTGTGCATTTCAATGAAGTCA
TAGGAAGAGGGCATTTTGCTTGTGTATATCATGGGACTTTGTTGGACAATGATGGCAAGAAAATT
CACTGTGCTGTGAAATCCTTGAACAGAATCACTGACATAGGAGAAGTTCCCCAGTTCTGACCGA

				GGGAATCATCATGAAAGATTTAGTCATCCAATGTCCTCTCGCTCCTGGAATCTGCCTGCGAA GTGAAGGGTCTCCGCTGGTGGTCCTACCCTACATGAAACATGGAGATCTTCGAAATTTCATTCGA AATGAGACTCATAATCCAACTGTAAAAGATCTTATTGGCTTTGGTCTTCAAGTAGCCAAAGGCAT CAAATATCTTGCAAGCAAAAAGTTTGTCCACACAGACTTGCCTCCAAGAAACTCTATGCTCCATC AAAAATTCACAGTCAAGGTTGCTGATTTTGGTCTTGCCAGAGACATGTATGATAAAGAATACTAT AGTGTGCACAACAAACACGTGCAAAGCTGCCAGTGAAGTGGATGGCTTTGGAAAGTCTGCAAAC TCAAAAGTTTACCACCAAGTCAGATGTGTGGTCCTTTGGTGTGCTCCTCTGGGAGCTCATGACAA GAGGAGCCCCCACCCTATCCTGATGTGAACACCTTTGATATAACTGTTTACTTGTTGCAAGGGAGA AGGCTCCTACAACCCGAATACTGCCCCAGACCCCTTATATGAAGTAATGCTAAAATGCTGGCACCC TAAAGCAGAAATGCGCCCATCCTTTTCTGAACTGGTGTCCCGGATATCAGCGATCTTCTCTACTT TCATTGGGGAGCACTACGTCCATGTAAACGCTACTTATGTGAACGTAAAATGTGTCGCTCCATAT CCTTCTCTGTTGTCATCACAAGATAACGCTGATGACGAGGTGGACACACTGA
789.	macaque cMET construct	artificial	aa	MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETAIQNVILHEHHIFLG ATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPCQDCSSKANLSGGVWKDNINMALVVDTYYDDQL ISCGSVNRGTCQRHVFPHNHTADIQSEVHCIFSPQIEEPNQCPDCVVSALGAKVLSSVKDRFINF FVGNTINSSYFPHHPLHSISVRRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYIHAFESNNFIY FLTVQRETLNAQTFHTRIIRFCSLNSGLHSYMEMPLECILTEKRKKRSTKKEVFNILQAAYVSKP GAQLARQIGASLNDDILFGVFAQSKPDSAEPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFY GPNHEHCFNRTLLRNSSGCEARRDEYRAEFTTALQRVDLFMGQFSEVLLTSISTFIKGDLTIANL GTSEGRFMQVVVSRSGPSTPHVNFLLDSHPVSPEVIVEHPLNQNGYTLVVTGKKITKIPLNGLGC RHFQSCSQCLSAPPFVQCGWCHDKCVRSEECPSGTWTQQICLPAIYKVFPTSAPLEGGTRLTICG WDFGFRRNNKFDLKKTRVLLGNESCTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTTQYS TFSYVDPIITSISPKYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLKSVSNSILECYTPAQT ISTEFAVKLKIDLANRETSIFSYREDPIVYEIHPTKSFISGGSTITGVGKNLIISVSVPRMVINVH EAGRNFTVACQHRSNSEIICCTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPFE KPVMISMGNENVLEIKGNDIDPEAVKGEVLKVGNKSCENIHLHSEAVLCTVPNDLLKLNSELNIE WKQAISSTVLGKVIVQPDQNFTGLIAGVVSISIALLLLLGLFLWLKKRKQIKDLGSELVRYDARV HTPHLDRLVSARSVSPTTEMVSNESVDYRATFPEDQFPNSSQNGSCRQVQYPLTDMSPILTSGDS DISSPLLQNTVHIDLSALNPELVQAVQHVVIGPSSLIVHFNEVIGRGHFGCVYHGTLLDNDGKKI HCAVKSLNRITDIGEVSQFLTEGIIMKDFSHPNVLSLLGICLRSEGSPLVVLPYMKHGDLRNFIR NETHNPTVKDLIGFGLQVAKGMKYLASKKFVHRDLAARNCMLDEKFTVKVADFGLARDMYDKEYY SVHNKTGAKLPVKWMALESLQTQKFTTKSDVWSFGVLLWELMTRGAPPYPDVNTFDITVYLLQGR RLLQPEYCPDPLYEVMLKCWHPKAEMRPSFSELVSRISAIFSTFIGEHYVHVNATYVNVKCVAPY PSLLSSEDNADDEVDT
790.	CM1-VH-A-XhoI	artificial	nt	CCATGTCTCGAGTCTGGGSCTGAASTGRWGARGCCTGGGGCTTCAGTGAAARTGTCCTGCARGGC TTCGGGCTATACCTTC

791.	CM1-VH-B	artificial	nt	ATCCACTCAAGCCYTTGTCCAGGCSYCTGTYTAACCCAGTGCAACCAGTAGCTGGTGAAGGTATA GCCCGAAGC
792.	CM1-VH-C	artificial	nt	GGCTTGAGTGGATKGGCATGATTGATCCTTCCAATAGTGACACTAGGTTTAATCCGAACTTCAAG GAC
793.	CM1-VH-D	artificial	nt	GCTGCTGAGCWSCATGTACGCTGTGYTGGMAGATSTGTCTMYAKTSAWTGTGRCCYTGTCCTTGA AGTTCGGATT
794.	CM1-VH-E	artificial	nt	GCCTACATGSWACTCAGCAGCCTGASATCTGMGGACACTGCAGTCTATTACTGTGCCASATATGG TAGCTACGTT
795.	CM1-VH-F-BstEII	artificial	nt	CATGTAGGTGACCGAGGTTCCTTGACCCCAGTAGTCCAGAGGGGAAACGTAGCTACCATA
796.	CM3-VH-A-XhoI	artificial	nt	CCATGTCTCGAGTCTGGGRCTGAASTGRWGAAGCCTGGGGCTTCAGTGAAGSTGTCCTGCAAGGC TTCT
797.	CM3-VH-B	artificial	nt	CTCAAGGCCTTGTCCAGGCSYCTGCYTCACCCAGTGTATCCAGTAACTGGTGAAGGTGTAGCCAG AAGCCTTGCAGGA
798.	CM3-VH-C	artificial	nt	CCTGGACAAGGCCTTGAGTGGATKGGAGAGATTAATCCTAGCAGCGGTCGTACTAACTACAACGA GAAATTC
799.	CM3-VH-D	artificial	nt	CTGTGGAGGTAGATKTGTCTMYAGTCAYTGTGACCYTGTTCTTGAATTTCTCGTTGTAGTT
800.	CM3-VH-E	artificial	nt	ATCTACCTCCACAGYCTACATGSAACTCAGCARCCTGASATCTGAGGACACTGCGGTCTATTACT GTGCA
801.	CM3-VH-F-BstEII	artificial	nt	CATGTAGGTGACCGTGGTCCTTGGCCCCAGTAGCCCCTWCTTGCACAGTAATAGACCGC
802.	CM1-VL-A-SacI	artificial	nt	CCTGTAGAGCTCGTGATGACCCAGACTCCAYYCTCCCTAMCTGTGACASYTGGAGAGMMGGYTTC TRTCAGCTGCAAGTCCAGT
803.	CM1-VL-B	artificial	nt	GTACCAGGCCAAGTAGTTCTTCTGACTGCTAGTATATAAAAGGGACTGGACTTGCAGCTGA
804.	CM1-VL-C	artificial	nt	TACTTGGCCTGGTACCWGCAGAAACCAGGTCAGTCTCCTMAACTGCTGATTTACTGGGCATCCAC TAGG
805.	CM1-VL-D	artificial	nt	GAGAGTGAAAATCTGTCCCAGATCCACTGCCTGAGAAGCGATCAGGGACCCCAGATTCCCTAGTGG ATGCCCAGTA
806.	CM1-VL-E	artificial	nt	ACAGATTTCACTCTCAMAATCTCCAGWGTGRAGGCTGASGACSTGGSAGTTTATTACTGTCAGCA ATAT
807.	CM1-VL-F-BsiWI/SpeI	artificial	nt	CCTCAGACTACGTACGTTTGATCTCCAACTTTGTGCCCCACCGAACGTCCACGGATAGGCAT AATATTGCTGACAGTAATA
808.	CM3-VL-A-SacI	artificial	nt	CCTGTAGAGCTCGTGATGACCCAATCTCCASYTTCTTTGSCTGTGACTCTAGGGCAGCSGGCCTC CATCTCCTGC
809.	CM3-VL-Ba	artificial	nt	GAACCAACTCATATAACTACCACCATCATAATCAACACTTTGGCTGGCCTTGCAGGAGATGGAGG C

810.	CM3-VL-Bb	artificial	nt	GAACCAACTCATATAACTACCACCATCATAATCAACACTAGATTGGCTGGCCTTGCAGGAGATGG AGGC
811.	CM3-VL-C	artificial	nt	AGTTATATGAGTTGGTTCCAACAGAGACCAGGACAGYCACCCARACKCCTCATCTMTGCTGCATC CAATCTA
812.	CM3-VL-D	artificial	nt	GGTGAAGTCTGTCCCAGACGCCACTGCCACTAAACCTGKCTGGGAYCCCAGATTCTAGATTGGATG CAGC
813.	CM3-VL-E	artificial	nt	TCTGGGACAGACTTCACCCTCAAKATCYMTCSTGTGGAGGMGGAGGATGTTGSARYCTATTACTG TCAGCAAAGT
814.	CM3-VL-F-BsiWI/SpeI	artificial	nt	CCTCAGACTAGTCGTACGTTTGATCTCCAGCTTGGTCCCCTGACCGAACGTGAGCGGATCCTCAT AACTTTGCTGACAGTAATA
815.	MET-1 L	artificial	aa	DIMMSQSPSSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVP DRFTGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEIK
816.	MET-1 L-CDR1	artificial	aa	KSSQSLLYTSSQKNYLA
817.	MET-1 L-CDR2	artificial	aa	WASTRES
818.	MET-1 L-CDR3	artificial	aa	QQYYAYPWT
819.	MET-1 L	artificial	nt	GATATTATGATGAGTCAGTCCCCCAGCAGCCTGACCGTGTCCGTGGGCGAGAAGGTGACCGTGTC TTGCAAGAGCAGCCAGAGCCTGCTGTACACCAGCAGCCAGAAGAACTACCTGGCTTGGTATCAGC AGAAGCCCGGCCAGAGCCCCAAAGCTGCTGATCTACTGGGCCAGCACCCGGGAGAGCGGAGTGCCC GACAGATTCACCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCACCAGCGTGAAGGCCGA CGACCTGGCCGTGTACTACTGCCAGCAGTACTACGCCTACCCCTGGACCTTCGGCGGAGGGACCA AGCTGGAGATCAAG
820.	MET-1 H	artificial	aa	QVQLQQSGPELVRPGASVKMSCRASGYTFTSYWLHWVKQRPGQGLEWIGMIDPSNSDTRFNPNFK DKATLNVDRSSNTAYMLLSSLTSADSAVYYCATYGSYVSPLDYWGQGTSVTVSS
821.	MET-1 H-CDR1	artificial	aa	SYWLH
822.	MET-1 H-CDR2	artificial	aa	MIDPSNSDTRFNPNFKD
823.	MET-1 H-CDR3	artificial	aa	YGSYVSPLDY
824.	MET-1 H	artificial	nt	CAGGTGCAGCTGCAGCAGAGCGGACCCGAGCTGGTGCGGCCAGGCGCCTCCGTGAAGATGAGCTG CAGGGCCAGCGGCTACACCTTCACCAGCTACTGGCTGCACTGGGTGAAACAGAGACCTGGACAGG GACTGGAGTGGATCGGCATGATCGACCCCAGCAACAGCGACACCAGGTTCAACCCCAACTTCAAG

				GACAAGGCCACCCTGAACCTGGACAGGTCCAGCAACACCGCCTACATGCTGCTGTCCAGCCTGAC CTCTGCCGACAGCAGCGCCGTCTATTACTGTGCCACCTACGGCAGCTACGTGTCCCCCCTGGACTACT GGGGCCAGGGCACCCTCTGTGACAGTGTCCTCC
825.	MET-1 HL	artificial	aa	QVQLQQSGPELVRPGASVKMSCRASGYTFTSYWLHWVKQRPGQGLEWIGMIDPSNSDTRFNPNFK DKATLNVDRSSNTAYMLLSSLTSADSAVYYCATYGSYVSPLDYWGQGTSVTVSSGGGGSGGGGSG GGGSDIMMSQSPSSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRE SGVPDRFTGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEIK
826.	MET-1 HL	artificial	nt	CAGGTGCAGCTGCAGCAGAGCGGACCCGAGCTGGTGCGGCCAGGCGCCTCCGTGAAGATGAGCTG CAGGGCCAGCGGCTACACCTTCACCAGCTACTGGCTGCACTGGGTGAAACAGAGACCTGGACAGG GACTGGAGTGGATCGGCATGATCGACCCCAGCAACAGCGACACCAGGTTCAACCCCAACTTCAAG GACAAGGCCACCCTGAACCTGGACAGGTCCAGCAACACCGCCTACATGCTGTCCAGCCTGAC CTCTGCCGACAGCGCCGTCTATTACTGTGCCACCTACGGCAGCTACGTGTCCCCCTGGACTACT GGGGCCAGGGCACCCTCTGTGACAGTGTCCTCCGGTGGTGGTTCTGGCGGCGGCTCCGGT GGTGGTGGTTCTGATATTATGATGAGTCAGTCCCCCAGCAGCCTGACCGTGTCCGTGGGCGAGAA GGTGACCGTGTCTTGCAACAGCAGCCAGAGCCTGCTGTACACCAGCAGCCAGAAGAACTATCTGG CTTGGTATCAGCAGAAGCCCGGCCAGAGCCCAAAGCTGCTGATCTACTGGGCCAGCACCCGGGAG AGCGGAGTGCCCGACAGATTCACCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCAGCAG CGTGAAGGCCGACGACCTGGCCGTGTACTACTGCCAGCAGTACTACGCCTACCCCTGGACCTTCG GCGGAGGGACCAAGCTGGAGATCAAG
827.	MET-1 LH	artificial	aa	DIMMSQSPSSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVP DRFTGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEIKGGGSGGGGSGGGGSQV QLQQSGPELVRPGASVKMSCRASGYTFTSYWLHWVKQRPGQGLEWIGMIDPSNSDTRFNPNFKDK ATLNVDRSSNTAYMLLSSLTSADSAVYYCATYGSYVSPLDYWGQGTSVTVSS
828.	MET-1 LH	artificial	nt	GATATTATGATGAGTCAGTCCCCCAGCAGCCTGACCGTGTCCGTGGGCGAGAAGGTGACCGTGTC TTGCAAGAGCAGCCAGAGCCTGCTGTACACCAGCAGCCAGAAGAACTACCTGGCTTGGTATCAGC AGAAGCCCGGCCAGAGCCCAAAGCTGCTGATCTACTGGGCCAGCACCCGGGAGAGCGGAGTGCCC GACAGATTCACCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCAGCAGCGTGAAGGCCGA CGACCTGGCCGTGTACTACTGCCAGCAGTACTACGCCTACCCCTGGACCTTCGGCGGAGGGACCA AGCTGGAGATCAAGGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG CAGCTGCAGCAGAGCGGACCCGAGCTGGTGCGGCCAGGCGCCTCCGTGAAGATGAGCTGCAGGGC CAGCGGCTACACCTTCACCAGCTACTGGCTGCACTGGGTGAAACAGAGACCTGGACAGGGACTGG AGTGGATCGGCATGATCGACCCCAGCAACAGCGACACCAGGTTCAACCCCAACTTCAAGGACAAG

				GCCACCCTGAACGTGGACAGGTCCAGCAACACCGCCTACATGCTGCTGTCCAGCCTGACCTCTGC CGACAGCGCCGTGTATTACTGTGCCACCTACGGCAGCTACGTGTCCCCCTGGACTACTGGGGCC AGGGCACCTCTGTGACAGTGTCCTCC
829.	MET-1 HL x I2C HL	artificial	aa	QVQLQQSGPELVRPGASVKMSCRASGYTFTSYWLHWVKQRPGQGLEWIGMIDPSNSDTRFNPNFK DKATLNVDRSSNTAYMLLSSLTSADSAVYYCATYGSYVSPLDYWGQGTSVTVSSGGGGSGGGGSG GGGSDIMMSQSPSSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRE SGVPDRFTGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEIKSGGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQIVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
830.	MET-1 HL x I2C HL	artificial	nt	CAGGTGCAGCTGCAGCAGAGCGGACCCGAGCTGGTGCGGCCAGGCGCCTCCGTGAAGATGAGCTG CAGGGCCAGCGGCTACACCTTCACCAGCTACTGGCTGCACTGGGTGAAACAGAGACCTGGACAGG GACTGGAGTGGATCGGCATGATCGACCCCAGCAACAGCGACACCAGGTTCAACCCCAACTTCAAG GACAAGGCCACCCTGAACGTGGACAGGTCCAGCAACACCGCCTACATGCTGCTGTCCAGCCTGAC CTCTGCCGACAGCGCCGTCTATTACTGTGCCACCTACGGCAGCTACGTGTCCCCCTGGACTACT GGGGCCAGGGCACCCTCTGTGACAGTGTCCTCCGGTGGTGGTTCTGGCGGCGGCTCCGGT GGTGGTGGTTCTGATATTATGATGACTCAGTCCCCCAGCAGCCTGACCGTGTCCGTGGGCGAGAA GGTGACCGTGTCTTGCAAGAGCAGCCAGAGCCTGCTGTACACCAGCAGCCAGAAGAACTATCTGG CTTGGTATCAGCAGAAGCCCGGCCAGAGCCCAAAGCTGCTGATCTACTGGGCCAGCACCCGGGAG AGCGGGAGTGCCCGACAGATTCACCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCAGCAG CGTGAAGGCCGACGACCTCGCCGTGTACTACTGCCAGCAGTACTACGCCTACCCCTGGACCTTCG GCGGAGGGACCAAGCTGGAGATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCT GGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTT CAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCA TAAGAAGTAAATATAATAATTATGCCGATTCAGTGAAAGACAGGTTCACCATC TCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGC CGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGT GGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCAC ACTCACTTGTGGCTCCTCCACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAA AACCAGGTCAGGCACCCCCTGGTCTAATAGGTGGACTAAGTTCCTCGCCCCCGGTACTCCTGCC AGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGA TGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
831.	MET-1 LH x I2C HL	artificial	aa	DIMMSQSPSSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVP DRFTGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEIKGGGGSGGGGSGGGGSQV

				QLQQSGPELVRPGASVKMSCRASGYTFTSYWLHWVKQRPGQGLEWIGMIDPSNSDTRFNPNFKDK ATLNVDRSSNTAYMLLSSLTSADSAVYYCATYGSYVSPLDYWGQGTSVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
832.	MET-1 LH x I2C HL	artificial	nt	GATATTATGATGAGTCAGTCCCCCAGCCTGACCGTGTCCGTGGGCGAGAGGTGACCGTGTC TTGCAAGAGCAGCCAGAGCCTGCTGTACACCAGCAGCCAGAAGAACTATCTTGGCTTGTATCAGC AGAAGCCCGGCCAGAGCCCAAAGCTGCTGATCTACTGGGCCAGCACCCGGGAGAGCGGAGTGCCC GACAGATTCACCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCAGCGTGAAGGCCGA CGACCTGGCCGTGTACTACTGCCAGCAGTACTACGCCTACCCCTGGACCTTCGGCGGAGGGACCA AGCTGGAGATCAAGGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGCAGCAGAGCGGACCCGAGCTGGTGCGGCCAGGCGCCTCCGTGAAGATGAGCTGCAGGGC CAGCGGCTACACCTTCACCAGCTACTGGCTGCACTGGGTGAAACAGAGACCTGGACAGGGACTGG AGTGGATCGGCATGATCGACCCCAGCAACAGCGACACCAGGTTCAACCCCAACTTCAAGGACAAG GCCACCCTGAACGTGGACAGGTCCAGCAACACCGCCTACATGCTGCTGTCCAGCCTGACCTCTGC CGACAGCGCCGTGTATTACTGTGCCACCTACGGCAGCTACGTGTCCCCCTGGACTACTGGGGCC AGGGCACCTCTGTGACAGTGTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTCGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
833.	MET-3 L-CDR1	artificial	aa	KASQSVDYDGGSYMS
834.	MET-3 L-CDR2	artificial	aa	AASNLES
835.	MET-3 L-CDR3	artificial	aa	QQSYEDPLT

836.	MET-3 H-CDR1	artificial	aa	SYWIH
837.	MET-3 H-CDR2	artificial	aa	EINPSSGRTNYNEKFKN
838.	MET-3 H-CDR3	artificial	aa	RGY
839.	MET 4 L	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFSGS GSGADFTLTISSLQPEDFATYYCQQANSFPLTFGGGTKVEIK
840.	MET-4 L-CDR1	artificial	aa	RASQGINTWLA
841.	MET-4 L-CDR2	artificial	aa	AASSLKS
842.	MET-4 L-CDR3	artificial	aa	QQANSFPLT
843.	MET-4 L	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGACCATCAC ATGTAGAGCTAGCCAGGGCATCAACACCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTGCTGATCTACGCCGCTTCCTCCTGAAATCTGGCGTGCCCAGCAGATTCAGCGGCAGC GGAAGCGGAGCCGACTTCACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTA CTGCCAGCAGGCCAACAGCTTCCCCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCAAG
844.	MET-4 H	artificial	aa	QVQLVQSGAEVKKPGASVKVSCEASGYTFTSYGFSWVRQAPGQGLEWMGWISASNGNTYYAQKLQ GRVTMTTDTSTSSAYMELRSLRSDDTAVYYCARVYADYADYWGQGTLVTVSS
845.	MET-4 H-CDR1	artificial	aa	SYGFS
846.	MET-4 H-CDR2	artificial	aa	WISASNGNTYYAQKLQG
847.	MET-4 H-CDR3	artificial	aa	VYADYADY
848.	MET-4 H	artificial	nt	CAGGTGCAGCTGGTGCAGAGCGGCGCTGAGGTGAAGAAGCCAGGCGCCAGCGTCAAGGTGTCCTG CGAGGCCAGCGGCTACACCTTCACCAGCTACGGCTTCAGCTGGGTGCGGCAGGCCCCTGGACAGG GACTGGAATGGATGGGCTGGATCAGCGCCAGCAACGGCAACACCTACTACGCCCAGAAGCTGCAG GGCCGCGTCACCATGACCACCGACACCAGCACCAGCGCCTACATGGAGCTGAGAAGCCTGAG ATCCGACGACACCGCCGTGTACTACTGCGCCAGGGTGTACGCCGACTACGCTGACTACTACTGGGGCC AGGGCACCCTGGTGACAGTGTCTTCC

849.	MET-4 HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCEASGYTFTSYGFSWVRQAPGQGLEWMGWISASNGNTYYAQKLQ GRVTMTTDTSTSSAYMELRSLRSDDTAVYYCARVYADYAWGQGTLVTVSSGGGGSGGGGSGGG GSDIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFS GSGSGADFTLTISSLQPEDFATYYCQQANSFPLTFGGGTKVEIK
850.	MET-4 HL	artificial	nt	CAGGTGCAGCTGGTGCAGAGCGGCGCTGAGGTGAAGAAGCCAGGCGCCAGCGTCAAGGTGTCCTG CGAGGCCAGCGGCTACACCTTCACCAGCTACGGCTTCAGCTGGGTGCGGCAGGCTCCTGGACAGG GACTGGAATGGATGGGCTGGATCAGCGCCAGCAACGGCAACACACCTACTACGCCCAGAAGCTGCAG GGCCGCGTCACCATGACCACACCGACACCAGCACAGCGCCTACATGGAGCTGAGAAGCCTGAG ATCCGACGACACCGCCGTCTACTACTGCGCCAGGGTGTACGCCGACTACGCTGACTACTGGGGCC AGGGCACCCTGGTGACAGTGTCTTCCGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGAC CATCACATGTAGAGCTAGCCAGGGCATCAACACCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCA AGGCCCCCAAGCTGCTGATCTACGCCGCTTCCTCCCTGAAATCTGGCGTCCCAGCAGATTCAGC GGCAGCGGAAGCGGAGCCGACTTCACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCAC CTACTACTGCCAGGCCAACAGCTTCCCCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCA AG
851.	MET-4 LH	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFSGS GSGADFTLTISSLQPEDFATYYCQQANSFPLTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSQVQLVQSG AEVKKPGASVKVSCEASGYTFTSYGFSWVRQAPGQGLEWMGWISASNGNTYYAQKLQGRVTMTTD TSTSSAYMELRSLRSDDTAVYYCARVYADYAWGQGTLVTVSS
852.	MET-4 LH	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGACCATCAC ATGTAGAGCTAGCCAGGGCATCAACACCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTGCTGATCTACGCCGCTTCCTCCCTGAAATCTGGCGTGCCCAGCAGATTCAGCGGCAGC GGAAGCGGAGCCGACTTCACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTA CTGCCAGGCAGGCCAACAGCTTCCCCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCAAGGGTG GTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTGGTGCAGAGCGGC GCTGAGGTGAAGAAGCCAGGCGCCAGCGTCAAGGTGTCCTGCGAGGCCAGCGGCTACACCTTCAC CAGCTACGGCTTCAGCTGGGTGCGGCAGGCTCCTGGACAGGGACTGGAATGGATGGGCTGGATCA GCGCCAGCAACGGCAACACCTACTACGCCCAGAAGCTGCAGGGCCGCGTCACCATGACCACCGAC ACCAGCACCAGCACGCCTACATGGAGCTGAGAAGCCTGAGATCCGACGACACCGCCGTGTACTA CTGCGCCAGGGTGTACGCCGACTACGCTGACTACTGGGGCCAGGGCACCCTGGTGACAGTGTCTT CC

853.	MET-4 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCEASGYTFTSYGFSWVRQAPGQGLEWMGWISASNGNTYYAQKLQ GRVTMTTDTSTSSAYMELRSLRSDDTAVYYCARVYADYAWGQGTLVTVSSGGGGSGGGGSGGG GSDIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFS GSGSGADFTLTISSLQPEDFATYYCQQANSFPLTFGGGTKVEIKSGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
854.	MET-4 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTGCAGAGCGGCGCTGAGGTGAAGAAGCCAGGCGCCAGCGTCAAGGTGTCCTG CGAGGCCAGCGGCTACACCTTCACCAGCTACGGCTTCAGCTGGGTGCGGCAGGCTCCTGGACAGG GACTGGAATGGATGGGCTGGATCAGCGCCACAACGGCAACACCTACTACGCCCAGAAGCTGCAG GGCCGCGTCACCATGACCACACCGACACCAGCACAGCGCCTACATGGAGCTGAGAAGCCTGAG ATCCGACGACACCGCCGTGTACTACTGCGCCAGGGTGTACGCCGACTACGCTGACTACTGGGGCC AGGGCACCCTGGTGACAGTGTCTTCCGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTGACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGAC CATCACATGTAGAGCTAGCCAGGGCATCAACACCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCA AGGCCCCCAAGCTGCTGATCTACGCCGCTTCCTCCCTGAAATCTGGCGTGCCCAGCAGATTCAGC GGCAGCGGAAGCGGAGCCGACTTCACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCAC CTACTACTGCCAGCAGGCCAACAGCTTCCCCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCA AGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGA GGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGT CCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATG CAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACT GCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGG GAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCT CCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACT CAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTCTGTGGCTCCTCGACTGG GGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTC TAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTGGA GGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCT ATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
855.	MET-4 LH x I2C HL	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFSGS GSGADFTLTISSLQPEDFATYYCQQANSFPLTFGGGTKVEIKGGGGSGGGGSGGGGSQVQLVQSG AEVKKPGASVKVSCEASGYTFTSYGFSWVRQAPGQGLEWMGWISASNGNTYYAQKLQGRVTMTTD TSTSSAYMELRSLRSDDTAVYYCARVYADYAWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGG

				SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTA YLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
856.	MET-4 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGACCATCAC ATGTAGAGCTAGCCAGGGCATCAACACCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTGCTGATCTACGCCGCTTCCTCCCTGAAATCTGGCGTGCCCAGCAGATTCAGCGGCAGC GGAAGCGGAGCCGACTTCACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTA CTGCCAGCAGGCCAACAGCTTCCCCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCAAGGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTGGTGCAGAGCGGC GCTGAGGTGAAGAAGCCAGGCGCCAGCGTCAAGGTGTCCTGCGAGGCCAGCGGCTACACCTTCAC CAGCTACGGCTTCAGCTGGGTGCGGCAGGCTCCTGGACAGGGACTGGAATGGATGGGCTGGATCA GCGCCAGCAACGGCAACACCTACTACGCCCAGAAGCTGCAGGGCCGCGTCACCATGACCACCGAC ACCAGCACCAGCAGCGCCTACATGGAGCTGAGAAGCCTGAGATCCGACGACACCGCCGTGTACTA CTGCGCCAGGGTGTACGCCGACTACGCTGACTACTGGGGCCAGGGCACCCTGGTGACAGTGTCTT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGG TCATTGAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCG CCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAA CATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCC TATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACCTCTGGTCACCGTCTCCT CAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAG GAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGC TGTTACATCTGGCAACTACCCAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAA TAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGC AAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
857.	MET-5 L	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYDISPMYSFGQGTKLEMK
858.	MET-5 L-CDR1	artificial	aa	RASQSVSNNYLA
859.	MET-5 L-CDR2	artificial	aa	GASSRAT

860.	MET-5 L-CDR3	artificial	aa	QQYDISPMYS
861.	MET-5 L	artificial	nt	GAGATCGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCAGGCGAGAGAGCCACCCTGAG CTGCAGAGCCAGCCAGAGCGTGTCCAACAACTATCTGGCTTGGTATCAGCAGAAACCAGGACAGG CTCCCAGACTGCTGATCTTCGGCGCCAGCTCTAGAGCCACCGGCATCCCCGACAGATTCAGTGGT AGCGGCTCCGGCACAGACTTCACCCTGACCATTTCCAGACTGGAACCCGAGGACTTCGCCGTGTA CTACTGCCAGCAGTACGACATCAGCCCCATGTACAGCTTCGGCCAGGGCACCAAGCTGGAGATCA AG
862.	MET-5 H	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGPLGYCSSTSCPVTGEYYYYGMDVWGQGTT VTVSS
863.	MET-5 H-CDR1	artificial	aa	SGGYYWS
864.	MET-5 H-CDR2	artificial	aa	YIYYSGSTYYNPSLKS
865.	MET-5 H-CDR3	artificial	aa	DGPLGYCSSTSCPVTGEYYYYGMDV
866.	MET-5 H	artificial	nt	CAGGTGCAGCTGCAGGAGAGCGGGGCCTGGACTGGTGAAGCCCAGCCAGACCCTGTCTCTGACCTG CACCGTGTCCGGCGGCAGCATCAGCAGCGGCGGCTACTACTGGTCCTGGATCAGGCAGCACCCAG GCAAGGGCCTGGAGTGGATCGGCTACATCTACTATTCTGGATCCACCTACTACAACCCCAGCCTG AAGTCCAGAGTGACCATCTCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGT GACAGCCGCCGACACCGCCGTGTATTATTGCGCCAGGGACGGCCCACTGGGATATTGTTCCTCCA CATCCTGCCCAGTGACCGCCGAGTACTACTACGGCATGGACGTGTGGGGACAGGGCACCACC GTGACCGTGTCTTCC
867.	MET-5 HL	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGPLGYCSSTSCPVTGEYYYYGMDVWGQGTT VTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAP RLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDISPMYSFGQGTKLEMK
868.	MET-5 HL	artificial	nt	CAGGTGCAGCTGCAGGAGAGCGGGGCCTGGACTGGTGAAGCCCAGCCAGACCCTGTCTCTGACCTG CACCGTGTCCGGCGGCAGCATCAGCAGCGGCGGCTACTACTGGTCCTGGATCAGGCAGCACCCAG GCAAGGGCCTGGAGTGGATCGGCTACATCTACTATTCTGGATCCACCTACTACAACCCCAGCCTG AAGTCCAGAGTGACCATCTCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGT GACAGCCGCCGACACCGCCGTGTATTATTGCGCCAGGGACGGCCCACTGGGATATTGTTCCTCCA

				CATCCTGCCCAGTGACCGCCGAGTACTACTACGGCATGGACGTGTGGGGACAGGGCACCACC GTGACCGTGTCTTCCGGTG-GTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTGAGAT CGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCAGGCGAGAGAGCCACCCTGAGCTGCA CAGCCACCCAGACCGTCTCCAACAACTATCTGCCTTGGTATCAGCACAAACCAGGCACAGCCTCCC AGACTGCTGATCTTCGGCGCCCAGCTCTAGAGCCACCGGCATCCCCCGACAGATTCAGTGGTAGCGG CTCCGGCACAGACTTCACCCTGACCATTTCCAGACTGGAACCCGAGGACTTCGCCGTGTACTACT GCCAGCAGTACGACATCAC-CCCCATGTACAGCTTCGGCCAGGGCACCAAGCTGGAGATGAAG
869.	MET-5 LH	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPRLL-FGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYDISPMYSFGQGTKLEMKGGGSGGGGSGGGGSQVQLQE SGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTI SVDTSKNQFSLKLSSVTAADTAVYYCARDGPLGYCSSTSCPVTGEYYYYGMDVWGQGTTVTVSS
870.	MET-5 LH	artificial	nt	GAGATCGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCAGGCGAGAGAGCCACCCTGAG CTGCAGAGCCAGCCAGAGCGTGTCCAACAACTATCTGGCTTGGTATCAGCAGAAACCAGGACAGG CTCCCAGACTGCTGATCTTCGGCGCCAGCTCTAGAGCCACCGGCATCCCCGACAGATTCAGTGGT AGCGGCTCCGGCACAGACTTCACCCTGACCATTTCCAGACTGGAACCCGAGGACTTCGCCGTGTA CTACTGCCAGCAGTACGACATCAGCCCCATGTACAGCTTCGGCCAGGGCACCAAGCTGGAGATGA AGGGTGGTGGTGGTTCTGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGCAGGAG AGCGGGCCTGGACTGGTGAAGCCCAGCCAGACCCTGTCTCTGACCTGCACCGTGTCCGGCGGCAG CATCAGCAGCGGCGGCTACTACTGGTCCTGGATCAGGCAGCACCCAGGGCAAGGGCCTGGAGTGGA TCGGCTACATCTACTATTCTGGATCCACCTACTACAACCCCAGCCTGAAGTCCAGAGTGACCATC TCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGTGACAGCCGCCGACACCGC CGTGTATTATTGTGCGCCAGCGACGGCCCACTGGGATATTGTTCCTCCACATCCTGCCCAGTGACCG GCGAGTACTACTACTACGGCATGGACGTGTGGGGACAGGGCACCACCGTGACCGTGTCTTCC
871.	MET-5 HL x I2C HL	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGPLGYCSSTSCPVTGEYYYYGMDVWGQGTT VTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAP RLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYD-SPMYS-GQGTKLEMKS GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY-SYWAYWGQGTLVTVSS GGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNY-PNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
872.	MET-5 HL x I2C HL	artificial	nt	CAGGTGCAGCTGCAGGAGAGCGGGGGCCTGGACTGGTGAAGCCCAGACCCTGTCTCTGACCTG CACCGTGTCCGGCGGCAGCATCAGCAGCGGCGGCTACTACTGGTCCTGGATCAGGCAGCACCCAG GCAAGGGCCTGGAGTGGATCGGCTACATCTACTATTCTGGATCCACCTACTACAACCCCAGCCTG

				AAGTCCAGAGTGACCATCTCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGT GACAGCCGCCGACACCGCCGTGTATTATTGCGCCAGGGACGGCCCACTGGGATATTGTTCCTCCA CATCCTGCCCAGTGACCGCCGAGTACTACTACGGCATGGACGTGTGGGGACAGGGCACCACC GTCACCGTGTCTTCCGCTCGTGCTGTCTGCCGCGCCGCTCCCCTGCTGCTGGTTCTCAGAT CGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCAGGCGAGAGCCACCCTGAGCTGCA GAGCCAGCCAGAGCGTGTCCAACAACTATCTGGCTTGGTATCAGCAGAAACCAGGACAGGCTCCC AGACTGCTGATCTTCGGCGCCAGCTCTAGAGCCACCGGCATCCCCGACAGATTCAGTGGTAGCGG CTCCGGCACAGACTTCACCCTGACCATTTCCAGACTGGAACCCGAGGACTTCGCCGTGTACTACT GCCAGCAGTACGACATCACCCCCATGTACAGCTTCGGCCAGGGCACCAAGCTGGAGATCAAGTCC GGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTC ATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCC AGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACA TATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTA TCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACT TCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCA GGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGA ACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGCTG TTACATCTGGCAACTACCCAAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATA GGTGGGACTAAGTTCCTCCCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAA GGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGT ACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
873.	MET-5 LH x I2C HL	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYDISPMYSFGQGTKLEMKGGGSGGGGSGGGGSQVQLQE SGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTI SVDTSKNQFSLKLSSVTAADTAVYYCARDGPLGYCSSTSCPVTGEYYYYGMDVWGQGTTVTVSSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
874.	MET-5 LH x I2C HL	artificial	nt	GAGATCGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCAGGCGAGAGAGCCACCCTGAG CTGCAGAGCCAGCCAGAGCGTGTCCAACAACTATCTGGCTTGGTATCAGCAGAAACCAGGACAGG CTCCCAGACTGCTGATCTTCGGCGCCAGCTCTAGAGCCACCGGCATCCCCGACAGATTCAGTGGT AGCGGCTCCGGCACAGACTTCACCCTGACCATTTCCAGACTGGAACCCGAGGACTTCGCCGTGTA CTACTGCCAGCAGTACGACATCAGCCCCATGTACAGCTTCGGCCAGGGCACCAAGCTGGAGATGA AGGGTGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGG

				AGCGGGCCTGGACTGGTGAAGCCCAGCCAGACCCTGTCTCTGACCTGCACCGTGTCCGGCGGCAG CATCAGCAGCGGCGGCTACTACTGGTCCTGGATCAGGCAGCACCCAGGCAAGGGCCTGGAGTGGA TCGGCTACATCTACTATTCTGGATCCACCTACTACAACCCCAGCCTGAAGTCCAGAGTCCATCATC TCCGTGCACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGTGACCGCCGCAGACACCGC CGTGTATTATTGCGCCAGCGGACGGCCCACTGGGATATTGTTCCTCCACATCCTGCCCAGTGACCG GCGAGTACTACTACGGCATGGACGTGTGGGGACAGGGCACCACCGTGACCGTGTCTTCCGGA GGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATT GAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGG CTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATATAATTATGCAACATAT TATGCCGATTCAGTGAAACACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCT ACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCG GTAATAGCTACATATCCTACTGGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGT GGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACC TTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTA CATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGT GGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGCGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACA GCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
875.	MET-6 L	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQSEDFATYYCQQANSFPITFGPGTKVEIK
876.	MET-6 L-CDR1	artificial	aa	RASQGISSWLA
877.	MET-6 L-CDR2	artificial	aa	AASSLQS
878.	MET-6 L-CDR3	artificial	aa	QQANSFPIT
879.	MET-6 L	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGACCATCAC CTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTCCTGATCTATGCTGCTTCCAGCCTGCAGAGCGGCGTGCCCAGCAGATTCAGCGGCAGC GGCTCCGGCACAGACTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTCGCCACCTACTA CTGCCAGCAGGCCAACAGCTTCCCCATCACCTTCGGCCCAGGCACCAAGGTGGAGATCAAG
880.	MET-6 H	artificial	aa	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYGGWIRQPPGKGLDWIGSIYYSGNTYYNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHSWDYFDYWDQGTLVTVSS

881.	MET-6 H-CDR1	artificial	aa	SSSYYGG
882.	MET-6 H-CDR2	artificial	aa	SIYYSGNTYYNPSLKS
883.	MET-6 H-CDR3	artificial	aa	HSWDYFDY
884.	MET-6 H	artificial	nt	CAGCTCCAGCTCCAGGAGAGCGGGCCTGGACTGGTGAAGCCCAGCGAGACACTGAGCCTGACCTG CACCGTGTCCGGCGGCAGCATCAGCAGCAGCTACTACGGCGGCTGGATCAGACAGCCACCCG GCAAAGGACTGGATTGGATCGGATCCATCTATTATAGTGGAAACACCTACAACCCCAGCCTG AAGTCCCGCGTGACCATCTCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGT GACAGCCGCCGACACCGCCGTGTACTACTGCGCCAGGCACAGCTGGGACTACTTCGACTACTGGG ACCAGGGCACCCTGGTGACCGTGTCTTCC
885.	MET-6 HL	artificial	aa	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYGGWIRQPPGKGLDWIGSIYYSGNTYYNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHSWDYFDYWDQGTLVTVSSGGGGSGGGGSGG GGSDIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQSEDFATYYCQQANSFPITFGPGTKVEIK
886.	MET-6 HL	artificial	nt	CAGCTCCAGCTCCAGGAGAGCGGGCCTGGACTGGTGAAGCCCAGCGAGACACTGAGCCTGACCTG CACCGTGTCCGGCGGCAGCATCAGCAGCAGCTACTACGGCGGCTGGATCAGACAGCCACCCG GCAAAGGACTGGATTGGATCGGATCCATCTATTATAGTGGAAACACCTACAACCCCAGCCTG AAGTCCCGCGTGACCATCTCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGT GACAGCCGCCGACACCGCCGTGTACTACTGCGCCAGGCACAGCTGGGACTACTTCGACTACTGGG ACCAGGGCACCCTGGTGACCGTGTCTTCCGGTGGTGGTTCTGGCGGCGGCTCCGGTGGT GGTGGTTCTGACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGT GACCATCACCTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCG GCAAGGCCCCCAAGCTCCTGATCTATGCTGCTTCCAGCCTGCAGAGCGGCGTGCCCAGCAGATTC AGCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTCGC CACCTACTACTGCCAGCAGGCCAACAGCTTCCCCATCACCTTCGGCCCCAGGCACCAAGGTGGAGA TCAAG
887.	MET-6 LH	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQSEDFATYYCQQANSFPITFGPGTKVEIKGGGGSGGGGSGGGGSQLQLQESG PGLVKPSETLSLTCTVSGGSISSSSYYGGWIRQPPGKGLDWIGSIYYSGNTYYNPSLKSRVTISV DTSKNQFSLKLSSVTAADTAVYYCARHSWDYFDYWDQGTLVTVSS

888.	MET-6 LH	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGACCATCAC CTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTCCTGATCTATGCTGCTTCCAGCCTGCAGAGCGGCGTGCCCAGCAGATTCAGCGGCAGC GGCTCCGGCACAGACTTCACCCTGACCATCAGCTCCCTGCAGTCCCAGGACTTCGCCACCTACTA CTGCCAGCAGGCCAACAGCTTCCCCATCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGCTCCAGGAGAGCGGG CCTGGACTGGTGAAGCCCAGCGAGACACTGAGCCTGACCTGCACCGTGTCCGGCGGCAGCATCAG CAGCAGCTACTACGGCGGCTGGATCAGACAGCCCACCCGGCAAAGGACTGGATTGGATCGGAT CCATCTATTATAGTGGAAACACCTACTACAACCCCAGCCTGAAGTCCCGCGTGACCATCTCCGTG GACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGTGACAGCCGCCGACACCGCCGTGTA CTACTGCGCCAGGCACAGCTGGGACTACTTCGACTACTGGGACCAGGGCACCCTGGTGACCGTGT CTTCC
889.	MET-6 HL x I2C HL	artificial	aa	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYGGWIRQPPGKGLDWIGSIYYSGNTYYNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHSWDYFDYWDQGTLVTVSSGGGGSGGGGSGG GGSDIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQSEDFATYYCQQANSFPITFGPGTKVEIKSGGGGSEVQLVESGGGLVQP GGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKN TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
890.	MET-6 HL x I2C HL	artificial	nt	CAGCTCCAGCTCCAGGAGAGCGGGCCTGGACTGGTGAAGCCCAGCGAGACACTGAGCCTGACCTG CACCGTGTCCGGCGGCAGCATCAGCAGCAGCTACTACGGCGGCTGGATCAGACAGCCACCCG GCAAAGGACTGGATTGGATCGGATCCATCTATTATAGTGGAAACACCTACTACAACCCCAGCCTG AAGTCCCGCGTGACCATCTCCGTGGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGT GACAGCCGCCGACACCGCCGTGTACTACTGCGCCAGGCACAGCTGGGACTACTTCGACTACTGGG ACCAGGGCACCCTGGTGACCGTGTCTTCCGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGT GGTGGTTCTGACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGT GACCATCACCTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCG GCAAGGCCCCCAAGCTCCTGATCTATGCTGCTTCCAGCCTGCAGAGCGGCGTGCCCAGCAGATTC AGCGGCAGCGGCTCCGGCACAGACTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTCGC CACCTACTACTGCCAGCAGGCCAACAGCTTCCCCATCACCTTCGGCCAGGGCACCAAGGTGGAGA TCAAGTCCGGAGGTGGTGGCATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCT GGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTG GGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATT ATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAAC

				ACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACA TGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCG TCTCCTCAGGTGGTGGTGCTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTG ACTCAGCAACCTTCACTCACCGTATCATCACCTGGTGAACACAGTCACACTCACTTCTGCCTCCTCGAC TGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTG GTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTT GGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGT TCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
891.	MET-6 LH x I2C HL	artificial	aa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQSEDFATYYCQQANSFPITFGPGTKVEIKGGGSGGGGSGGGGSQLQLQESG PGLVKPSETLSLTCTVSGGSISSSSYYGGWIRQPPGKGLDWIGSIYYSGNTYYNPSLKSRVTISV DTSKNQFSLKLSSVTAADTAVYYCARHSWDYFDYWDQGTLVTVSSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
892.	MET-6 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGACCATCAC CTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTCCTGATCTATGCTGCTTCCAGCCTGCAGAGCGGCGTGCCCAGCAGATTCAGCGGCAGC GGCTCCGGCACAGACTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTCGCCACCTACTA CTGCCAGCAGGCCAACAGCTTCCCCATCACCTTCGGCCCAGGCACCAAGGTGGAGATCAAGGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGCTCCAGCTGCAGGAGAGCGGG CCTGGACTGGTGAAGCCCAGCGAGACACTGAGCCTGACCTGCACCGTGTCCGGCGGCAGCATCAG CAGCAGCAGCTACTACGGCGGCTGGATCAGACAGCCACCCGGCAAAGGACTGGATTGGATCGGAT CCATCTATTATAGTGGAAACACCTACTACAACCCCAGCCTGAAGTCCCGCGTGACCATCTCCGTG GACACCAGCAAGAACCAGTTCAGCCTGAAGCTGTCCAGCGTGACAGCCGCCGACACCGCCGTGTA CTACTGCGCCAGGCACAGCTGGGACTACTTCGACTACTGGGACCAGGGCACCCTGGTGACCGTGT CTTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGA GGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGT CCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATAATATTATG CAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACT GCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGG GAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCT CCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACT CAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTCTGCCTCCTCGACTGG

				GGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACACAAAAACCAGGTCAGGCACCCCGTGGTC TAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGA GGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCT ATGCTACAGCAACCGCTGCCTGTTCCGTCCAGGAACCAAACTGACTCTCCTA
893.	MET-7 L	artificial	aa	DIQMTQSPSSVSASVGDRVIITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFSGS GSGTDFTVTISSLQPEDFATYYCQQSNSLPWTFGQGTKVEIK
894.	MET-7 L-CDR1	artificial	aa	RASQGISSWLA
895.	MET-7 L-CDR2	artificial	aa	AASSLKS
896.	MET-7 L-CDR3	artificial	aa	QQSNSLPWT
897.	MET-7 L	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGATCATCAC CTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTGCTCATCTATGCTGCTTCCAGCCTGAAGTCCGGCGTGCCCAGCAGATTCAGCGGCAGC GGCTCCGGCACAGACTTCACCGTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTA CTGCCAGAGCAACAGCCTGCCCTGGACCTTCGGCCAGGGCACCAAGGTGGAGATCAAG
898.	MET-7 H	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMNWVRQAPGKGLEWVSYISSRSSTIYYADSVK GRFTMSRDNAKNSLYMQMNSLRDEDTAVYYCGYGDYDYFDYWGQGTLVTVSS
899.	MET-7 H-CDR1	artificial	aa	RYSMN
900.	MET-7 H-CDR2	artificial	aa	YISSRSSTIYYADSVKG
901.	MET-7 H-CDR3	artificial	aa	GDYDYFDY
902.	MET-7 H	artificial	nt	GAGGTGCAGCTGGTCGAGTCTGGCGGAGGACTGGTGCAGCCAGGCGGCAGCCTGAGACTGTCCTG TGCTGCTTCTGGATTCACCTTCAGCAGGTACAGCATGAACTGGGTCCGCCAGGCTCCTGGTAAAG GACTGGAGTGGGTCTCCTACATCAGCAGCAGGTCCAGCACCATCTACTACGCCGACAGCGTGAAG GGCAGGTTCACCATGAGCAGGGACAACGCCAAGAACAGCCTGTACATGCAGATGAACAGCCTGAG GGACGAGGACACCGCCGTGTACTACTGCGGCTACGGCGACTACGACTACTTCGACTACTGGGGCC AGGGAACCCTGGTGACCGTGTCTTCC
903.	MET-7 LH	artificial	aa	DIQMTQSPSSVSASVGDRVIITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFSGS GSGTDFTVTISSLQPEDFATYYCQQSNSLPWTFGQGTKVEIKGGGGSGGGGSGGGGSEVQLVESG

				GGLVQPGGSLRLSCAASGFTFSRYSMNWVRQAPGKGLEWVSYISSRSSTIYYADSVKGRFTMSRD NAKNSLYMQMNSLRDEDTAVYYCGYGDYDYFDYWGQGTLVTVSS
904.	MET-7 LH	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGATCATCAC CTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTGCTCATCTATGCTGCTTCCAGCCTGAAGTCCGGCGTGCCCAGCAGATTCAGCGGCAGC GGCTCCGGCACAGACTTCACCGTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTA CTGCCAGCAGGCAACAGCCTGCCCTGGACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGGTGCAGCTGGTCGAGTCTGGC GGAGGACTGGTGCAGCCAGGCGGCAGCCTGAGACTGTCCTGTGCTGCTTCTGGATTCACCTTCAG CAGGTACAGCATGAACTGGGTCCGCCAGGCTCCTGGTAAAGGACTGGAGTGGGTCTCCTACATCA GCAGCAGGTCCAGCACCATCTACTACGCCGACAGCGTGAAGGGCAGGTTCACCATGAGCAGGGAC AACGCCAAGAACAGCCTGTACATGCAGATGAACAGCCTGAGGGACGAGGACACCGCCGTGTACTA CTGCGGCTACGGCGACTACGACTACTTCGACTACTGGGGCCAGGGAACCCTGGTGACCGTGTCTT CC
905.	MET-7 LH x I2C HL	artificial	aa	DIQMTQSPSSVSASVGDRVIITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLKSGVPSRFSGS GSGTDFTVTISSLQPEDFATYYCQQSNSLPWTFGQGTKVEIKGGGSGGGGSGGGGSEVQLVESG GGLVQPGGSLRLSCAASGFTFSRYSMNWVRQAPGKGLEWVSYISSRSSTIYYADSVKGRFTMSRD NAKNSLYMQMNSLRDEDTAVYYCGYGDYDYFDYWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTA YLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
906.	MET-7 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGAGCCCCAGCAGCGTGTCTGCCAGCGTGGGCGACAGAGTGATCATCAC CTGCAGAGCTTCCCAGGGCATCTCTAGCTGGCTGGCCTGGTATCAGCAGAAGCCCGGCAAGGCCC CCAAGCTGCTCATCTATGCTGCTTCCAGCCTGAAGTCCGGCGTGCCCAGCAGATTCAGCGGCAGC GGCTCCGGCACAGACTTCACCGTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTA CTGCCAGCAGAGCAACAGCCTGCCCTGGACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGGTGCAGCTGGTCGAGTCTGGC GGAGGACTGGTGCAGCCAGGCGGCAGCCTGAGACTGTCCTGTGCTGCTTCTGGATTCACCTTCAG CAGGTACAGCATGAACTGGGTCCGCCAGGCTCCTGGTAAAGGACTGGAGTGGGTCTCCTACATCA GCAGCAGGTCCAGCACCATCTACTACGCCGACAGCGTGAAGGGCAGGTTCACCATGAGCAGGGAC AACGCCAAGAACAGCCTGTACATGCAGATGAACAGCCTGAGGGACGAGGACACCGCCGTGTACTA CTGCGGCTACGGCGACTACGACTACTTCGACTACTGGGGCCAGGGAACCCTGGTGACCGTGTCTT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGG

				TCATTGAAACTCTCATGTCCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCG CCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAA CATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCC TATCTACAAATGAACAACTTGAAAACTCAGGACACTGCCGTCTACTACTGTGTGACACATCCGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCT CAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAG GAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGC TGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAA TAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGC AAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
907.	ENSI L-CDR1	artificial	aa	RASQNVGTAVA
908.	ENSI L-CDR2	artificial	aa	SASNRYT
909.	ENSI L-CDR3	artificial	aa	QQYTNYPMYT
910.	ENSI H-CDR1	artificial	aa	DYVIH
911.	ENSI H-CDR2	artificial	aa	YINPYDDDTTYNQKFKG
912.	ENSI H-CDR3	artificial	aa	RGNSYDGYFDYSMDY
913.	Human endosialin	artificial	nt	ATGCTGCTGGCGCCTGTTGCTGGCCTGGGCGGCCGCAGGGCCCACACTGGGCCAGGACCCCTGGGC TGCTGAGCCCCGTGCCGCCTGCGGCCCCAGCAGCTGCTACGCTCTCTTCCCACGGCGCCGCACCT TCCTGGAGGCCTGGCGGCCCTGCCGCGAGCTGGGGGGCGACCTGGCCACTCCTCGGACCCCCGAG GAGGCCCAGCGTGTGGACAGCCTGGTGGGTCGGGCCCAGCCAGCGGCTGCTGTGGATCGGGCT GCAGCGGCAGGCCCGGCAATGCCAGCTGCAGCGCCCACTGCGCGGCTCACGTGGACCACAGGGG ACCAGGACACGGCTTTCACCAACTGGGCCCAGCCACGCCTCTGGAGGCCCCTGCCCGGCCCAGCGC TGTGTGGCCCTGGAGGCAAGTGGCGACACCGCTGGCTGGAGGGCTCGTGCACGCTGGCTGTCGA CGGCTACCTGTGCCAGTTTGGCTTCGAGGGCGCCTGCCCGGCGCTGCAAGATGAGGCGGGCCAGG CCGGCCCAGCCGTGTATACCACGCCCTTCCACCTGGTCTCCACACAGAGTTTGAGTGGCTGCCCTTC GGCTCTGTGGCCGCTGTCCAGTGCCAGGCTGGCAGGGAGGCCTCTCTGCTCGTGCAAGCAGCC TGAGGGAGGTGTGGGCTCGTCACGGGCTGGGCCCCCTGTGCCTGGGGACTGGCTGCAGCCCTGACA ACGGGGGCTGCGAACACCAATGTGTGGAGGAGGTGGATGGTCACGTGTCCTGCCGCTGCACTGAG GGCTTCCGGCTGGCAGCAGACGGGCGCAGTTGCGAGGACCCCTGTGCCCAGGCTCCGTGCGAGCA GCAGTGTGAGCCCGGTGGGCCACAAGGCTACAGCTGCCACTGTCGCCTGGGTTTCCGGCCAGCGG AGGATGATCCGCACCGCTGTGTGGACACAGATGAGTGCCAGATTGCCGGTGTGTGCCAGCAGATG TGTGTCAACTACGTTGGTGGCTTCGAGTGTTATTGTAGCGAGGGACATGAGCTGGAGGCTGATGG CATCAGCTGCAGCCCTGCAGGGGCCATGGGTGCCCAGGCTTCCCAGGACCTCGGAGATGAGTTGC TGGATGACGGGGAGGATGAGGAAGATGAAGACGAGGCCTGGAAGGCCTTCAACGGTGGCTGGACG GAGATGCCTGGGATCCTGTGGATGGAGCCTACGCAGCCGCCTGACTTTGCCCTGGCCTATAGACC

				GAGCTTCCCAGAGGACAGAGAGCCACAGATACCCTACCCGGAGCCCACCTGGCCACCCCCGCTCA GTGCCCCCAGGGTCCCCTACCACTCCTCAGTGCTCTCCGTCACCCGGCCTGTGGTGGTCTCTGCC ACGCATCCCACACTGCCTTCTGCCCACCAGCCTCCTGTGATCCCTGCCACACACCCAGCTTTGTC CCCTGACCACCAGATCCCCCTGATCGCAGCCAACTATCCAGATCTGCCTTCTGCCTACCAACCCG GTATTCTCTCTGTCTCTCATTCAGCACAGCCTCCTGCCCACCAGCCCCCTATGATCTCAACCAAA TATCCGGAGCTCTTCCCIGCCCACCAGTCCCCCATGTTCCAGACACCCGGGTCGCTGGCACCCA GACCACCACTCATTTGCCTGGAATCCCACCIAACCATGCCCCCTCTGGTCACCACCCTCGGTGCCC AGCTACCCCCCTCAAGCCCCCAGATGCCCTTGICCTCAGAACCCAGGCCACCCAGCTTCCCATTATC CCAACTGCCCCAGCCCCTCTCTGACCACCACCICCAGGTCCCCCTGTGTCTCCTGCCCATCAAATCTC TGTGCCTGCTGCCACCCAGCCCGCAGCCCTCCCCACCCTCCTGCCCTCTCAGAGCCCCCACTAACC AGACCTCACCCATCAGCCCTACACATCCCCATTCCCAAAGCCCCCCCAAATCCCAAGGGAAGATGGC CCCAGTCCCAAGTTGGCCCTGTGGCTGCCCICACCAGCTCCCACAGCAGCCCCAACAGCCCTGGG GGAGGCTGGTCTTGCCGAGCACAGCCAGAGGGATGACCGGTGGCTGCTGGTGGCACTCCTGGTGC CAACGTGTGTCTTTTTGCTGGTCCTGCTTGCACTGGGCATCGTCGTGTACTGCACCCGCTGTGGCCCC CATGCACCCAACAAGCGCATCACTGACTGCTATCGCTGGGTCATCCATGCTGGGAGCAAGAGCCC AACAGAACCCATGCCCCCCCAGGGGCAGCCTCACAGGGGTGCAGACCTGCAGAACCAGCGTGGACT ACAAAGATGATGACGATAAGTGA
914.	Human endosialin	artificial	aa	MTTTTTAWAAAGPTTGQDPWAAFPRAACGPSSCYATFPRRRTFTEAWRACREIGGDLATPRTPE EAQRVDSLVGAGPASRLLWIGLQRQARQCQLQRPLRGFTWTTGDQDTAFTNWAQPASGGPCPAQR CVALEASGEHRWLEGSCILAVDGYLCQFGFEGACPALQDEAGQAGPAVYTTPFHLVSTEFEWLPF GSVAAVQCQAGRGASLLCVKQPEGGVGWSRAGPLCLGTGCSPDNGGCEHECVEEVDGHVSCRCTE GFRLAADGRSCEDPCAQAPCEQQCEPGGPQGYSCHCRLGFRPAEDDPHRCVDTDECQIAGVCQQM CVNYVGGFECYCSEGHELEADGISCSPAGAVGAQASQDLGDELLDDGEDEDEDEAWKAFNGGWT EMPGILWMEPTQPDPFALAYRPSFPEDREPQIPYPEPTWPPPLSAPRVPYHSSVLSVTRPVVVSA THPTLPSAHQPPVIPATHPALSRDHQIPVIAANYPDLPSAYQPGILSVSHSAQPPAHQPPMISTK YPELFPAHQSPMEPDTRVAGTQTTTHLPGIPPNHAPLVTTLGAQLPPQAPDALVLRTQATQLPII PTAQPSLTTTSRSPVSPAHQISVPAATQPAALPTLLPSQSPTNQTSPSPTHPHSKAPQIPREDG PSPKLALWLPSPAPTAAFTALGEAGLAEHSQRDDRWLLVALLVPTCVFLVVLLALGIVYCTRCGP HAPNKRITDCYRWVIHAGSKSPTETMPPRGSLTGVQTCRTSVDYKDDDDK
915.	Macaque endosialin	artificial	nt	ATGCTGCTGCTGGCCTGTTGCTGGCCTGGGCGGCCGCAGGAGGCCCACACTGGGCCAGGACCCCTGGGC TGCTGAGCCCCCGCTCCGCCTGCGGCCCCAGCAGCTGCTACGCTCTCTCT-TCCACGGCGCCGCACCT TTCTGGAGGCCTGGCGGCCCTGCCGCGAGCIGGGGGGCGCGACCTGGCCACTCCTCGGACCCCCGAG GAGGCCCAGCGTGTGGACAACCTGGTGGGTGCAGGCCCGGCCAGCCGGCTGCTGTGGATCGGCCT GCAGCGGCAGGCCCGGCAATGCCAGCTGCAGCCGCCCACTGCGAGGCTCTCACGTGGACCACAGGGG ACCAGGACACGGCTTTCACCAACTGGGCCCAGCCAGCCACTGGAGGCCCCCTGCCCGGCCCAGCGC TGTGTGGCCCTGGAGGCGAGTGGCGAGCACCGCTGGCTGGAGAGGCTCATGCACGCTGGCTGTCGA CGGCTACTTGTGCCAGTTTGGCTTCGAGGGTGCCTGCCCAGCGCTGCAAGACGAAGCGGGCCAGG

				CCGGCCCAGCCGTCTATACCACGCCCTTCCACCTGGTCTCCACAGAGTTTGAGTGGCTACCTTC
				GGCTCTGTGGCCGCTGTGCCAGTGCCAGGCTGGCAGGGAGCCTCTCTGCTCTGCGTGAAGCAGCC
				CGAGGGAGGTGTGGGCTCGTCACGGGCAGGGCCCCTGTGCCTGGGGGCTGGCTGCAGCCCTGACA
				ACGGGGCTGCCAACACCAATGTGTGCACGAGGTGCATCGTCACGTGTCCTGCCCGCTGCACTGAG
				GGCTTCCGGCTGGCAGCAGACGGGCGCAGTTGCGAGGATCCCTGTGCCCAGGCTCCATGCGAGCA
				GCAGTGTGAGCCCGGTGGCCACAAGGCTACAGCTGCCACTGTCGCCTGGGTTTCCGACCTGCAG
				AGGATGATCCGCACCGCTGTGTGGACACAGATGAGTGCCAGATTGCCGGTGTGTGCCAGCAGATG
				TGTGTCAACTACGTTGTGGTGGCTTCGAGTGTTATTGTAGTGAGGGTCACTGAGCTGGAGGCTGATGG
				CATCAGCTGCAGCCCTGCAGGGCCATGGGTGCCCGGGCTTCCCAGGACCTCGGAGATGAGTTGC
				TGGATGATGGGGAGGGATGAGGAAGATGAAGACGAGGCCTGGGAGGCCTTTGGCGGTGGCTGGACG
				GAGATGCCTGGGATCCTGTGGATGGAGCCTACTCAGCCGCCTGACTTTGCCCTGGCCTATAGACC
				GAGCTTCCCAGAGGACAGAGAGCCACAGATACCCTACCCGGAGCCCACCTGGCCGCCCCCGCTCA
				GTGCCCCCCAGGGTCCCCTACCACTCCTCAGTGCTCTCCGTCACCCGGCCTGTGGTGGTCTCTGCC
				ACGCGCCCCCACACTGCCTTCCGCCCACCAGCCTCCTGTGATCCCTGCCACACACCCAGCTTTGTC
				CCGTGACCACCAGATCCCCGTGATCGCAGCCAACTATCCAGATCTGCCTTCTGCCTACCAACCCG
				GTATTCTCTCTGTCTCTCATCCAGCACAGCCCCCCTGCCCACCAGCCCCCCCATGATCTCAACCAGA
				TATCCTGAGCTGTTCCCTGCCCACCAGTCCCCCATGTTTCCAGACACCCAGGTCGCTGGCACCCA
				GACCACCACTCATTTGCCTGCAATCCCACCTAACCGTGCCCCTCTGGTCACCACACTCGGTGCCC
				ATCAACCCCCTCAAGCCCCAGATGCCCCTGTCCTCAGAACCCAGGCTACCCAGCTTCCCATTATC
				CCTACTGCCCAGCCGTCTCTGACCACCAGCTCCAGGTCCCCTGTGTCTCCTGCCCATCAAGTCTC
				TGTGCCTGCTGCCACCCAGCCCCCAGCCCTCCCCACCCTCCTGCCCCTCTCAGAGCCCCCACTAACC
				AGACCTCACCCATCAGCCCTACACATCCCCATTCCCAAAGTCCCCCAAATCCCAAGGGAAGATGGC
				CCCAGTCCCAAGCTGGCCCCTGTGGCTGCCCICAGCAGCTCCCCACAGCAGCCCCCAACAGCCCTGGG
				GCAGGCTACTCTTGCCCAGCACATCCACAGCGCATGACCCGTGGCCTTCTCGTCGCACTCCTCGTGC
				CAACGTGTGTCTTTTTGGTGGTCCTGCTTGCTGCACTGGGCATTGTGTACTGCACCCGCTGTGGCCCC
				CATGCACCCAACAAGCGCATCACTGACTGCIATCGCTGGGTCACCCACTGCTGGGAGCAAGAGTCC
				AACAGAACCCATGCCCCCCCAGGGGCAGCCTCACAGGGGTGCAGACCTGCAGAACCAGCGTGGACT
				ACAAAGATGATGACGATAAGTGA
			aa	MLLRLLLAWAAAGPTLGQDFWAAETRSACGPSSCYALFPRRRTFLEAWRACRELGGDLATPRTPE
				EAQRVDNLVGAGPASRLLWIGLQRQARQCQLQRPLRGFTWTTGLQDTAFTNWAQPAIGGPCPAQR
				CVALEASGEHRWLEGSCTLAVDGYLCQFGFEGACPALQDEAGQAGPAVYTTPFHLVSTEFEWLPF
				GSVAAVQCQAGRGASLLCVKQPEGGVGWSRAGPLCLGAGCSPDNGGCEHECVEEVDGHVSCRCTE
				GFRLAADGRSCEDPCAQAPCEQQCEPGGPQGYSCHCRLGFRPAEDDPHRCVDTDECQIAGVCQQM
				CVNYVGGFECYCSEGHELEADGISCSPAGAMGARASQDLGDELLDDGEDEDEDEAWEAFGGGWT
				EMPGILWMEPTQPPDFALAYRPSFPEDREPQIPYPEPTWPPPLSAPRVPYHSSVLSVTRPVVVSA
				TRPTLPSAHQPPVIPATHPALSRDHQIPVIAANYPCLPSAYQPGILSVSHPAQPPAHQPPMISTR
				YPELFPAHQSPMEPDTQVAGTQTTHLPAIPPNRAPLVTTLGAHQPPQAPDAPVLRTQATQLPII
	916.	Macaque endosialin	artificial	

				PTAQPSLTTSSRSPVSPAHQVSVPAATQFPALPTLLPSQSPTNQTSP-SPTHPHSKVPQIPREDG PSPKLALWLPSAAPTAAPTALGEASLAEHIQRDDRWLLVALLVPTCVFLVVLLALGIVYCTRCGP HAPNKRITDCYRWVTHACSKSPTE?MPPRGSLTGVQTCRTSVDYKDDDDK
917.	Forward primer	artificial	nt	ATATGAATTCGCCACCATGCTGCTGCCCTGTTGCTGGCC
918.	Reverse primer	artificial	nt	GTCTTCATCTTCCTCATCCTCCCC
919.	Forward primer	artificial	nt	GTCAACTACGTTGGTGGCTTCGAGTG
920.	Reverse primer	artificial	nt	GGTCTAGATCACTTATCGTCATCATCTTTGTAGTCCACGCTGGTTCTGCAGGTCTGC
921.	Primer 5'ED-VH-A-XhoI	artificial	nt	CCAGCTCTCGAGTCAGGASCTGAGSTGRWGAAGCCTGGGGCTTCAGTGAAGRTGTCCTGCAAGGC TTCTGGATACACATTCACT
922.	Primer 3'ED-VH-B	artificial	nt	AAT ATA TCC MAT CCA CTC AAG GCK CTK TCC AKK TSY CTG CYT CAY CCA GTG TAT AAC ATA GTC AGT GAA TGT GTA TCC AGA
923.	Primer 5'ED-VH-C	artificial	nt	CTT GAG TGG ATK GCA TAT ATT AAT CCT TAT GAT GAT ACTA CC TAC AAC CAG AAG TTC AAG GGC
924.	Primer 3'ED-VH-D	artificial	nt	T GAG CTS CAT GTA GGC TGT GYT GGM GGA TKT GWC TMS AGT MAW TGT GRC CYG GCC CTT GAA CTT CTG GTT
925.	Primer 5'ED-VH-E	artificial	nt	C ACA GCC TAC ATG SAA CTC ARC AGC CTG ASA TCT GAG GAC ACT GCA GTC TAT TAC TGT GCA ACA AGG GGG
926.	Primer 3'ED-VH-F-BstEII	artificial	nt	CCT GAT GGT GAC CAA GGT TCC TTG ACC CCA GTA GTC CAT AGA ATA GTC GAA GTA ACC ATC ATA GGA GTT CCC CCT TCT TGC ACA GTA
927.	Primer 5'ED-VL-A-SacI	artificial	nt	CCA GTC GAG CTC CAG CTG ACC CAG TCT CMA ARM TTC MTG TCC RCA TCA GTA GGA GAC AGA GTC NNS ATC ACC TGC AGG GCC AG
928.	Primer 3'ED-VL-B	artificial	nt	TCC TGG TTT CTG TTG ATA CCA GGC TAC AGC AGT ACC CAC ATT CTG ACT GGC CCT GCA GGT GAT
929.	Primer 5'ED-VL-C	artificial	nt	TAT CAA CAG AAA CCA GGA MAA KCC CCT AAA TTA CTG ATT TACT CG GCA TCG AAT CGG TAC ACT GGA GTC CCT
930.	Primer 3'ED-VL-D	artificial	nt	GCT GAT GGT GAG ACT GAA MTC TGT CCC AGA TCC ACT GCC TGA GAA GCG AYY AGG GAC TCC AGT GTA CCG
931.	Primer 5'ED-VL-E	artificial	nt	TTC ACT CTC ACC AIC AGC ART MTG CAG YCT GAA GAC YTS GCA RMT TAT TWC TGC CAG CAA TAT ACC AAC
932.	Primer 3'ED-VL-F-BsiWI/SpeI	artificial	nt	CCT GAT ACT AGT CGT ACG TTT TAT TTC CAG CTT GGT CCC CTG TCC AAA CGT ATA CAT GGG ATA GTT GGT ATA TTG CTG GCA
933.	Flag-tag	artificial	nt	DYKDDDDK
934.	Ep 5-10 VL	artificial	aa	ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVP DRFTGSGSGTDFTLTISVQAEDLAVYYCQNDYSYPLTFGAGTKLEIK
935.	Ep 5-10 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT

936.	Ep 5-10 LCDR2	artificial	aa	WASTRES
937.	Ep 5-10 LCDR3	artificial	aa	QNDYSYPLT
938.	Ep 5-10 VL	artificial	nt	GAGCTCGTGATGACACAGACTCTCCATCCTCCCTGACTGTGACAGCAGGAGAGAAGGTCACTATGAG CTGCAAGTCCAGTCAGAGCTCTGTTAACACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGCCTCCTAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA AGACCTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTGCTGGGACCA ACCTTCAGATCAAA
939.	Ep 5-10 HL	artificial	aa	EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKF KGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS
940.	Ep 5-10 HCDR1	artificial	aa	NYWLG
941.	Ep 5-10 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
942.	Ep 5-10 HCDR3	artificial	aa	LRNWDEPMDY
943.	Ep 5-10 HL	artificial	nt	GAGGTGCAGCTGCTCGAGCCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAGTGAAGATATC CTGCAAGGCTTCTGGATACGCCTTCACTAACTACTGGCTAGGTTGGGTAAAGCAGAGGCCTGGAC ATGGACTTGAGTGGATTGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTC AAGGGCAAAGCCACACTGACTGCAGACAAAATCTTCGAGCACAGCCTACATGCAGCTCAGTAGCCT GACATTTGAGGACTCTGCTGTCTATTTCTGTGCAAGACTGAGGACGAGCCTATGGACT ACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCC
944.	Ep 5-10 LH x I2C HL	artificial	aa	ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVP DRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGGGGSGGGGSEV QLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKFKG KATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSSGGGGSGGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
945.	Ep 5-10 LH x I2C HL	artificial	nt	GAGCTCGTGATGACACAGACTCTCCATCCTCCCTGACTGTGACAGCAGGAGAGAAGGTCACTATGAG CTGCAAGTCCAGTCAGAGCTCTGTTAACACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGCCTCCTAAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA AGACCTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTGCTGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGGTG

				CAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAGTGAAGATATCCTGCAA GGCTTCTGGATACGCCTTCACTAACTACTGGCTAGTTGGGTAAAGCAGAGGCCTGGACATGGAC TTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGC AAAGCCACACTCACTCCAGACAAATCTTCGACGCACAGCCTATAGTGCAGCTCAGTAGCCTCACATT TGAGGACTCTGCTGTCTATTTCTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGG GCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCT GGAGGAGGATTGGTGCAGCCTGGAGGGTCAITGAAACTCTCATGTGCAGCCTCTGGATTCACCTT CAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCA TAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATC TCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGC ACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAA CGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG AACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGACTAAGTTCCTCGCCCCCGGTACTCCTGCC GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGT AGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGA GGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCTGGTGGAACACAGTCAC TGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
946.	Ep 5-10 LH x H2C HL	artificial	aa	ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVP DRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGSGGGGSGGGGSEV QLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKFKG KATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSSGGGGSGGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
947.	Ep 5-10 LH x H2C HL	artificial	nt	GAGCTCGTGATGACACACTCTCCATCCTCCCTGACTGTGACAGCAGGAGAGAAGGTCACTATGAG CTGCAAGTCCAGTCAGATCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGCCTCCTAAACTGTTGATCTACTGGGCATCCACTAGGAATCTGGGTCCCT GATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA AGACCTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTGCTGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTGAGGTG CAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAGTGAAGATATCCTGCAA GGCTTCTGGATACGCCTTCACTAACTACTGGCTAGGTTGGGTAAAGCAGAGGCCTGGACATGGAC TTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGC AAAGCCACACTGACTGCAGACAAATCTTCGAGCACAGCCTATAGTGCAGCTCAGTAGCCTGACATT

				TGAGGACTCTGCTGTCTATTTCTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGG GCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCT GGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTT CAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGCGAATGGCTTGCTCGCA TAAGAAGTAAATATAATTATATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATC TCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGC CGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGT GGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCAC ACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAA AACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCC AGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGA TGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
948.	Ep 5-10 LH x F12Q HL	artificial	aa	ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVP DRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGSGGGGSGGGGSEV QLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKFKG KATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDFPMDYWGQGTTVTVSSGGGGSFVQIVFS GGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
949.	Ep 5-10 LH x F12Q HL	artificial	nt	GAGCTCGTGATGACACAGTCTCCATCCTCCCTGACTGTGACAGCAGGAGAAGGTCACTATGAG CTGCAAGTCCAGTCAGAGCTCTGTTAACAGATGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGCCTCCTAAACTGTTGATCTACTGGGCATCCACTAGGAATCTGGGGTCCCT GATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA AGACCTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTGCTGGGACCA AGCTTGAGATCAAAGGTCGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGGTG CAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAGTGAAGATATCCTGCAA GGCTTCTGGATACGCCTTCACTAACTACTGGCTAGGTTGGGTAAAGCAGAGGCCTGGACATGGAC TTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGC AAAGCCACACTGACTGCAGACAAATCTTCGAGCACAGCCTATATGCAGCTCAGTAGCCTGACATT TGAGGACTCTGCTGTCTATTTCTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGG GCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCT GGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTT CAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCA TAAGAAGTAAATATAATTATATGCAACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATC

				TCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGC CGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGT GCTGGTTCTCACACTCTTGTGACTCAGGAACCTTCACTCACCCTATCACCTGGTCGAACACTCAC ACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAA AACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCC AGATTCTCAGGCTCCCTCCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGA TGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
950.	hEp 14-A1 L	artificial	aa	DIVMTQTPLSLPVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVQAEDVGVYYCQNDYSYPLTFGQGTKLEIK
951.	hEp 14-A1 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
952.	hEp 14-A1 LCDR2	artificial	aa	WASTRES
953.	hEp 14-A1 LCDR3	artificial	aa	QNDYSYPLT
954.	hEp 14-A1 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGACTCTGTTAACACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGAICTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCAGTGTGCAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
955.	hEp 14-A1 H	artificial	aa	QVQLVQSGAEVKKPGSSVKISCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
956.	hEp 14-A1 HCDR1	artificial	aa	NYWLG
957.	hEp 14-A1 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
958.	hEp 14-A1 HCDR3	artificial	aa	LRNWDEPMDY
959.	hEp 14-A1 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGATATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTGACCTGAC ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
960.	hEp 14-A1 LH x I2C HL	artificial	aa	DIVMTQTPLSLPVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVQAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV

				QLVQSGAEVKKPGSSVKISCKASGYTFSNYWLGWVRQAPGQGLEWIGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHCNFCNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
961.	hEp 14-A1 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACACTCTCACAATCAGCAGTGTGCAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATATTATGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGATATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCCGCCTGGACAGGGACTTG AGTGGATTGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGGGACGAGCCTATGGACTACTGGGGCCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
962.	hEp 14-D2 L	artificial	aa	DIVMTQTPLSLPVTPGEQVSISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
963.	hEp 14-D2 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
964.	hEp 14-D2 LCDR2	artificial	aa	WASTRES
965.	hEp 14-D2 LCDR3	artificial	aa	QNDYSYPLT

966.	hEp 14-D2 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGCAGCCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
967.	hEp 14-D2 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
968.	hEp 14-D2 HCDR1	artificial	aa	NYWLG
969.	hEp 14-D2 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
970.	hEp 14-D2 HCDR3	artificial	aa	LRNWDEPMDY
971.	hEp 14-D2 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
972.	hEp 14-D2 LH x I2C HL	artificial	aa	DIVMTQTPLSLPVTPGEQVSISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGSGGGGSGGGGSQV QLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
973.	hEp 14-D2 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTCGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGA

				GGACACTGCTGTCTATTACTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGCAAAGGGTTTGGCTGGGTTGCTCCCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAGGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
974.	hEp 14-H8 L	artificial	aa	DIVMTQTPLSLPVTPGEPASISCKSSQSLLNSGNQKNYLTWYQQKPGQSPKLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
975.	hEp 14-H8 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
976.	hEp 14-H8 LCDR2	artificial	aa	WASTRES
977.	hEp 14-H8 LCDR3	artificial	aa	QNDYSYPLT
978.	hEp 14-H8 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGCCTCTATCAG CTGCAAGTCCAGTCAGAGCTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGTCTCCTAAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
979.	hEp 14-H8 H	artificial	aa	QVQLVQSGAELKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLRSEDTAVYYCARLRNWDFPMDYWGQGTTVTVSS
980.	hEp 14-H8 HCDR1	artificial	aa	NYWLG
981.	hEp 14-H8 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
982.	hEp 14-H8 HCDR3	artificial	aa	LRNWDFPMDY
983.	hEp 14-H8 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGCGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG

				GGCAGAGTCACAAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAG ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
984.	hEp 14-H8 LH x I2C HL	artificial	aa	DIVMTQTPLSLPVTPGEPASISCKSSQSLLNSGNQKNYLTWYQQKPGQSPKLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGSGGGGSGGGGSQV QLVQSGAELKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLRSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
985.	hEp 14-H8 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGCCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGTCTCCTAAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTCGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGCTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAGATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
986.	hEp 14-A6 L	artificial	aa	DIVMTQTPFSLTVTPGEIVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK

987.	hEp 14-A6 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
988.	hEp 14-A6 LCDR2	artificial	aa	WASTRES
989.	hEp 14-A6 LCDR3	artificial	aa	QNDYSYPLT
990.	hEp 14-A6 L	artificial	nt	GACATCGTGATGACACAGACTCCATTCTCCCTGACTGTGACACCAGGAGAGACGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCAGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
991.	hEp 14-A6 H	artificial	aa	QVQLVQSGAELVKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GKVTITADKSTSTAYMELSSLRFEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
992.	hEp 14-A6 HCDR1	artificial	aa	NYWLG
993.	hEp 14-A6 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
994.	hEp 14-A6 HCDR3	artificial	aa	LRNWDEPMDY
995.	hEp 14-A6 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGGTAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAAAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAG ATTTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
996.	hEp 14-A6 LH x I2C HL	artificial	aa	DIVMTQTPFSLTVTPGETVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGSGGGGSGGGGSQV QLVQSGAELVKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWIGDIFPGSGNIHYNEKFKGK VTITADKSTSTAYMELSSLRFEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
997.	hEp 14-A6 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCATTCTCCCTGACTGTGACACCAGGAGAGACGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCAGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA

				AGCTTGAGATCAAAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGCTGGTAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGGGACTTG ACTGGATTCGACATATTTCCCTGCAACTGCTAATATCCACTACAATGACAAGTTCAAGGCCAAA GTCACAATCACTGCCAGACAAATCTACGAGCCACAGCCTATATGGAACTCAGTAGCCTGAGATTTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
998.	hEp 14-D1 L	artificial	aa	DIVMTQTPFSLTVTPGEPASISCKSSQSLLNSGNQKNYLTWYQQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVAVYYCQNDYSYPLTFGQGTKLEIK
999.	hEp 14-D1 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1000.	hEp 14-D1 LCDR2	artificial	aa	WASTRES
1001.	hEp 14-D1 LCDR3	artificial	aa	QNDYSYPLT
1002.	hEp 14-D1 L	artificial	nt	GACATCGTGATGACACAGACTCCATTCTCCCTGACTGTGACACCAGGAGAGCCGGCCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1003.	hEp 14-D1 H	artificial	aa	QVQLVQSGAELKKPGSSVKISCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTLTADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1004.	hEp 14-D1 HCDR1	artificial	aa	NYWLG

1005.	hEp 14-D1 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1006.	hEp 14-D1 HCDR3	artificial	aa	LRNWDEPMDY
1007.	hEp 14-D1 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGAAAAAGCCTGGGTCTTCAGTGAAGATATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACACTCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACCGTCACCGTCTCCTCC
1008.	hEp 14-D1 LH x I2C HL	artificial	aa	DIVMTQTPFSLTVTPGEPASISCKSSQSLLNSGNQKNYLTWYQQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVAVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAELKKPGSSVKISCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFKGR VTLTADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1009.	hEp 14-D1 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCATTCTCCCTGACTGTGACACCAGGAGAGCCGGCCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGAAAAAGCCTGGGTCTTCAGTGAAGATATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACACTCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGA GGACACTGCTGTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCACTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCCTGGTGGAACAGTCACACT

				CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GCCAGAATATTACTGTGTCTTCTATGCTACAGCAACCCCTCGGTCTTCGGTGCAGGAACCAAACTGA CTGTCCTA
1010.	hEp 14-G6 L	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVQAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1011.	hEp 14-G6 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1012.	hEp 14-G6 LCDR2	artificial	aa	WASTRES
1013.	hEp 14-G6 LCDR3	artificial	aa	QNDYSYPLT
1014.	hEp 14-G6 L	artificial	nt	GACATCGTGATGACACAGACACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGACGTCTGTTAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTTCTCAGGCAGTGGATCTGGAACAGATTTTCACTCTCAAAATCAGCCGTGTGCAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1015.	hEp 14-G6 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1016.	hEp 14-G6 HCDR1	artificial	aa	NYWLG
1017.	hEp 14-G6 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1018.	hEp 14-G6 HCDR3	artificial	aa	LRNWDEPMDY
1019.	hEp 14-G6 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCCTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATGGGGATCATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGCCACACAATCACTGCAGACAAATCTACCGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACGAGGACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1020.	hEp 14-G6 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVQAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFKGR ATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG

				GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1021.	hEp 14-G6 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGACTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGAICTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGCAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GCCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGA GGACACTGCTGTCTATTACTGTGCAAGAGTCGGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA.
1022.	hEp 14-H4 L	artificial	aa	DIVMTQTPLSLPVTPGEIASISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1023.	hEp 14-H4 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1024.	hEp 14-H4 LCDR2	artificial	aa	WASTRES
1025.	hEp 14-H4 LCDR3	artificial	aa	QNDYSYPLT
1026.	hEp 14-H4 L	artificial	nt	GACATCGTGATGACACAGACACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGCCTCTATCAG CTGCAAGTCCAGTCAGACTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGTCTCCTCAACTGTTGAICTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCAGTGTGGAGGCTGA

				AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1027.	hEp 14-H4 H	artificial	aa	QVQLVQSGAEVVKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1028.	hEp 14-H4 HCDR1	artificial	aa	NYWLG
1029.	hEp 14-H4 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1030.	hEp 14-H4 HCDR3	artificial	aa	LRNWDEPMDY
1031.	hEp 14-H4 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGGTAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1032.	hEp 14-H4 LH x I2C HL	artificial	aa	DIVMTQTPLSLPVTPGETASISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAEVVKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1033.	hEp 14-H4 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGACGGCCTCTATCAG CTGCAAGTCCAGTCAGACGTCTGTTAACACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCAGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCAGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGGTAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCCGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCCTATATGGAACTCAGTAGCCTGACATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA

				GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCCTCTCCTCAGGTGGTCGTTCTGGCGGCGGCGGCTCCGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1034.	hEp 17-A6 L	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1035.	hEp 17-A6 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1036.	hEp 17-A6 LCDR2	artificial	aa	WASTRES
1037.	hEp 17-A6 LCDR3	artificial	aa	QNDYSYPLT
1038.	hEp 17-A6 L	artificial	nt	GACATCGTGATGACACAGACACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGCTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGAICTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1039.	hEp 17-A6 H	artificial	aa	QVQLVQSGAEVKRPGSSVKISCKASGYTFSNYWLGWVKQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLTSEDTAVYFCARLRNWDEPMDYWGQGTTVTVSS
1040.	hEp 17-A6 HCDR1	artificial	aa	NYWLG
1041.	hEp 17-A6 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1042.	hEp 17-A6 HCDR3	artificial	aa	LRNWDEPMDY
1043.	hEp 17-A6 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGATATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAAGCAGGCGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTTCCCCGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTCTATTTCTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC

1044.	hEp 17-A6 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAEVKRPGSSVKISCKASGYTFSNYWLGWVKQAPGQGLEWMGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLTSEDTAVYFCARLRNWDEPMDYWGQGTTVTVSSGGCGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1045.	hEp 17-A6 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAACAGTGGAAATCAACTTGACCTTGGTACCTGC AGAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAGGCCTGGGTCTTCAGTGAAGATATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAAGCAGGCGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTTCCCCGGAAGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGA GGACACTGCTGTCTATTTCTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGIAATAGCTACATATCCTACTGGGCTTACTGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1046.	hEp 17-E9 L	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPKLLIYWASTRESGVP DRFSGSGSGTDFTLNISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1047.	hEp 17-E9 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT

1048.	hEp 17-E9 LCDR2	artificial	aa	WASTRES
1049.	hEp 17-E9 LCDR3	artificial	aa	QNDYSYPLT
1050.	hEp 17-E9 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGACTCTGTTAACACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAACATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATATATGTTATCCGCTCACGTTCGGTCAAGGGACCA ACCTTCAGATCAAA
1051.	hEp 17-E9 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVKQAPGHGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLRSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1052.	hEp 17-E9 HCDR1	artificial	aa	NYWLG
1053.	hEp 17-E9 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1054.	hEp 17-E9 HCDR3	artificial	aa	LRNWDEPMDY
1055.	hEp 17-E9 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAAGCAGGCGCCTGGACATG GACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAG ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1056.	hEp 17-E9 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPKLLIYWASTRESGVP DRFSGSGSGTDFTLNISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVKQAPGHGLEWMGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLRSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1057.	hEp 17-E9 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGACTCTGTTAACACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAACATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATATATGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG

				CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAAGCAGGCGCCTGGACATGGACTTG AGTGGATGGGAGATATTTCCCTGGAAGTGSTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACAATCACTGCCACACAAATCTACCACCACAGCCTATATGCAACTCAGTACCCTGAGATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCIGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCICCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1058.	hEp 18-A6 L	artificial	aa	DIVMTQTPLSLPVTPGEQVSMSCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLNISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1059.	hEp 18-A6 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1060.	hEp 18-A6 LCDR2	artificial	aa	WASTRES
1061.	hEp 18-A6 LCDR3	artificial	aa	QNDYSYPLT
1062.	hEp 18-A6 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGTCTCTATGAG CTGCAAGTCCAGTCAGACGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGIGGATCTGGAACAGATTTCACTCTCAACATCAGCAGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1063.	hEp 18-A6 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1064.	hEp 18-A6 HCDR1	artificial	aa	NYWLG
1065.	hEp 18-A6 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG

1066.	hEp 18-A6 HCDR3	artificial	aa	LRNWDEPMDY
1067.	hEp 18-A6 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTCTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTCTATTACTGTGCAACACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1068.	hEp 18-E3 L	artificial	aa	DIVMTQTPLSLPVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVQAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1069.	hEp 18-E3 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1070.	hEp 18-E3 LCDR2	artificial	aa	WASTRES
1071.	hEp 18-E3 LCDR3	artificial	aa	QNDYSYPLT
1072.	hEp 18-E3 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGCTCTGTTAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1073.	hEp 18-E3 H	artificial	aa	QVQLVQSGAELVRPGSSVKISCKASGYAFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTLTADKSTSTAYMQLSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1074.	hEp 18-E3 HCDR1	artificial	aa	NYWLG
1075.	hEp 18-E3 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1076.	hEp 18-E3 HCDR3	artificial	aa	LRNWDEPMDY
1077.	hEp 18-E3 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGTCTCAGTGAAGATATCCTG CAAGGCTTCTGGATACGCCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACACTCACTGCAGACAAATCTACGAGCACAGCCTATATGCAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1078.	hEp 18-E3 LH x I2C HL	artificial	aa	DIVMTQTPLSLPVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVQAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAELVRPGSSVKISCKASGYAFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFKGR

				VTLTADKSTSTAYMQLSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1079.	hEp 18-E3 LH x I2C HL	artificial	nt	GACATCGTGATGACACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA AGACGTGGGAGTTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGTCTTCAGTGAAGATATCCTGCAAGGC TTCTGGATACGCCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACACTCACTGCAGACAAATCTACGAGCACAGCCTATATGCAACTCAGTAGCCTGACATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGCTTACTGGGGCCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1080.	hEp 18-F11 L	artificial	aa	DIVMTQTPPSLTVTAGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISSVQAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1081.	hEp 18-F11 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1082.	hEp 18-F11 LCDR2	artificial	aa	WASTRES
1083.	hEp 18-F11 LCDR3	artificial	aa	QNDYSYPLT

1084.	hEp 18-F11 L	artificial	nt	GACATCGTGATGACACAGACTCCACCCTCCCTGACTGTGACAGCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGCATCTGGAACAGATTTCACTCTCAAAATCAGCAGTGTGCAGCCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1085.	hEp 18-F11 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSGNIHYNEKFK GRVTITADKSTSTAYMELSSLRFEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1086.	hEp 18-F11 HCDR1	artificial	aa	NYWLG
1087.	hEp 18-F11 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1088.	hEp 18-F11 HCDR3	artificial	aa	LRNWDEPMDY
1089.	hEp 18-F11 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGGCCTGGGTCTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGG GACTTGAGTGGATTGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAG ATTTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1090.	hEp 18-F11 LH x I2C HL	artificial	aa	DIVMTQTPPSLTVTAGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISSVQAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGSGGGGSGGGSQV QLVQSGAEVKRPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWIGDIFPGSGNIHYNEKFKGR VTITADKSTSTAYMELSSLRFEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1091.	hEp 18-F11 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACCCTCCCTGACTGTGACAGCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCAGTGTGCAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTCGTGGTGGTTCTGGCCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGCCTGGACAGGGACTTG AGTGGATTGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAGATTTGA

				GGACACTGCTGTCTATTACTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGCGATGGTTGCTCCCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1092.	hEp 18-F12 L	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1093.	hEp 18-F12 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1094.	hEp 18-F12 LCDR2	artificial	aa	WASTRES
1095.	hEp 18-F12 LCDR3	artificial	aa	QNDYSYPLT
1096.	hEp 18-F12 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGCTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1097.	hEp 18-F12 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQRPGQGLEWMGDIFPGSGNIHYNEKFK GRATITADKSTSTAYMELSSLRSEDTAVYYCARLRNWDFPMDYWGQGTTVTVSS
1098.	hEp 18-F12 HCDR1	artificial	aa	NYWLG
1099.	hEp 18-F12 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1100.	hEp 18-F12 HCDR3	artificial	aa	LRNWDEPMDY
1101.	hEp 18-F12 L	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCCTGGACAGG GACTTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG

				GGCAGAGCCACACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAG ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1102.	hEp 18-F12 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGSGGGGSGGGGSQV QLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQRPGQGLEWIGDIFPGSGNIHYNEKFKGR ATITADKSTSTAYMELSSLRSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1103.	hEp 18-F12 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGCCTCCTCAACTGTTGAICTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTCGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGAGGCCTGGACAGGGACTTG AGTGGATTGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GCCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAGATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1104.	hEp 18-G1 L	artificial	aa	DIVMTQTPLSLTVTPGEIVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK

1105.	hEp 18-G1 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1106.	hEp 18-G1 LCDR2	artificial	aa	WASTRES
1107.	hEp 18-G1 LCDR3	artificial	aa	QNDYSYPLT
1108.	hEp 18-G1 L	artificial	nt	GACATCGTGATGACACAGACACTCCACTCTCCCTGACTGTGACACCAGGAGACGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCAGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1109.	hEp 18-G1 H	artificial	aa	QVQLVQSGAEVVKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSGNIHYNEKFK GKVTITADKSTSTAYMELSSLGSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1110.	hEp 18-G1 HCDR1	artificial	aa	NYWLG
1111.	hEp 18-G1 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1112.	hEp 18-G1 HCDR3	artificial	aa	LRNWDEPMDY
1113.	hEp 18-G1 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAGCCCTGGGTCCTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGCCTGGACAGG GACTTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAAAGTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGGG ATCTGAGGACACTGCTGTCTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GGGGCCAAGGGACCACGGTCACCGTCTCCTCC
1114.	hEp 18-G1 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGETVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLTISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGSGGGGSGGGGSQV QLVQSGAEVVKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWIGDIFPGSGNIHYNEKFKGK VTITADKSTSTAYMELSSLGSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1115.	hEp 18-G1 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACACTCCACTCTCCCTGACTGTGACACCAGGAGACGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCACAATCAGCAGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA

				AGCTTGAGATCAAAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGGTAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGCCTGGACAGGGACTTG ACTGGATTCGACATATTTCCCTGCAACTGCTAATATCCACTACAATGACAAGTTCAAGGCCAAA GTCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGGGATCTGA GGACACTGCTGTCTATTACTGTGCAAGACTGAGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
1116.	hEp 18-G9 L	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1117.	hEp 18-G9 LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1118.	hEp 18-G9 LCDR2	artificial	aa	WASTRES
1119.	hEp 18-G9 LCDR3	artificial	aa	QNDYSYPLT
1120.	hEp 18-G9 L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAA
1121.	hEp 18-G9 H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSGNIHYNEKFK GRATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTTVTVSS
1122.	hEp 18-G9 HCDR1	artificial	aa	NYWLG

1123.	hEp 18-G9 HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1124.	hEp 18-G9 HCDR3	artificial	aa	LRNWDEPMDY
1125.	hEp 18-G9 H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGCCTGGACAGG GACTTGAGTGGATGGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAG GGCAGAGCCCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGAC ATCTGAGGACACTGCTGTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACT GCGGCCAAGCGGACCACCCTCACCGTCTCCTCC
1126.	hEp 18-G9 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWASTRESGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGGSGGGGSGGGGSQV QLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSGNIHYNEKFKGR ATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWCEPMDYWGQGTTVTVSSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1127.	hEp 18-G9 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGTCTCTATCAG CTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGACCTGGTACCTGC AGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCT GATCGCTTCTCAGGCAGTGGATCTGGAACAGATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGA AGACGTGGGAGTTTATTACTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCA AGCTTGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTG CAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTGCAAGGC TTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGCCTGGACAGGGACTTG AGTGGATGGGAGATATTTCCCTGGAAGTGGTAATATCCACTACAATGAGAAGTTCAAGGGCAGA GCCACAATCACTGCAGACAAATCTACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGA GGACACTGCTGTATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCC AAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCACTGAAAGACACGTTCACCATCTCC AGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGT GTACTACTGTGTGAGACATGGGAACTTCGGIAATAGCTACATATCCTACTGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGT GGTTCTCAGACTGTTGTCACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT

				CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGA TTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGA GCCAGAATATTACTGTGTCTTCTATGCTACAGCAACCCCTCGGTCTTCGGTGCAGGAACCAAACTGA CTGTCCTA
1128.	human EpCAM	human	aa	MAPPQVLAFGLLLAAATATFAAAQEECVCENYKLAVNCFVNNNRQCQCTSVGAQNTVICSKLAAK CLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSTCWCVNTAGVRRTDKD TEITCSERVRTYWIIIELKHKAREKPYDSKSLRTALQKEITTRYQLDPKFITSILYENNVITIDL VQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLTVNGEQLDLDPGQTLIYYVDEKAPEFS MQGLKAGVIAVIVVVVLAVVAGLVVLVISRKKRMAKYEKAEIKEMGEMHRELNA
1129.	human EpCAM cDNA	human	nt	cggcgagcgagcacctcgacgcggtccgggggaccccctcgtcgtcctcccgacgcggacccgcgtgcc ccaggcctcgcgctgcccggccggctcctcgtgtcccactcccggcgcacgccctcccgcgagtcccgggcc cctcccgcgcccctcttctcggcgcgcgcgcagcatggcgccccgcaggtcctcgcgttcgggcttctgct tgccgcggcgacggcgacttttgccgcagctcaggaagaatgtgtctgtgaaaactacaagctggccgtaaa ctgctttgtgaataaatcgtcaatgccagtgtacttcagttggtgcacaaaatactgtcatttgctcaaa gctggctgccaaaatgttttggtgatgaaggcagaaatgaatggctccaaaaacttgggagaagagcaaaacctga agcggccctccagaacaatgatgggcttttatgatccctgactgcgatgcgagcgggctcttaaggccaagca gtgcaacggcgcacctccacgtgctggtgtgtgaacactgctgcgaagaacagacaagcactgaaat aacctgctctgagcgagtgagaacctactggatcatcattgaactaaaacacaaagcaagagaaaaacctta tgatagtaaaagtttgcggactgcacttcagaaggagatcacaacgcgttatcaactggatccaaaatttat cacgagtatttttgtatgagataatgttatcactattgatctggttccaaaatcttctcaaaaaactcagaa tgatgtggacataagctgatgtggcttattatttttgaaaaaagatgttaaaggtgaatcctgtttcattctaa gaaaatggacctgacagtaaatgggggaacaactggatctggatcctcgtcaaacttttaatttattatgttga tgaaaaagcacctgaattctcaatgcagggtctaaaagctggtgttattgctgttattgtggttgtggtgat agcagttgttgctggaattgttgtgctggttatttccagaaaagagagaatggcaaagtatgagaaggctga gataaaggagatgggtgagatgcataggaactcaatgcatataatattgtgaaggattatagaagaaggg gaaatagcaaatggacacacaaattacaaaatgtgtgtgcgtgggacgaagacatctttgaaggtcatgagtttg ttagtttaacatcatatatttgtaatagtgaaacctgtactcaaaatataagcagcttgaaactggctttac caatcttgaaatttgaccacaagtgtcttatatatgcagatctaatgctaaaa-ccagaacttggactccatc gttaaaatttatttatgtgtaacattcaaatgtgtgcattaaatatgcttccacagtaaaatctgaaaaactg atttgtgattgaaagctgccttctatttactttgagtcttgtacatacatactttttatgagctatgaaat aaaacatttaaactg
1130.	aa 26-61 of the EGF-like domain 1 of human EpCAM, encoded by exon 2	human	aa	ECVCENYKLAVNCFVNNNRQCQCTSVGAQNTVICSK
1131.	FAP L	artificial	aa	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQQKPGQPPKLLIFWASTRESGVP DRFSGSGFGTDFTLTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIK
1132.	FAP L-CDR1	artificial	aa	KSSQSLLYSRNQKNYLA

1133.	FAP L-CDR2	artificial	aa	WASTRES
1134.	FAP L-CDR3	artificial	aa	QQYFSYPLT
1135.	FAP L	artificial	nt	GACATTGTGATGACCCACACTCTCCACAGACTCTTTGGCTGTGTCTCTAGGGGAGAGGGCCACCATCAA CTGCAAGTCCAGTCAGAGCCTTTTATATTCTAGAAATCAAAAGAACTACTTGGCCTGGTATCAGC AGAAACCAGGACAGCCACCCAAACTCCTCATCTTTGGGCTAGCACTAGGGAATCTGGGGTACCT GATAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATTAGCAGCCTGCAGGCTGA AGATGTGGCAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTCGGACAAGGGACCA AGGTGGAAATAAAA
1136.	FAP H	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIGGINPNNGIPNYNQKFK GRVTITVDTSASTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQGTLVTVSS
1137.	FAP H-CDR1	artificial	aa	EYTIH
1138.	FAP H-CDR2	artificial	aa	GINPNNGIPNYNQKFKG
1139.	FAP H-CDR3	artificial	aa	RRIAYGYDEGHAMDY
1140.	FAP H	artificial	nt	CAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAGAAACCCGGTGCTTCCGTGAAAGTCAGCTG TAAACTAGTAGATACACCTTCACTGAATACTACCATACACTGGGTTAGACAGGCCCCTGGCCAAA GGCTGGAGTGGATAGGATGGTATTAATCCTAACAATGGTATTCCTACAACCAGAAGTTCAAG GGCCGGGTCACCATCACCGTAGACACCTCTACCAGCACCGCCTACATGGAACTGTCCAGCCTGCG CTCCGAGGACACTGCAGTCTACTACTGCGCCAGAAGAATCGCCTATGGTTACGACGAGGGCC ATGCTATGGACTACTGGGGTCAAGGAACCCTTGTCACCGTCTCCTCC
1141.	FAP LH	artificial	aa	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQQKPGQPPKLLIFWASTRESGVP DRFSGSGFGTDFTLTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIKGGGGSGGGGSGGGGSQV QLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIGGINPNNGIPNYNQKFKGR VTITVDTSASTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQGTLVTVSS
1142.	FAP LH	artificial	nt	GACATTGTGATGACCCAGTCTCCAGACTCTTTGGCTGTGTCTCTAGGGGAGAGGGCCACCATCAA CTGCAAGTCCAGTCAGAGCCTTTTATATTCTAGAAATCAAAAGAACTACTTGGCCTGGTATCAGC AGAAACCAGGACAGCCACCCAAACTCCTCATCTTTGGGCTAGCACTAGGGAATCTGGGGTACCT GATAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCACCATTAGCAGCCTGCAGGCTGA AGATGTGGCAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTCGGACAAGGGACCA AGGTGGAAATAAAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAACTAGTGCAGTCCGGCGCCGAAGTGAAGAAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAAC TAGTAGATACACCTTCACTGAATACACCATACACTGGGTTAGACAGGCCCCTGGCCAAAGGCTGG AGTGGATAGGAGGTATTAATCCTAACAATGGTATTCCTAACTACAACCAGAAGTTCAAGGGCCGG GTCACCATCACCGTAGACACCTCTGCCAGCACCGCCTACATGGAACTGTCCAGCCTGCGCTCCGA GGACACTGCAGTCTACTACTGCGCCAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTA TGGACTACTGGGGTCAAGGAACCCTTGTCACCGTCTCCTCC
1143.	FAP LH x I2C HL	artificial	aa	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQQKPGQPPKLLIFWASTRESGVP

				DRFSGSGFGTDFTLTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIKGGGSGGGGSGGGGSGV QLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIGGINPNNGIPNYNQKFKGR VTITVDTSASTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQGTLVTVSSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALILSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1144.	FAP LH x I2C HL	artificial	nt	GACATTGTGATGACCCAGTCTCCAGACTCTTTGGCTGTGTCTCTAGGGGAGAGGGCCACCATCAA CTGCAAGTCCAGTCAGAGCCTTTTATATTCTAGAAATCAAAAGAACTACTTGGCCTGGTATCAGC AGAAACCAGGACAGCCACCCAAACTCCTCATCTTTTGGGCTAGCACTAGGAATCTGGGGTACCT GATAGGTTCAGTGGCAGTGGGTTTGGGACAGACTTCACCCTCACCATCAGCAGCCTGCAGGCTGA AGATGTGGCAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTCGGACAAGGGACCA AGGTGGAAATAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAACTAGTGCAGTCCGGCGCCGAAGTGAAGAAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAAC TAGTAGATACACCTTCACTGAATACACCATACACTGGGTTAGACAGGCCCCTGGCCAAAGGCTGG AGTGGATAGGAGGTATTAATCCTAACAATGGTATTCCTAACTACAACCAGAGATTCAAGGGCCGG GTCACCATCACCGTAGACACACCTCTGCCAGCACCGCCTACATGGAACTGTCCAGCCTGCGCTCCGA GGACACTGCAGTCTACTACTGCGCCAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTA TGGACTACTGGGGTCAAGGAACCCTTGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTC TGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAAT GGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCCACATATTATGCCGATTCAGTGAAAGAC AGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAAC TGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACT GGGCTTACTGGGGCCAACGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGG TGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACT GGGTCCAACAAAACCACGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCC GGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGT ACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTG GAGGAACCAAACTGACTGTCCTA
1145.	FAP LH x H2C HL	artificial	aa	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQQKPGQPPKLLIFWASTRESGVP DRFSGSGFGTDFTLTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIKGGGGSGGGGSGGGGSQV QLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIGGINPNNGIPNYNQKFKGR VTITVDTSASTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQGTLVTVSSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGG

				GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1146.	FAP LH x H2C HL	artificial	nt	GACATTGTGATGACCCAGACTCTCCAGACTCTTTGGCTGTGTCTCTAGGGGAGAGGGCCACCATCAA CTGCAAGTCCAGTCAGACCCTTTTATATTCTAGAAATCAAAAGAACTACTTGGCCTGGTATCAGC AGAAACCAGGACAGCCACCCAAACTCCTCAICTTTTGGGCTAGCACTAGGGAATCTGGGGTACCT GATAGGTTCAGTGGCAGIGGGTTTGGGACAGACTTCACCCTCACCATTAGCAGCCTGCAGGCTGA AGATGTGGCAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTCGGACAAGGGACCA AGGTGGAAATAAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAACTAGTGCAGTCCGGGCGCCGAAGTGAAGAAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAAC TAGTAGATACACCTTCACTGAATACACCATACACTGGGTTAGACAGGCCCCTGGCCAAAGGCTGG AGTGGATAGGAGGTATTAATCCTAACAATGGTATTCCTAACTACAACCAGAAGTTCAAGGGCCGG GTCACCATCACCGTAGACACCTCTGCCAGCACCGCCTACATGGAACTGTCCAGCCTGCGCTCCGA GGACACTGCAGTCTACTACTGCGCCAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTA TGGACTACTGGGGTCAAGGAACCCTTGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTC TGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAAT GGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGAC AGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAAC TGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACT GGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGG TGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACT GGGTCCAACAAAAACCACGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCC GGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGT ACAGCCAGAGGATGAGGCAGAATATTACTGTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTG GAGGAACCAAACTGACTGTCCTA
1147.	FAP LH x F12Q HL	artificial	aa	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQQKPGQPPKLLIFWASTRESGVP DRFSGSGFGTDFTLTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIKGGGSGGGGSGGGGSQV QLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIGGINPNNGIPNYNQKFKGR VTITVDTSASTAYMELSSLRSEDTAVYYCARRRIAYGYDEGFAMDYWGQGTLVTVSSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARISSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1148.	FAP LH x F12Q HL	artificial	nt	GACATTGTGATGACCCAGACTCTCCAGACTCTTTGGCTGTGTCTCTAGGGGAGAGGGCCACCATCAA CTGCAAGTCCAGTCAGACCCTTTTATATTCTAGAAATCAAAAGAACTACTTGGCCTGGTATCAGC AGAAACCAGGACAGCCACCCAAACTCCTCAICTTTTGGGCTAGCACTAGGGAATCTGGGGTACCT

				GATAGGTTCAGTGGCAGTGGGTTTGGGACAGACTTCACCCTCACCATCAGCAGCCTGCAGGCTGA AGATGTGGCAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTCGGACAAGGGACCA AGGTGGAAATAAAAGGTCGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTG CAACTAGTCCACTCCCCGCCCGAACTCAACAAACCCGCTGCTTCCCTGAAACTCACGTGTAAAAC TAGTAGATACACCTTCACTGAATACACCATACGGGTTAGACAGGCCCCTGGCCAAAGGCCTGG AGTGGATAGGAGGTATTAATCCTAACAATGGTATTCCTAACTACAACCAGAAGTTCAAGGGCCGG GTCACCATCACCGTAGACACCTCTGCCAGCACCGCCTACATGGAACTGTCCAGCCTGCGCTCCGA GGACACTGCAGTCTACTACTGCGCCAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTA TGGACTACTGGGGTCAAGGAACCCTTGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTC TGGATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAAT GGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGGC AGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAAC TGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACGTTTCCTGGT GGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGC GGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGG TGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACT GGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCC GGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGT ACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTG GAGGAACCAAACTGACTCTCCTA
1149.	FAP alpha	human	nt	ATGAAGACTTGGGTAAAAATCGTATTTGGAGTTGCCACCTCTGCTGTGCTTGCCTTATTGGTGAT GTGCATTGTCTTACGCCCTTCAAGAGTTCATAACTCTGAAGAAATACAATGAGAGCACTCACAC TGAAGGATATTTTAAATGGAACATTTTCTTATAAAACATTTTTTCCAAACTGGATTTCAGGACAA GAATATCTTCATCAATCTGCAGATAACAATATAGTACTTTATAATATTGAAACAGGACAATCATA TACCATTTTGAGTAATAGAACCATGAAAAGTGTGAATGCTTCAAATTACGGCTTATCACCTGATC GGCAATTTGTATATCTAGAAAGTGATTATTCAAAGCTTTGGAGATACTCTTACACAGCAACATAT TACATCTATGACCTTAGCAATGGAGAATTTGTAAGAGGAAATGAGCTCCCTCGTCCAATTCAGTA TTTATGCTGGTCGCCTGTTGGGAGTAAATTAGCATATGTCTATCAAAACAATATCTATTTGAAAC AAAGACCAGGAGATTCCACCTTTTTCAAATAACATTTTAATGGAAGAGAAAATAAAATATTTAATGGA ATCCCAGACTGGGTTTATGAAGAGGAAATGCTTGCTACAAAATATGCTCTCTGGTGGTCTCCTAA TGGAAATTTTTGGCATATGCGGATTTAATGATACGGATATACCAGTATTGCCTATTCCTATTATT ATGGCGATGAACAATATCCTAGAACAATAAATATTCCATACCCAAGGCTGGAGCTAAGAATCCC GTTGTTCGGATATTTATATCGATACCACTTACCCTGCGTATGTAGGTCCCCAGGAAGTGCCTGT TCCAGCAATGATAGCCTCAAGTGATTATTTATTTCAGTTGGCTCACGTGGGTTACTGATGAACGAG TATGTTTGCAGTGGCTAAAAAGAGTCCAGAATGTTTCGGTCCTGTCTATATGTGACTTCAGGGAA GACTGGCAGACATGGGATTGTCCAAGACCCAGGAGCATATAGAAGAAAGCAGAACTGGATGGGC

				TGGTGGATTCTTTGTTTCAACACCAGTTTTCAGCTATGATGCCATTTCGTACTACAAAATATTTA GTGACAAGGATGGCTACAAACATATTCACTATATCAAAGACACTGTGGAAAATGCTATTCAAATT ACAAGTGGCAAGTGGGACGCCATAAATATATTCAGAGTAACACAGGATTCACTGTTTTATTCTAG CAATGAATTTCAAGAATACCCTGGAACAAGAAACATCTACAGAATTAGCATTGGAAGCTATCCTC CAAGCAAGAAGTGTGTTACTTGCCATCTAAGAAGAAGGTGCCAATATTACACAGCAAGTTTC AGCGACTACGCCAAGTACTATGCACTTGTCTGCTACGGCCCAGGCATCCCCATTTCCACCCTTCA TGATGGACGCACTGATCAAGAAATTAAAATCCTGGAAGAAAACAAGGAATTGGAAAATGCTTTGA AAAATATCCAGCTGCCTAAAGAGGAAATTAAGAAACTTGAAGTAGATGAAATTACTTTATGGTAC AAGATGATTCTTCCTCCTCAATTTGACAGAICAAAGAAGTATCCCTTGCTAATTCAAGTGTATGG TGGTCCCTGCAGTCAGACGTGTAAGGTCTGTATTTGCTGTTAATTGGACATCTTATCTTGCAAGTA AGGAAGGGATGGTCATTGCCTTGGTGGATGGTCGAGGAACAGCTTTCCAAGGTGACAAACTCCTC TATGCAGTGTATCGAAAGCTGGGTGTTTATGAAGTTGAAGACCAGATCACAGCTGTCAGAAAATT CATAGAAATGGGTTTCATTGATGAAAAAAGAATAGCCATATGGGGCTGGTCCTATGGAGGATACG TTTCATCACTGGCCCTTCCATCTGGAACTGGTCTTTTCAAATGTGGTATAGCAGTGGCTCCAGTC TCCAGCTGGGAATATTACGCGTCTGTCTACACAGAGAGATTCATGGGCTCTCCCAACAAGGATGA TAATCTTGAGCACTATAAGAATTCAACTGTGATGGCAAGAGCAGAATATTTCAGAAATGTAGACT ATCTTCTCATCCACGGAACAGCAGATGATAATGTGCACTTTCAAAACTCAGCACAGATTGCTAAA GCTCTGGTTAATGCACAAGTGGATTTCCAGGCAATGTGGTACTCTGACCAGAACCACGGCTTATC CGGCCTGTCCACGAACCACTTATACACCCACATGACCCACTTCCTAAAGCAGTGTTTCTCTTTGT CAGACTAA
1150.	FAP alpha	human	aa	MKTWVKIVFGVATSAVLALLVMCIVLRPSRVHNSEENTMRALTLKDILNGTFSYKTFFPNWISGQ EYLHQSADNNIVLYNIETGQSYTILSNRTMKSVNASNYGLSPDRQFVYLESDYSKLWRYSYTATY YIYDLSNGEFVRGNELPRPIQYLCWSPVGSKLAYVYQNNIYLKQRPGDPPFQITFNGRENKIFNG IPDWVYEEEMLATKYALWWSPNGKFLAYAEFNDTDIPVIAYSYYGDEQYPRTINIPYPKAGAKNP VVRIFIIDTTYPAYVGPQEVPVPAMIASSDYYFSWLTWVTDERVCLQWLKRVQNVSVLSICDFRE DWQTWDCPKTQEHIEESRTGWAGGFFVSTPVFSYDAISYYKIFSDKDGYKHIHYIKDTVENAIQI TSGKWEAINIFRVTQDSLFYSSNEFEEYPGRRNIYRISIGSYPPSKKCVTCHLRKERCQYYTASF SDYAKYYALVCYGPGIPISTLHDGRTDQEIKILEENKELENALKNIQLPKEEIKKLEVDEITLWY KMILPPQFDRSKKYPLLIQVYGGPCSQSVRSVFAVNWISYLASKEGMVIALVDGRGTAFQGDKLL YAVYKKLGVYEVEDQITAVRKFLEMGFIDEKRIAIWGWSYGGYVSSLALASGTGLFKCGIAVAPV SSWEYYASVYTERFMGLPTKDDNLEHYKNSTVMARAEYFRNVDYLLIHGTADDNVHFQNSAQIAK ALVNAQVDFQAMWYSDQNHGLSGLSTNHLYTHMTHFLKQCFSLSD
1151.	FAP alpha	Macaque (cynomol-gus)	nt	ATGAAGACTTGGGTAAAAATCGTATTTGGAGTTGCCACCTCTGCTGTGCTTGCCTTATTGGTGAT GTGCATTGTCTTACGCCCTCCAAGAGTTCATAACTCTGAAGAAATACAATGAGAGCACTCACAC TGAAGGATATTTTAAATGGGACATTTTCTTATATAAACATTTTTTCCAAACTGGATTTCAGGACAA GAATATCTTCATCAATCTGCAGATAACAATATAGTACTTTATAATATTGAAACAGGACAATCATA TACCATTTTGAGTAACACAACCATGAAAGTGTGAATGCTTCAAATTATGGCTTATCACCTGATC

				GGCAATTTGTATATCTACAAAGTGATTATTCAAAGCTTGGAGATACTCTTACACAGCAACATAT TACATCTATGACCTTAGCAATGGAGAATTTGTAAGAGGAAATGAGCTCCTCGTCCAATTCAGTA TTTATGCTGGTCGCCTGTTGGGAGTAAATTAGCATATGTCTATCAAAACAATATCTATTTGAAAC AAAGACCACGACATCCACCTTTTCAAATAACATTTAATCGAACAGAAAATAAAATATTTAATGCA ATCCCAGACTGGGTTTATGAAGAGGAAATGCTTGCTACAAAATATGCCTCTGGTGGTCTCCTAA TGGAAAATTTTTGGCATATGCGGAATTTAATGATACAGATATACCAGTATTGCCTATTCCTATT ATGGCGATGAACAATATCCCAGAACAATAAATATTCCATACCCAAAGGCYGGAGCTAAGAATCCT TTTGTTCGGATATTTATTATCGATACCACTTACCCTGCGTATGTAGGTCCCCAGGAAGTGCCTGT TCCAGCAATGATAGCCTCAAGTGATTATTATTTCAGTTGGCTCACGTGGGTTACTGATGAACGAG TATGTTTGCAGTGGCTAAAAAGAGTCCAGAATGTTTCGGTCTTGTCTATATGTGATTTCAGGGAA GACTGGCAGACATGGGATTGTCCAAAGACCCAGGAGCATATAGAAGAAAGCAGAACTGGATGGGC TGGTGGATTCTTTGTTTCAACACCAGTTTCAGCTATGATGCCATTTCATACTACAAAAATATTTA GTGACAAGGATGGCTACAAACATATTCACTATATCAAAGACACTGTGGAAAATGCTATTCAAATT ACAAGTGGCAAGTGGGACGCCATAAATATATTCAGAGTAACACAGGATTCACTGTTTATTCTAG CAATGAATTTGAAGATTACCCTGGAAGAAGAAACATCTACAGAATTAGCATTGGAAGCTATCCTC CAAGCAAGAAGTGTGTTACTTGCCATCTAAGGAAAGAAGGTGCCAATATTACACAGCAAGTTTC AGCGACTACGCCAAGTACTATGCACTTGTCTGCTATGGCCCCAGGCATCCCCATTTCCACCCTTCA TGACGGACGCACTGATCAAGAAATTAAAATCCTGGAAGAAAACAAGGAATTGGAAAATGCTTTGA AAAATATCCAGCTGCCTAAAGAGGAAATTAAGAAACTTGAAGTAGATGAAATTACTTTATGGTAC AAGATGATTCTTCCTCCTCCICAATTTGACAGAICAAAGAAGTATCCCTTGCTAATTCAAGTGTATGG TGGTCCCTGCAGTCAGACGTGTRAGGTCTGTATTTGCTGTTAATTGGATATCKTATCTTGCAAGTA AGGAAGGGATGGTCATTCCCTTGGTGGATGSTCGAGGAACAGCTTTCCAAGGTGACAAACTCCTG TATGCAGTGTATCGAAACCTGGGTGTTTATGAAGTTGAAGACCAGATTACAGCTGTCAGAAAATT CATAGAAATGGCGTTTCATTGATGAAAAAAGAATAGCCATATGGCGCTGCTCCTATGCAGCATAYG TTTCATCACTGGCCCTTTGCATCTGGAACTGSTCTTTTCAAATGTGGGATAGCAGTGGCTCCAGTC TCCAGCTGGGAATATTACGCGTCTGTCTACACAGAAAGATTCATGGGYCTTCCCACAAAGGATGA TAATCTTGAGCACTACAAAAATTCAACTGTGATGGCAAGAGCAGAATATTTCAGAAATGTAGACT ATCTTCTCATCCACGGAACAGCAGATGATAATGTGCACTTTCAAAACYCAGCACAGATTGCTAAA GCTCTGGTTAATGCACAAGTGGATTTCCAGSCAATGTGGTACTCTGACCAGAACCACGGCTTATC CGGCCTGTCCACGAACCACTTATACACCCACATGACCCACTTTCTAAAGCAGTGTTTTCTTTGT CGGACTAA
1152.	FAP alpha	Macaque (cynomol-gus)	aa	MKTWVKIVFGVATSAVLALLVMCIVLRPPRVHNSEENTMRALTLKDILNGTFSYKTFFPNWISGQ EYLHQSADNNIVLYNIETGQSYTILSNRTMKSVNASNYGLSPDRQFVYLESDYSKLWRYSYTAT Y YIYDLSNGEFVRGNELPRPIQYLCWSPVGSKLAYVYQNNIYLKQRPGDPPFQITFNGRENKIFNG IPDWVYEEEMLATKYALWWSPNGKFLAYAEFNDTDIPVIAYSYYGDEQYPRTINIPYPKAGAKNP FVRIFIIDTTYPAYVGPQEVPVPAMIASSDYYFSWLTWVTDERVCLQWLKRVQNVSVLSICDFRE DWQTWDCPKTQEHIEESRTGWAGGFFVSTPVFSYDAISYYKIFSDKDGYKHIHYIKDTVENAIQI

				TSGKWEAINIFRVTQDSLFYSSNEFEDYPGRRNIYRISIGSYPPSKKCVTCHLRKERCQYYTASF SDYAKYYALVCYGPGIPISTLHDGRTDQEIKILEENKELENALKNIQLPKEEIKKLEVDEITLWY KMILPPQFDRSKKYPLLIQVYGGPCSQSVRSVFAVNWISYLASKEGMVIALVDGRGTAFQGDKLL YAVYRKLGVYEVEDQITAVRKFIEMGFIDEKRIAIWGWSYGGYVSSLALASGTGLFKCGIAVAPV SSWEYYASVYTERFMGLPTKDDNLEHYKNSTVMARAEYFRNVDYLLIHGTADDNVHFQNSAQIAK ALVNAQVDFQAMWYSDQNHGLSGLSTNHLYTHMTHFLKQCFSLSD
1153.	forward primer	artificial	nt	CAGCTTCCAACTACAAGACAGAC
1154.	reverse primer	artificial	nt	TTTCCTCTTCATAACCCAGTCTGG
1155.	forward primer	artificial	nt	TTGAAACAAAGACCAGGAGATCCACC
1156.	reverse primer	artificial	nt	AGATGGCAAGTAACACACTTCTTGC
1157.	forward primer	artificial	nt	GAAGAAACATCTACAGAATTAGCATTGG
1158.	reverse primer	artificial	nt	CACATTTGAAAAGACCACTTCCAGATGC
1159.	forward primer	artificial	nt	AGATTACAGCTGTCAGAAAATTCATAGAAATGG
1160.	reverse primer	artificial	nt	ATATAAGGTTTTCAGATTCTGATACAGGC
1161.	5'FAP-VH-A-XhoI	artificial	nt	CCG CTA CTC GAG TCT GGA SCT GAG STG RWG AAG CCT GGG GCT TCA GTA AAG
1162.	3'FAP-VH-B	artificial	nt	CTG TCT CAC CCA GTG TAT GGT GTA TTC AGT GAA TGT GTA TCY AGA AGY CTT GCA GGA CAY CTT TAC TGA AGC CCC
1163.	5'FAP-VH-C	artificial	nt	CAC TGG GTG AGA CAG KCC CMT GGA MAG AGM CTT GAG TGG ATK GGA GGT ATT AAT CCT AAC AAT GGT ATT CCI AAC
1164.	3'FAP-VH-D	artificial	nt	CAT GTA GGC GGT GCT GGM GGA CKT GYC TMY AGT TAW TGT GRC CCT GCC CTT GAA CTT CTG ATT GTA GTT AGG AAT ACC
1165.	5'FAP-VH-E	artificial	nt	AGC ACC GCC TAC ATG GAG CTC MGC AGC CTG ASA TCT GAG GAT ACT GCG GTC TAT TWC TGT GCA AGA AGA AGA ATC GCC
1166.	3'FAP-VH-F-BstEII	artificial	nt	CCA GTA GGT GAC CAG GGT TCC TTG ACC CCA GTA GTC CAT AGC ATG GCC CTC GTC GTA ACC ATA GGC GAT TCT TCT TCT TGC ACA
1167.	5'FAP-VL-A-SacI	artificial	nt	CGA CCT GAG CTC GTG ATG ACA CAG ACT CCA YYC TCC CTA SCT GTG ACA SYT GGA GAG MMG GYT TCT ATG AGC TGC AAG TCC AGT CAG
1168.	3'FAP-VL-B	artificial	nt	AGA CTG CCC TGG CTT CTG CWG GWA CCA GGC CAA GTA GTT CTT TTG ATT ACG ACT ATA TAA AAG GCT CTG ACT GGA CTT GCA GCT
1169.	5'FAP-VL-C	artificial	nt	CAG AAG CCA GGG CAG TCT CCT MAA CTG CTG ATT TWC TGG GCA TCC ACTA GG GAA TCT GGG GTC CCT GAT CGC TTC TCA GGC AGT GGA
1170.	3'FAP-VL-D	artificial	nt	ATA TTG CTG ACA GTM ATA AAC TSC CAS GTC CTC AGC CTS CAC WCT GCT GAT CKT GAG AKT GAA ATC CGT CCC ARA TCC ACT GCC TGA GAA

1171.	3'FAP-VL-E-BsiWI/SpeI	artificial	nt	CCA GTA ACT AGT CGT ACG TTT GAT CTC CAC CTT GGT CCC ACC ACC GAA CGT GAG CGG ATA GCT AAA ATA TTG CTG ACA GT
1172.	PC32B8-H	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQAPGRGLEWIGRIDPSDSEI HYDQKFKDRVTITADKSTNTAYIELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS
1173.	PC32B8-HCDR1	artificial	aa	NYWLN
1174.	PC32B8-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
1175.	PC32B8-HCDR3	artificial	aa	TGIYAMAY
1176.	PC32B8-H	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGGCGCCCGGCAGGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACAA GAGCACCAACACCGCCTACATCGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCA
1177.	PC32B8-L	artificial	aa	DIVMTQSPPSLPVTPGEPASISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK
1178.	PC32B8-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1179.	PC32B8-LCDR2	artificial	aa	RMSNLAS
1180.	PC32B8-LCDR3	artificial	aa	LQHLEYPYT
1181.	PC32B8-L	artificial	nt	GACATCGTGATGACCCAGTCACCTCCAAGCCTGCCAGTGACCCCAGGCGAGCCAG CGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTA CCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGG ATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGGCTCTGGAA CCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGGGCGTGTACTA CTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACCAAGCTGGAA ATCAAG
1182.	PC32B8-HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQAPGRGLEWIGRIDPSDSEI HYDQKFKDRVTITADKSTNTAYIELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPPSLPVTPGEPASISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIK

1183.	PC32B8-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGGCGCCCGGCAGGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACAA GAGCACCAACACCGCCTACATCGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCCAAGCCTGCCAGTGACCCCA GGCGAGCCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAG
1184.	PC32B8 HL x I2C HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQAPGRGLEWIGRIDPSDSEI HYDQKFKDRVTITADKSTNTAYIELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPPSLPVTPGEPASISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1185.	PC32B8 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGGCGCCCGGCAGGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACAA GAGCACCAACACCGCCTACATCGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCCAAGCCTGCCAGTGACCCCA GGCGAGCCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC

				AAGCTGGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1186.	PC32D5-H	artificial	aa	EVQLVQSGAEVVKPGATVKISCKVSGYTFTNYWLNWVKQAPGRGLEWIGRIDPSDSEI HYDQKFKDRVTITADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS
1187.	PC32D5-HCDR1	artificial	aa	NYWLN
1188.	PC32D5-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
1189.	PC32D5-HCDR3	artificial	aa	TGIYAMAY
1190.	PC32D5-H	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGGTGAAGCCTGGCGCCACAGTG AAGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGT GAAACAGGCGCCCGGCAGGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGA CAGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACA AGAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGC CGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGC ACCACGGTCACCGTCTCCTCA
1191.	PC32D5-L	artificial	aa	DIVMTQSPLSLPVTPGESASISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK
1192.	PC32D5-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1193.	PC32D5-LCDR2	artificial	aa	RMSNLAS
1194.	PC32D5-LCDR3	artificial	aa	LQHLEYPYT
1195.	PC32D5-L	artificial	nt	GACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCAGGCGAGTCAG CGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTA CCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGG ATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGGCTCTGGAA CCGACTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGACGTGGGCGTGTACTA

				CTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACCAAGCTGGAA ATCAAG
1196.	PC32D5-HL	artificial	aa	EVQLVQSGAEVVKPGATVKISCKVSGYTFTNYWLNWVKQAPGRGLEWIGRIDPSDSEI HYDQKFKDRVTITADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGESASISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIK
1197.	PC32D5-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGGTGAAGCCTGGCGCCACAGTG AAGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGT GAAACAGGCGCCCGGCAGGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGA CAGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACA AGAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGC CGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGC ACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGTCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGACGTG GGCGTGTACTACTGCCTGCAGCACCTGGAATACCCCCTACACCTTCGGCCAAGGGA CCAAGCTGGAAATCAAG
1198.	PC32D5 HL x I2C HL	artificial	aa	EVQLVQSGAEVVKPGATVKISCKVSGYTFTNYWLNWVKQAPGRGLEWIGRIDPSDSEI HYDQKFKDRVTITADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGESASISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1199.	PC32D5 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGGTGAAGCCTGGCGCCACAGTG AAGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGT GAAACAGGCGCCCGGCAGGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGA CAGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACA

				AGAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGC CGTGTACTATTGCGCCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGC ACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGTCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGACGTG GGCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGA CCAAGCTGGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTC TGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTG GATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGT TTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1200.	PC17D10-H	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQTPGKGLEWIGRIDPSDSEIH YDQKFKDKVTITADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS
1201.	PC17D10-HCDR1	artificial	aa	NYWLN
1202.	PC17D10-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
1203.	PC17D10-HCDR3	artificial	aa	TGIYAMAY
1204.	PC17D10-H	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGACGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGACA GCGAGATCCACTACGACCAGAAGTTCAAGGACAAAGTCACCATAACCGCGGACAAG AGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCCG TGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCAC CACGGTCACCGTCTCCTCA

1205.	PC17D10-L	artificial	aa	DIVMTQAPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK
1206.	PC17D10-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1207.	PC17D10-LCDR2	artificial	aa	RMSNLAS
1208.	PC17D10-LCDR3	artificial	aa	LQHLEYPYT
1209.	PC17D10-L	artificial	nt	GACATCGTGATGACCCAGGCACCTCTAAGCCTGCCAGTGACCCCAGGCGAGCCAG TGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTA CCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGG ATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGGCTCTGGAA CCGACTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGACGTGGGCGTGTACTA CTGCCTGCAGCACCTGGAATACCCCCTACACCTTCGGCCAAGGGACCAAGCTGGAA ATCAAG
1210.	PC17D10-HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQTPGKGLEWIGRIDPSDSEIH YDQKFKDKVTITADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSSG GGGSGGGGSGGGGSDIVMTQAPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYLQ KPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCLQHLEYPYT FGQGTKLEIK
1211.	PC17D10-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGACGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGACA GCGAGATCCACTACGACCAGAAGTTCAAGGACAAAGTCACCATAACCGCGGACAAG AGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCCG TGTACTATTGCGCCCTGACCGGCATCTACGCCATGGACTACTGGGGCCAGGGCAC CACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGT GGTGGTTCTGACATCGTGATGACCCAGGCACCTCTAAGCCTGCCAGTGACCCCAG GCGAGCCAGTGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGG CAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGA TCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGG CTCTGGAACCGACTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGACGTGGGC GTGTACTACTGCCTGCAGCACCTGGAATACCCCCTACACCTTCGGCCAAGGGACCAA GCTGGAAATCAAG
1212.	PC17D10 HL x I2C HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQTPGKGLEWIGRIDPSDSEIH YDQKFKDKVTITADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSSG GGGSGGGGSGGGGSDIVMTQAPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYLQ KPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCLQHLEYPYT

				FGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1213.	PC17D10 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGACGCCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGACA GCGAGATCCACTACGACCAGAAGTTCAAGGACAAAGTCACCATAACCGCGGACAAG AGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCCG TGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCAC CACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGT GGTGGTTCTGACATCGTGATGACCCAGGCACCTCTAAGCCTGCCAGTGACCCCAG GCGAGCCAGTGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGG CAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGA TCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGG CTCTGGAACCGACTTCACCCTGAGGATCAGCAGGGTGGAGGCCGAGGACGTGGGC GTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACCAA GCTGGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA ACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1214.	PC16E12-H	artificial	aa	EVQLVQSGAEVKKPGAPVKISCKVSGYTFTNYWLNWVKQRPGKGLEWIGRIDPSDSEI HYDQKFKDRVTITVDKSTSTAYIELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS
1215.	PC16E12-HCDR1	artificial	aa	NYWLN
1216.	PC16E12-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD

1217.	PC16E12-HCDR3	artificial	aa	TGIYAMAY
1218.	PC16E12-H	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCCCAGTG AAGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGT GAAACAGAGGCCCGGCAAGGGCCTGGAATGGATAGGTAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGTGGACAA GAGCACCAGCACCGCCTACATGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCA
1219.	PC16E12-L	artificial	aa	DIVMTQSPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK
1220.	PC16E12-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1221.	PC16E12-LCDR2	artificial	aa	RMSNLAS
1222.	PC16E12-LCDR3	artificial	aa	LQHLEYPYT
1223.	PC16E12-L	artificial	nt	GACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCAGGCGAGCCAG TGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTA CCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGG ATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGGCTCTGGAA CCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGGGCGTGTACTA CTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACCAAGCTGGAA ATCAAG
1224.	PC16E12-HL	artificial	aa	EVQLVQSGAEVKKPGAPVKISCKVSGYTFTNYWLNWVKQRPGKGLEWIGRIDPSDSEI HYDQKFKDRVTITVDKSTSTAYIELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIK
1225.	PC16E12-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCCCAGTG AAGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGT GAAACAGAGGCCCGGCAAGGGCCTGGAATGGATAGGTAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGTGGACAA GAGCACCAGCACCGCCTACATCGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGCCAGTGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG

				GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAG
1226.	PC16E12 HL x I2C HL	artificial	aa	EVQLVQSGAEVKKPGAPVKISCKVSGYTFTNYWLNWVKQRPGKGLEWIGRIDPSDSEI HYDQKFKDRVTITVDKSTSTAYIELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1227.	PC16E12 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCCCAGTG AAGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGT GAAACAGAGGCCCGGCAAGGGCCTGGAATGGATAGGTAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCATAACCGTGGACAA GAGCACCAGCACCGCCTACATGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGCCAGTGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC

				AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1228.	PC08F4-H	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVQQRPGKGLEWIGRIDPSDSEI HYDQKFKDRVTLTADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVS S
1229.	PC08F4-HCDR1	artificial	aa	NYWLN
1230.	PC08F4-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
1231.	PC08F4-HCDR3	artificial	aa	TGIYAMAY
1232.	PC08F4-H	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG CAACAGAGGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCCTAACCGCGGACAA GAGCACCAGCACACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCA
1233.	PC08F4-L	artificial	aa	DIVMTQSPLSLPVTPGESASISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK
1234.	PC08F4-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1235.	PC08F4-LCDR2	artificial	aa	RMSNLAS
1236.	PC08F4-LCDR3	artificial	aa	LQHLEYPYT
1237.	PC08F4-L	artificial	nt	GACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCAGGCGAGTCAG CGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTA CCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGG ATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGGCTCTGGAA CCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGGGCGTGTACTA CTGCCTGCAGCACCTGGAATACCCCCTACACCTTCGGCCAAGGGACCAAGCTGGAA ATCAAG
1238.	PC08F4-HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVQQRPGKGLEWIGRIDPSDSEI HYDQKFKDRVTLTADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVS SGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGESASISCRSSKSLLHSNGNTYLYWY LQKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP

				YTFGQGTKLEIK
1239.	PC08F4-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG CAACAGAGGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCCTAACCGCGGACAA GAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGTCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAG
1240.	PC08F4 HL x I2C HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVQQRPGKGLEWIGRIDPSDSEI HYDQKFKDRVTLTADKSTSTAYMELSSLRSEDTAVYYCALTGIYAMAYWGQGTTVTVS SGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGESASISCRSSKSLLHSNGNTYLYWY LQKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1241.	PC08F4 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG CAACAGAGGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCCTAACCGCGGACAA GAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGAGAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGTCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG

				GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAGTCCGGAGGTGGTGGATCCGGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1242.	PC16F5-H	artificial	aa	EVQLVQSGAEVMKPGATVKISCKVSGYTFTNYWLNWVKQAPGKGLEWIGRIDPSDSEI HYDQKFKDRVTITANKSTSTAYMELSSLTSEDTAVYYCALTGIYAMAYWGQGTTVTVSS
1243.	PC16F5-HCDR1	artificial	aa	NYWLN
1244.	PC16F5-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
1245.	PC16F5-HCDR3	artificial	aa	TGIYAMAY
1246.	PC16F5-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGATGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGGCACCTGGAAAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACAAATC CGCCAGCACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1247.	PC16F5-L	artificial	aa	DIVMTQSPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK
1248.	PC16F5-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1249.	PC16F5-LCDR2	artificial	aa	RMSNLAS
1250.	PC16F5-LCDR3	artificial	aa	LQHLEYPYT
1251.	PC16F5-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAGCTTCATGTCCGCATCAGTAGGAGACAGAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGACAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATC

				AGCAGTCTGCAGTCTGAAGACTTCGCAACTTATTACTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAAA
1252.	PC16F5-HL	artificial	aa	EVQLVQSGAEVMKPGATVKISCKVSGYTFTNYWLNWVKQAPGKGLEWIGRIDPSDSEI HYDQKFKDRVTITANKSTSTAYMELSSLTSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIK
1253.	PC16F5-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGATGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGGCGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACCGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGAACAA GAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGACAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA CCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGCCAGTGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAG
1254.	PC176F5 HL x I2C HL	artificial	aa	EVQLVQSGAEVMKPGATVKISCKVSGYTFTNYWLNWVKQAPGKGLEWIGRIDPSDSEI HYDQKFKDRVTITANKSTSTAYMELSSLTSEDTAVYYCALTGIYAMAYWGQGTTVTVSS GGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPVSISCRSSKSLLHSNGNTYLYWYL QKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1255.	PC16F5 HL x I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGATGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGGCGCCCGGCAAGGGCCTGGAATGGATAGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACCGACCAGAAGTTCAAGGACAGAGTCACCATAACCGCGAACAA GAGCACCAGCACCGCCTACATGGAGCTGTCCAGCCTGACAAGCGAGGACACCGCC GTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGCA

				CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGTCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGCCAGTGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1256.	PC17H10-H	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQTPGKGLEWMGRIDPSDSEI HYDQKFKDRVTLTADTSTDTAYMELSSLTSEDTAVYYCALTGIYAMAYWGQGTTVTVS S
1257.	PC17H10-HCDR1	artificial	aa	NYWLN
1258.	PC17H10-HCDR2	artificial	aa	RIDPSDSEIHYDQKFKD
1259.	PC17H10-HCDR3	artificial	aa	TGIYAMAY
1260.	PC17H10-H	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGACGCCCGGCAAGGGCCTGGAATGGATGGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACCGACCAGAAGTTCAAGGACAGAGTCACCCTAACCGCGGACA CGAGCACCGACACCGCCTACATGGAGCTGTCCAGCCTGACAAGCGAGGACACCGC CGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGC ACCACGGTCACCGTCTCCTCA
1261.	PC17H10-L	artificial	aa	DIVMTQAPLSLPVTPGEPASISCRSSKSLLHSNGNTYLYWYLQKPGQSPQLLIYRMSNL ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYPYTFGQGTKLEIK

1262.	PC17H10-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1263.	PC17H10-LCDR2	artificial	aa	RMSNLAS
1264.	PC17H10-LCDR3	artificial	aa	LQHLEYPYT
1265.	PC17H10-L	artificial	nt	GACATCGTGATGACCCAGGCACCTCTAAGCCTGCCAGTGACCCCAGGCGAGCCAG CGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACGGCAACACCTA CCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCTGATCTACAGG ATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGCGGCTCTGGAA CCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGGGCGTGTACTA CTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACCAAGCTGGAA ATCAAG
1266.	PC17H10-HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQTPGKGLEWMGRIDPSDSEI HYDQKFKDRVTLTADTSTDTAYMELSSLTSEDTAVYYCALTGIYAMAYWGQGTTVTVS SGGGGSGGGGSGGGGSDIVMTQAPLSLPVTPGEPASISCRSSKSLLHSNGNTYLYWY LQKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIK
1267.	PC17H10-HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGACGCCCGGCAAGGGCCTGGAATGGATGGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCCTAACCGCGGACA CGAGCACCGACACCGCCTACATGGAGCTGTCCAGCCTGACAAGCGAGGACACCGC CGTGTACTATTGCGCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGC ACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGGCACCTCTAAGCCTGCCAGTGACCCCA GGCGAGCCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAG
1268.	PC17H10 HL X I2C HL	artificial	aa	EVQLVQSGAEVKKPGATVKISCKVSGYTFTNYWLNWVKQTPGKGLEWMGRIDPSDSEI HYDQKFKDRVTLTADTSTDTAYMELSSLTSEDTAVYYCALTGIYAMAYWGQGTTVTVS SGGGGSGGGGSGGGGSDIVMTQAPLSLPVTPGEPASISCRSSKSLLHSNGNTYLYWY LQKPGQSPQLLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQHLEYP YTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS

				PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1269.	PC17H10 HL X I2C HL	artificial	nt	GAGGTGCAGCTGGTCCAGTCAGGCGCCGAAGTGAAGAAGCCTGGCGCCACAGTGA AGATATCCTGCAAGGTCAGCGGCTACACCTTCACCAACTACTGGCTGAACTGGGTG AAACAGACGCCCGGCAAGGGCCTGGAATGGATCGGCAGGATCGACCCCAGCGAC AGCGAGATCCACTACGACCAGAAGTTCAAGGACAGAGTCACCCTAACCGCGGACA CGAGCACCGACACCGCCTACATGGAGCTGTCCAGCCTGACAAGCGAGGACACCGC CGTGTACTATTGCGCCCCTGACCGGCATCTACGCCATGGCCTACTGGGGCCAGGGC ACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGGCACCCTCTAAGCCTGCCAGTGACCCCA GGCGAGCCAGCGTCCATCAGCTGCAGGTCCAGCAAGAGCCTGCTGCACAGCAACG GCAACACCTACCTGTACTGGTATCTGCAGAAGCCAGGCCAGGAGCCCCCAGCTGCT GATCTACAGGATGAGCAACCTGGCTAGCGGCGTGCCAGACAGATTCAGCGGCAGC GGCTCTGGAACCGACTTCACCCTGAAGATCAGCAGGGTGGAGGCCGAGGACGTGG GCGTGTACTACTGCCTGCAGCACCTGGAATACCCCTACACCTTCGGCCAAGGGACC AAGCTGGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1270.	hCD19 5-A9-H	artificial	aa	QVQLVQSGAEVVRPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTVGRYYYAMDY WGQGTTVTVSS
1271.	hCD19 5-A9-HCDR1	artificial	aa	SYWMN
1272.	hCD19 5-A9-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1273.	hCD19 5-A9-HCDR3	artificial	aa	RETTVGRYYYAMDY
1274.	hCD19 5-A9-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGGCTGAGGTGGTGAGGCCTGGGGCCTCAGTG

				AAGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTG AGGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATG GTGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAAT CCACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGT CTATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGG ACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1275.	hCD19 5-A9-L	artificial	aa	DIQMTQSPSSLSVSVGERVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISSLQKEDFATYYCQQSTEDPWTFGQGTKVEIK
1276.	hCD19 5-A9-LCDR1	artificial	aa	KASQSVDYDGTSYLN
1277.	hCD19 5-A9-LCDR2	artificial	aa	DASNLVS
1278.	hCD19 5-A9-LCDR3	artificial	aa	QQSTEDPWT
1279.	hCD19 5-A9-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCAAAGTGTTGATTATGATGGTACCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGCAGAAGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1280.	hCD19 5-A9-LH	artificial	aa	DIQMTQSPSSLSVSVGERVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISSLQKEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVRPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTV GRYYYAMDYWGQGTTVTVSS
1281.	hCD19 5-A9-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGCAGAAGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCCGGTGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAGGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCA

1282.	hCD19 5-A9 LH x I2C HL	artificial	aa	DIQMTQSPSSLSVSVGERVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISSLQKEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVRPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1283.	hCD19 5-A9 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGCAGAAGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAGGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC

				CTA
1284.	hCD19 2-C6-H	artificial	aa	QVQLVQSGAEVKKPGASVKISCKASGYAFTSYWMNWVRQAPGQGLEWIGQIWPGDG DTNYNGKFKGRVTLTADTSTSTAYMELSSLQSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSS
1285.	hCD19 2-C6-HCDR1	artificial	aa	SYWMN
1286.	hCD19 2-C6-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1287.	hCD19 2-C6-HCDR3	artificial	aa	RETTTVGRYYYAMDY
1288.	hCD19 2-C6-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGGCCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTCTGACTGCTGACACATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTACAATCTGAGGACACTGCGGTCT ATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGAC TACTGGGGCCAAGGGACCACCGTCACCGTCTCCTCA
1289.	hCD19 2-C6-L	artificial	aa	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLV SGVPPRFSGSGSGTDFTLTIHSLQPEDFATYYCQQSTEDPWTFGQGTKVEIK
1290.	hCD19 2-C6-LCDR1	artificial	aa	KASQSVDYDGSSYLN
1291.	hCD19 2-C6-LCDR2	artificial	aa	DASNLVS
1292.	hCD19 2-C6-LCDR3	artificial	aa	QQSTEDPWT
1293.	hCD19 2-C6-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTCGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCCATTCTCTGCAGCCGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1294.	hCD19 2-C6-LH	artificial	aa	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLV SGVPPRFSGSGSGTDFTLTIHSLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVKKPGASVKISCKASGYAFTSYWMNWVRQAPGQGLE WIGQIWPGDGDTNYNGKFKGRVTLTADTSTSTAYMELSSLQSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSS
1295.	hCD19 2-C6-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTCGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA

				ATCTAGTTTCTGGGTCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCCATTCTCTGCAGCCGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGGCCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTCTGACTGCTGACACATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTACAATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACCGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCA
1296.	hCD19 2-C6 LH x I2C HL	artificial	aa	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLV SGVPPRFSGSGSGTDFTLTIHSLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVKKPGASVKISCKASGYAFTSYWMNWVRQAPGQGLE WIGQIWPGDGDTNYNGKFKGRVTLTADTSTSTAYMELSSLQSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1297.	hCD19 2-C6 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTCGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCCATTCTCTGCAGCCGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGGCCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTCTGACTGCTGACACATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTACAATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACCGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA

				AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
1298.	hCD19 4-C7-H	artificial	aa	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTVGRYYYAMDY WGQGTTVTVSS
1299.	hCD19 4-C7-HCDR1	artificial	aa	SYWMN
1300.	hCD19 4-C7-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1301.	hCD19 4-C7-HCDR3	artificial	aa	RETTVGRYYYAMDY
1302.	hCD19 4-C7-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC TATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1303.	hCD19 4-C7-L	artificial	aa	DIQMTQSPSSLSASLGDRVTITCKASQSVDYDGTSYLNWYQQKPGQPPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISPLEQEDFATYYCQQSTEDPWTFGQGTKVEIK
1304.	hCD19 4-C7-LCDR1	artificial	aa	KASQSVDYDGSSYLN
1305.	hCD19 4-C7-LCDR2	artificial	aa	DASNLVS
1306.	hCD19 4-C7-LCDR3	artificial	aa	QQSTEDPWT
1307.	hCD19 4-C7-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTTGTCTGCGTCTCTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCA

				ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTCCTCTGGAGCAGGAGGATTTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1308.	hCD19 4-C7-LH	artificial	aa	DIQMTQSPSSLSASLGDRVTITCKASQSVDYDGTSYLNWYQQKPGQPPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISPLEQEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSS
1309.	hCD19 4-C7-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTCTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTCCTCTGGAGCAGGAGGATTTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
1310.	hCD19 4-C7 LH x I2C HL	artificial	aa	DIQMTQSPSSLSASLGDRVTITCKASQSVDYDGTSYLNWYQQKPGQPPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISPLEQEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1311.	hCD19 4-C7 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTCTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTCCTCTGGAGCAGGAGGATTTCGCAACCTATTACTGTCAGCA

				AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
1312.	hCD19 2-D7-H	artificial	aa	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDY WGQGTTVTVSS
1313.	hCD19 2-D7-HCDR1	artificial	aa	SYWMN
1314.	hCD19 2-D7-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1315.	hCD19 2-D7-HCDR3	artificial	aa	RETTTVGRYYYAMDY
1316.	hCD19 2-D7-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC

				CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC TATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1317.	hCD19 2-D7-L	artificial	aa	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLV SGVPPRFSGSGSGTDFTLTIHSLQPEDFATYYCQQSTEDPWTFGQGTKVEIK
1318.	hCD19 2-D7-LCDR1	artificial	aa	KASQSVDYDGSSYLN
1319.	hCD19 2-D7-LCDR2	artificial	aa	DASNLVS
1320.	hCD19 2-D7-LCDR3	artificial	aa	QQSTEDPWT
1321.	hCD19 2-D7-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTCGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCCATTCTCTGCAGCCGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1322.	hCD19 2-D7-LH	artificial	aa	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLV SGVPPRFSGSGSGTDFTLTIHSLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTV GRYYYAMDYWGQGTTVTVSS
1323.	hCD19 2-D7-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTCGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCCATTCTCTGCAGCCGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCA
1324.	hCD19 2-D7 LH x I2C HL	artificial	aa	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLV SGVPPRFSGSGSGTDFTLTIHSLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE

				WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1325.	hCD19 2-D7 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTTCGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCCATTCTCTGCAGCCGGAGGATTTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
				QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDY
1326.	hCD19 2-D4-H	artificial	aa	

				WGQGTTVTVSS
1327.	hCD19 2-D4-HCDR1	artificial	aa	SYWMN
1328.	hCD19 2-D4-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1329.	hCD19 2-D4-HCDR3	artificial	aa	RETTTVGRYYYAMDY
1330.	hCD19 2-D4-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC TATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1331.	hCD19 2-D4-L	artificial	aa	DIQMTQSPASLSVSVGERVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSTEDPWTFGQGTKVEIK
1332.	hCD19 2-D4-LCDR1	artificial	aa	KASQSVDYDGSSYLN
1333.	hCD19 2-D4-LCDR2	artificial	aa	DASNLVS
1334.	hCD19 2-D4-LCDR3	artificial	aa	QQSTEDPWT
1335.	hCD19 2-D4-L	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCAAAGTGTTGATTATGATGGTACCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGCAGCCGGAGGATTTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1336.	hCD19 2-D4-LH	artificial	aa	DIQMTQSPASLSVSVGERVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTV GRYYYAMDYWGQGTTVTVSS
1337.	hCD19 2-D4-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCAAAGTGTTGATTATGATGGTACCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGCAGCCGGAGGATTTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG

				GTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCA
1338.	hCD19 2-D4 LH x I2C HL	artificial	aa	DIQMTQSPASLSVSVGERVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1339.	hCD19 2-D4 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCAGCTTCTTTGTCTGTGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCAAAGTGTTGATTATGATGGTACCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGCAGCCGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA

				GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
1340.	hCD19 5-G3-H	artificial	aa	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTVGRYYYAMDY WGQGTTVTVSS
1341.	hCD19 5-G3-HCDR1	artificial	aa	SYWMN
1342.	hCD19 5-G3-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1343.	hCD19 5-G3-HCDR3	artificial	aa	RETTVGRYYYAMDY
1344.	hCD19 5-G3-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC TATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1345.	hCD19 5-G3-L	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGLSYLNWYQQKPGQAPKLLIYDASNLV SGIPSRFSGSGSGTDFTLTISSLEPEDFATYYCQQSTEDPWTFGQGTKVEIK
1346.	hCD19 5-G3-LCDR1	artificial	aa	KASQSVDYDGSSYLN
1347.	hCD19 5-G3-LCDR2	artificial	aa	DASNLVS
1348.	hCD19 5-G3-LCDR3	artificial	aa	QQSTEDPWT
1349.	hCD19 5-G3-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCTCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGATCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGGAGCCGGAGGATTTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA

1350.	hCD19 5-G3-LH	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGLSYLNWYQQKPGQAPKLLIYDASNLV SGIPSRFSGSGSGTDFTLTISSLEPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGS QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDY WGQGTTVTVSS
1351.	hCD19 5-G3-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCTCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGATCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGGAGCCGGAGGATTTTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
1352.	hCD19 5-G3 LH x I2C HL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGLSYLNWYQQKPGQAPKLLIYDASNLV SGIPSRFSGSGSGTDFTLTISSLEPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1353.	hCD19 5-G3 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTCTCAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGATCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAGTTCTCTGGAGCCGGAGGATTTTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT

				GGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
1354.	hCD19 4-E10-H	artificial	aa	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDY WGQGTTVTVSS
1355.	hCD19 4-E10-HCDR1	artificial	aa	SYWMN
1356.	hCD19 4-E10-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1357.	hCD19 4-E10-HCDR3	artificial	aa	RETTTVGRYYYAMDY
1358.	hCD19 4-E10-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC

				TATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1359.	hCD19 4-E10-L	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLNISSVQPEDVATYYCQQSTEDPWTFGQGTKVEIK
1360.	hCD19 4-E10-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1361.	hCD19 4-E10-LCDR2	artificial	aa	RMSNLAS
1362.	hCD19 4-E10-LCDR3	artificial	aa	LQHLEYPYT
1363.	hCD19 4-E10-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCAACATCAGTTCTGTGCAGCCGGAGGATGTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1364.	hCD19 4-E10-LH	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLNISSVQPEDVATYYCQQSTEDPWTFGQGTKVEIKGGGGS GGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGL EWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTT VGRYYYAMDYWGQGTTVTVSS
1365.	hCD19 4-E10-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCAACATCAGTTCTGTGCAGCCGGAGGATGTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
1366.	hCD19 4-E10 LH x	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGTSYLNWYQQKPGQAPKLLIYDASNLV

	I2C HL			SGVPSRFSGSGSGTDFTLNISSVQPEDVATYYCQQSTEDPWTFGQGTKVEIKGGGS GGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGL EWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTT VGRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1367.	hCD19 4-E10 LH x I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGACAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCAACATCAGTTCTGTGCAGCCGGAGGATGTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA

1368.	hCD19 4-E3-H	artificial	aa	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTVGRYYYAMDY WGQGTTVTVSS
1369.	hCD19 4-E3-HCDR1	artificial	aa	SYWMN
1370.	hCD19 4-E3-HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1371.	hCD19 4-E3-HCDR3	artificial	aa	RETTVGRYYYAMDY
1372.	hCD19 4-E3-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC TATTACTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1373.	hCD19 4-E3-L	artificial	aa	DIQMTQSPSSLAASVGERVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTINSLEKEDFATYYCQQSTEDPWTFGQGTKVEIK
1374.	hCD19 4-E3-LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1375.	hCD19 4-E3-LCDR2	artificial	aa	RMSNLAS
1376.	hCD19 4-E3-LCDR3	artificial	aa	LQHLEYPYT
1377.	hCD19 4-E3-L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGGCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAATTCTCTGGAGAAGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1378.	hCD19 4-E3-LH	artificial	aa	DIQMTQSPSSLAASVGERVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTINSLEKEDFATYYCQQSTEDPWTFGQGTKVEIKGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTV GRYYYAMDYWGQGTTVTVSS
1379.	hCD19 4-E3-LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGGCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAATTCTCTGGAGAAGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG

				TCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCA
1380.	hCD19 4-E3 LH X I2C HL	artificial	aa	DIQMTQSPSSLAASVGERVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLTINSLEKEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSG GGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLE WIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTV GRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1381.	hCD19 4-E3 LH X I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGGCTGCGTCTGTAGGGGAGAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCACCATCAATTCTCTGGAGAAGGAGGATTTCGCAACCTATTACTGTCAGCAA AGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGTG GTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTTCTCAGGTGCAGCTGG TCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAA GGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCTG GACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTAC AATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAGC CTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCAA GACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCAA GGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGG

				ACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
1382.	hCD19 3-H7 -H	artificial	aa	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDG DTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDY WGQGTTVTVSS
1383.	hCD19 3-H7 – HCDR1	artificial	aa	SYWMN
1384.	hCD19 3-H7 – HCDR2	artificial	aa	QIWPGDGDTNYNGKFKG
1385.	hCD19 3-H7 – HCDR3	artificial	aa	RETTTVGRYYYAMDY
1386.	hCD19 3-H7 -H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGCCTCAGTGA AGATTTCCTGCAAGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGA GGCAGCGCCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGG TGATACTAACTACAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATC CACCAGCACAGCCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTC TATTACTGTGCAAGACGGGAGACTACCGACGGTAGGCCGTTATTACTATGCTATGGA CTACTGGGGCCAAGGGACCACCGTCACCGTCTCCTCA
1387.	hCD19 3-H7 –L	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLNISSLQPEDVATYYCQQSTEDPWTFGQGTKVEIK
1388.	hCD19 3-H7 – LCDR1	artificial	aa	RSSKSLLHSNGNTYLY
1389.	hCD19 3-H7 – LCDR2	artificial	aa	RMSNLAS
1390.	hCD19 3-H7 – LCDR3	artificial	aa	LQHLEYPYT
1391.	hCD19 3-H7 -L	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC

				ACCCTCAACATCAGTTCTCTGCAGCCGGAGGATGTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAA
1392.	hCD19 3-H7 -LH	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLNISSLQPEDVATYYCQQSTEDPWTFGQGTKVEIKGGGGS GGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGL EWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTT VGRYYYAMDYWGQGTTVTVSS
1393.	hCD19 3-H7 -LH	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCAACATCAGTTCTCTGCAGCCGGAGGATGTCGCAACCTATTACTGTCAGCA AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
1394.	hCD19 3-H7 LH X I2C HL	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLV SGVPSRFSGSGSGTDFTLNISSLQPEDVATYYCQQSTEDPWTFGQGTKVEIKGGGGS GGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGL EWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTT VGRYYYAMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1395.	hCD19 3-H7 LH X I2C HL	artificial	nt	GACATCCAGATGACCCAGTCTCCATCTTCTTTGTCTGCGTCTGTAGGGGACAGAGT CACCATCACCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTACGAGTTATTTGAA CTGGTACCAACAGAAACCAGGAAAGGCACCCCAAACTCCTCATCTATGATGCATCCA ATCTAGTTTCTGGGGTCCCATCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTC ACCCTCAACATCAGTTCTCTGCAGCCGGAGGATGTCGCAACCTATTACTGTCAGCA

				AAGTACTGAGGATCCGTGGACGTTCGGTCAAGGGACCAAGGTGGAGATCAAAGGT GGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTG GTCCAGTCTGGGGCTGAGGTGGTGAAGCCTGGGGGCCTCAGTGAAGATTTCCTGCA AGGCTTCTGGCTATGCATTCACTAGCTACTGGATGAACTGGGTGAGGCAGCGCCCT GGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA CAATGGAAAGTTCAAGGGTAGAGTCACTATGACTGCTGACGAATCCACCAGCACAG CCTACATGGAACTCAGCAGCCTGCGATCTGAGGACACTGCGGTCTATTACTGTGCA AGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTACTGGGGCCA AGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTC GAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAG CCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGA AAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATT ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTG CCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGA GACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGGCTTACTGGGGCCAAGGG ACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGT GGAACAGTCACACTCACTTGTGGCTCCTCCGACTGGGGCTGTTACATCTGGCAACTA CCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGGG ACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCCTGCTTGGAGG CAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACT GTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTC CTA
1396.	cMET-1	artificial	nt	atgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtacactccgagtgtaaagaggcactag caaagtccgagatgaatgtgaatatgaagtatcagcttcccaacttcaccgcggaaacacccatccagaatgtc attctacatgagcatcacatttccttggtgccactaactacatttatgttttaaatgaggaagacctcagaaggttgc tgagtacaagactgggcctgtgctggaacacccagattgtttcccatgtcaggactgcagcagcaaagccaatttt atcaggaggtgtttggaaagataacatcaacatggctctagttgtggacacctactatgatgatcaactcattagct gtggcagcgtcaacagaggggacctgccagcgacatgtctttcccacaatcatactactgctgacatacagtcggag gttcactgcatattctcccccacagatagaagagcccagccagtgtcctgactgtgtggtgagcgccctgggagcc aaagtcctttcatctgtaaaggaccggttcatcaacttcttgtaggcaataccataaattcttcttattttcccagatcat ccattgcattcgatatcagtgagaaggctaaaggaaacgaaagatggttttatgttttgacggaccagtcctacat tgatgtttacctgagttcagagatctacccccattaagtatgtccatgccttgaaagcaacaatttattacttcttga cggtccaaagggaaactctagatgctcagactttcacacaagaataatcaggttctgttccataaactctggattg

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				aataataaatttgatttaaagaaaactagagttctcctggaaatgagagctgcaccttgactttaagtgagagcac
				gatgaatacattgaaatgcacagttggtcctgccatgaataagcatttcaatatgtccataattatttcaaatggcca
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				aacatgtacttaaaaagtgtgtcaaacagtatttctgaatgttataccccagcccaaaccatttcaactgagttgct
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				attgttgctggaattgttgtgctggtttatttccagaaaagaagagaatggcaaagtatgagaaggctgagataaagg
				agatgggtgagatgcatagggaactcaatgcataa
1397.	cMET-2	artificial	aa	mgwsciilfvatatgvhseckealaksemnvnmkyqlpnftaetpiqnvilhehhiflgatnyiyvlneedlqkva eyktgpvlehpdctpcqdcsskanlsggvwkdninmalvvdtyyddqliscgsvnrgtcqrivfphnhtadiqs evhcifspqieepsqcpdcvvsalgakvlssvkdrfinffvgntinssyfpdhplhsisvrrlketkdgfmfltdqsyi dvlpefrdsypikyvhafesnnfiyfltvqretldaqtfhtriirfcsinsglhsymempleciltekrkkrstkkevfnilq aayvskpgaqlarqigasldditlgvfaqskpdsaepmdrsamcafpikyvndffnkivnknnvrclqhfygpn

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1398.	cMET-3	artificial	nt	atgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtaacactccgagtgtaaagaggcactag caaagtccgagatgaatgtgaatatgaagtatcagcttccaacttcaccgcggaaacagccatccagaatgtc attctacatgagcatcacatttcctcggtgccaccaactacattatgtttaaatgaggaagaccttcagaaggttg ctgagtacaagaccgggcctgtgctggaacacccagatgtttcccgtgtcaggactgcagcagcaaagccaat ttatcaggaggcgtttggaaagataacatcaacatggctctggttgtggacacctactatgatgatcaactcattag ctgtggcagcgtcaacagagggacctgccagcgacatgtctttcccataatcatactgctgacatacagtcgga ggttcactgcatattctcccacagatagaagagcccaaccagtgccctgactgtgtggtgagcgccctgggag ccaaagtcctttcatctgtaaaggaccggttcatcaacttcttgtaggcaataccataaattcttcttattttcccacatc atccgttgcattcgatatcagtgagaaaggctaaaggaaacgaaagatggtttatgttttgacagaccagtcctac attgatgtttacctgagttcagagattcttaccccattaagtacatccacgctttgaaagcaacaatttattacttctt gacggtccaaagggaaactctaaatgctcagacttttcacacaagaataatcaggttctgttccttaaactctggat tgcactcctacatggaaatgcctctagagtgtattctcacagaaaagagaaaaaagagatccacaaagaagg aagtgtttaatatccttcaggctgcatatgtcagcaagcccgggggcccagcttgctagacaaaatagggagccagcc tgaatgatgacattctctttgggtgttcgcacaaagcaagccagattctgccgaaccaatggatcgatctgcaat gtgtgcatttcctatcaaatatgtcaacgacttcttcaacaagatcgtcaacaaaaacaatgtgagatgtctccagc attttatggacccaatcatgagcactgtttaataggacacttctgagaaaattcatcaggctgtgaagccgccgctg atgaatatcgagcagagtttaccacagctttgcagcgggttgacttattcatgggtcaattcgcggaagtcctcttaa catctatatccaccttcgtgaaaggagacctcaccatcgctaatctgggacatcagagggtcgcttcatgcaggtt gtggtttctcgatcaggaccatcaaccctcatgtgaatttctcctggactctcacccggtgtctccagaagtgattg tggagcatccattaaaccagaatggctacacactggttgtcacgggggaagaagatcaccaagatcccattgaat ggcttgggctgcagacatttccagtcctgcagtcagtgcctctctgccccaccctttgtgcagtgtggctggtgccac gacaaatgtgtgcgatcggaggaatgccccagtgggacatggactcaacagatctgtctgcctgcaatctacaa ggtttccaactagtgcaccccttgaaggagggacaaggctgaccatatggctgggacttggatttcggaggg aataataaatttgatttaaagaaaactagagttcttcctggaaatgagagctgcaccttgacttaagtgagagcac gatgaatacattgaaatgcacagttggttcctgccatgaataaacatttcaatatgtccataatttcaaatggcca

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1399.	cMET-4	artificial	aa	mgwsciilfvatatgvhseckealaksemnvnmkyqlpnftaetaiqnvilhehhiflgatnyiyvlneedlqkva eyktgpvlehpdcfpcqdcsskanlsggvwkdninmalvvdtyyddqlisegsvnrgtcqrivfphnhtadiqs evhcifspqieepnqcpdcvvsalgakvlssvkdrfinffvgntinssyfphhplhsisvnrlketkdgfmfltdqsyi dvlpefrdsypikyihafesnnfiyfltvqretlnaqtfhtriirfcslnsglhsymemplecilteklrkkrstkkevfnilqa ayvskpgaqlarqigaslnddilfgvfaqskpdsaepmdrsamcafpikyvndffnkivnknnvrclqhfygpnh ehcfnrtllrnssgceardeyraefttalqrvdlfmgqfsevlltsistfvkgdltianlgtsegrfmqvvvsrsgpstph vnflldshpvspevivehplnqngytlvvtgkkitkiplnglgcrhfqscsqclsappfvqcgwchdkcvrseecps gtwtqqiclpaiykvfptsapleggtrlticgwdfgfrrnkfdlkktrvllgnesctltlsestmntlkctvgpamnkhfn msiiisnghgttqystfsyvdpiitsispkygpmaggtlltltgnylnsgnsrhisiggktctlksvsnsilecytpaqtist efavklkidlanretsifsyredpivyeihptksfisggstitgvgknlhsvsvprmvinvheagrnftvacqhrsnsei icctpslqqlnlqlplktkaffmldgilskyfdliyvhnpvfkpfekpvmismgnenvleikgndidpeavkgevlkv gnkscenihllhseavlctvpndllklnselniewkqaisstvlgkvivqpdqnftsggggsgagviavivvvviaiva givvlvisrkkrmakyekaeikemgemhrelna
1400.	ME86H11-H	artificial	aa	QVQLVQSGAEVKRPGASVKVSCRASGYTFTSYWLHWVRQGPGQRLEWIGMIDPSNS DTRFNPNFKDRATFTVDTSASTAYMELSSLTSEDTAVYYCATYGSYVSPLDYWGQGTS VTVSS
1401.	ME86H11-HCDR1	artificial	aa	SYWLH
1402.	ME86H11-HCDR2	artificial	aa	MIDPSNSDTRFNPNFKD
1403.	ME86H11-HCDR3	artificial	aa	YGSYVSPLDY
1404.	ME86H11-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGAAGAGGCCTGGGGCTTCAGTGA

				AAGTGTCCTGCAGGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGGGGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGCCACATTCACTGTAGACACATC TGCCAGCACAGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCA
1405.	ME86H11-L	artificial	aa	DIVMTQTPFSLPVTLGETVSISCKSSQSLLYTSSQKNYLAWYLQKPGQSPQLLIYWASTR ESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYAYPWTFGGGTKLEIK
1406.	ME86H11-LCDR1	artificial	aa	KSSQSLLYTSSQKNYLA
1407.	ME86H11-LCDR2	artificial	aa	WASTRES
1408.	ME86H11-LCDR3	artificial	aa	QQYYAYPWT
1409.	ME86H11-L	artificial	nt	GACATCGTGATGACCCAGACTCCATTCTCCCTACCTGTGACACTTGGAGAGACGGT TTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAAGAACTA CTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACGTGGGAGTTTATTACTGT CAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAGTTGGAGATCAA A
1410.	ME86H11-HL	artificial	aa	QVQLVQSGAEVKRPGASVKVSCRASGYTFTSYWLHWVRQGPGQRLEWIGMIDPSNS DTRFNPNFKDRATFTVDTSASTAYMELSSLTSEDTAVYYCATYGSYVSPLDYWGQGTS VTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTLGETVSISCKSSQSLLYTSSQKNY LAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQ YYAYPWTFGGGTKLEIK
1411.	ME86H11-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGAAGAGGCCTGGGGCTTCAGTGA AAGTGTCCTGCAGGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGGGGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGCCACATTCACTGTAGACACATC TGCCAGCACAGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCATTCTCCCTACCTGTGACACTT GGAGAGACGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACGTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG

				TTGGAGATCAAA
1412.	ME86H11 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASVKVSCRASGYTFTSYWLHWVRQGPGQRLEWIGMIDPSNS DTRFNPNFKDRATFTVDTSASTAYMELSSLTSEDTAVYYCATYGSYVSPLDYWGQGTS VTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTLGETVSISCKSSQSLLYTSSQKNY LAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQ YYAYPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1413.	ME86H11 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGAAGAGGCCTGGGGCTTCAGTGA AAGTGTCCTGCAGGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGGGGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGCCACATTCACTGTAGACACATC TGCCAGCACAGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCATTCTCCCTACCTGTGACACTT GGAGAGACGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAG GAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTC ACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGA ATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATCTACAA ATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTC TCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCA CACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGG GTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCT CGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCC CTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG

				GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1414.	ME62A12-H	artificial	aa	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYWLHWVRQTPGQGLEWIGMIDPSNSD TRFNPNFKDKVTFTVDTSASTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSS
1415.	ME62A12-HCDR1	artificial	aa	SYWLH
1416.	ME62A12-HCDR2	artificial	aa	MIDPSNSDTRFNPNFKD
1417.	ME62A12-HCDR3	artificial	aa	YGSYVSPLDY
1418.	ME62A12-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGGTGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGACGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAAGGTCACATTCACTGTAGACACATC TGCCAGCACAGCCTACATGGAACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCA
1419.	ME62A12-L	artificial	aa	DIVMTQTPLSLPVTLGEKVSVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWAST RESGVPDRFSGSGSGTDFTLTISRVEAEDLGVYYCQQYYAYPWTFGGGTKLEIK
1420.	ME62A12-LCDR1	artificial	aa	KSSQSLLYTSSQKNYLA
1421.	ME62A12-LCDR2	artificial	aa	WASTRES
1422.	ME62A12-LCDR3	artificial	aa	QQYYAYPWT
1423.	ME62A12-L	artificial	nt	GACATCGTGATGACCCAGACTCCACTCTCCCTACCTGTGACACTTGGAGAGAAGGT TTCTGTCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAAGAACTA CTTGGCCTGGTACCAGCAGAAACCAGGTCAGTCTCCTAAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GATTTCACTCTCACAATCTCCAGAGTGGAGGCTGAGGACCTGGGAGTTTATTACTGT CAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAGTTGGAGATCAA A
1424.	ME62A12-HL	artificial	aa	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYWLHWVRQTPGQGLEWIGMIDPSNSD TRFNPNFKDKVTFTVDTSASTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTLGEKVSVSCKSSQSLLYTSSQKNY LAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISRVEAEDLGVYYCQQ YYAYPWTFGGGTKLEIK
1425.	ME62A12-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGGTGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGACGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAAGGTCACATTCACTGTAGACACATC TGCCAGCACAGCCTACATGGAACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT

				ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCACTCTCCCTACCTGTGACACTT GGAGAGAAGGTTTCTGTCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGTCAGTCTCCTAAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCACAATCTCCAGAGTGGAGGCTGAGGACCTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAA
1426.	ME62A12 HL x I2C HL	artificial	aa	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYWLHWVRQTPGQGLEWIGMIDPSNSD TRFNPNFKDKVTFTVDTSASTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTLGEKVSVSCKSSQSLLYTSSQKNY LAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISRVEAEDLGVYYCQQ YYAYPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1427.	ME62A12 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGGTGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGACGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAAGGTCACATTCACTGTAGACACATC TGCCAGCACAGCCTACATGGAACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCACTCTCCCTACCTGTGACACTT GGAGAGAAGGTTTCTGTCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGTCAGTCTCCTAAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCACAATCTCCAGAGTGGAGGCTGAGGACCTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAG GAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTC ACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGA ATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAA

				ATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTC TCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCA CACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGG GTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCT CGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCC CTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1428.	ME63F2-H	artificial	aa	QVQLVQSGAEVKRPGASVKVSCKASGYTFTSYWLHWVRQTPGQRLEWIGMIDPSNSD TRFNPNFKDRVTMTVDTSANTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTS VTVSS
1429.	ME63F2-HCDR1	artificial	aa	SYWLH
1430.	ME63F2-HCDR2	artificial	aa	MIDPSNSDTRFNPNFKD
1431.	ME63F2-HCDR3	artificial	aa	YGSYVSPLDY
1432.	ME63F2-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGAAGAGGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGACGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATGACTGTAGACACATC TGCCAACACAGCCTACATGGAACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCA
1433.	ME63F2-L	artificial	aa	DIVMTQTPLSLPVTVGEQASISCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCQQYYAYPWTFGGGTKLEIK
1434.	ME63F2-LCDR1	artificial	aa	KSSQSLLYTSSQKNYLA
1435.	ME63F2-LCDR2	artificial	aa	WASTRES
1436.	ME63F2-LCDR3	artificial	aa	QQYYAYPWT
1437.	ME63F2-L	artificial	nt	GACATCGTGATGACCCAGACTCCACTCTCCCTACCTGTGACAGTTGGAGAGCAGGC TTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAAGAACTA CTTGGCCTGGTACCAGCAGAAACCAGGTCAGTCTCCTAAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACCTGGGAGTTTATTACTGT CAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAGTTGGAGATCAA A
1438.	ME63F2-HL	artificial	aa	QVQLVQSGAEVKRPGASVKVSCKASGYTFTSYWLHWVRQTPGQRLEWIGMIDPSNSD TRFNPNFKDRVTMTVDTSANTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTS

				VTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTVGEQASISCKSSQSLLYTSSQKNY LAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCQQ YYAYPWTFGGGTKLEIK
1439.	ME63F2-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGAAGAGGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGACGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATGACTGTAGACACATC TGCCAACACAGCCTACATGGAACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCACTCTCCCTACCTGTGACAGTT GGAGAGCAGGCTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGTCAGTCTCCTAAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACCTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAA
1440.	ME63F2 HL x I2C HL	artificial	aa	QVQLVQSGAEVKRPGASVKVSCKASGYTFTSYWLHWVRQTPGQRLEWIGMIDPSNSD TRFNPNFKDRVTMTVDTSANTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTS VTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTVGEQASISCKSSQSLLYTSSQKNY LAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCQQ YYAYPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1441.	ME63F2 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGAAGAGGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGACGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATGACTGTAGACACATC TGCCAACACAGCCTACATGGAACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCACTCTCCCTACCTGTGACAGTT GGAGAGCAGGCTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGTCAGTCTCCTAAACTGCT

				GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACCTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAG GAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTC ACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGA ATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAA ATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTC TCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCA CACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGG GTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCT CGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCCTGCTTGGAGGCAAGGCTGCC CTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1442.	ME62D11-H	artificial	aa	QVQLVQSGPEVVKPGASVKVSCKASGYTFTSYWLHWVKQAPGQGLEWIGMIDPSNSD TRFNPNFKDRATLTVDTSASTAYMLLSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSS
1443.	ME62D11-HCDR1	artificial	aa	SYWLH
1444.	ME62D11-HCDR2	artificial	aa	MIDPSNSDTRFNPNFKD
1445.	ME62D11-HCDR3	artificial	aa	YGSYVSPLDY
1446.	ME62D11-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCCTGAAGTGGTGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AAACAGGCGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGCCACATTGACTGTAGACACATC TGCCAGCACAGCCTACATGCTACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCA
1447.	ME62D11-L	artificial	aa	DIVMTQTPSSLPVTLGETVSISCKSSQSLLYTSSQKNYLAWYLQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLTISRVKAEDVAVYYCQQYYAYPWTFGGGTKLEIK
1448.	ME62D11-LCDR1	artificial	aa	KSSQSLLYTSSQKNYLA
1449.	ME62D11-LCDR2	artificial	aa	WASTRES
1450.	ME62D11-LCDR3	artificial	aa	QQYYAYPWT
1451.	ME62D11-L	artificial	nt	GACATCGTGATGACCCAGACTCCATCCTCCCTACCTGTGACACTTGGAGAGACGGT

				TTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAAGAACTA CTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GATTTCACTCTCACAATCTCCAGAGTGAAGGCTGAGGACGTGGCAGTTTATTACTGT CAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAGTTGGAGATCAA A
1452.	ME62D11-HL	artificial	aa	QVQLVQSGPEVVKPGASVKVSCKASGYTFTSYWLHWVKQAPGQGLEWIGMIDPSNSD TRFNPNFKDRATLTVDTSASTAYMLLSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQTPSSLPVTLGETVSISCKSSQSLLYTSSQKNYL AWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLTISRVKAEDVAVYYCQQY YAYPWTFGGGTKLEIK
1453.	ME62D11-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGCCTGAAGTGGTGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AAACAGGCGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGCCACATTGACTGTAGACACATC TGCCAGCACAGCCTACATGCTACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCATCCTCCCTACCTGTGACACTT GGAGAGACGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAA
1454.	ME62D11 HL x I2C HL	artificial	aa	QVQLVQSGPEVVKPGASVKVSCKASGYTFTSYWLHWVKQAPGQGLEWIGMIDPSNSD TRFNPNFKDRATLTVDTSASTAYMLLSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQTPSSLPVTLGETVSISCKSSQSLLYTSSQKNYL AWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLTISRVKAEDVAVYYCQQY YAYPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1455.	ME62D11 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGCCTGAAGTGGTGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT

				AAACAGGCGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGCCACATTGACTGTAGACACATC TGCCAGCACAGCCTACATGCTACTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCATCCTCCCTACCTGTGACACTT GGAGAGACGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCACAATCTCCAGAGTGAAGGCTGAGGACGTGGCA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAG GAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTC ACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAGGGTTTGGA ATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAA ATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTC TCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCA CACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGG GTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCT CGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCC CTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1456.	ME62C10-H	artificial	aa	QVQLVQSGAELKKPGASVKVSCKASGYTFTSYWLHWVKQAPGQRLEWIGMIDPSNSD TRFNPNFKDRVTITVDTSANTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSS
1457.	ME62C10-HCDR1	artificial	aa	SYWLH
1458.	ME62C10-HCDR2	artificial	aa	MIDPSNSDTRFNPNFKD
1459.	ME62C10-HCDR3	artificial	aa	YGSYVSPLDY
1460.	ME62C10-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAACTGAAGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AAACAGGCGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATCACTGTAGACACATC TGCCAACACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT

				ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCA
1461.	ME62C10-L	artificial	aa	DIVMTQTPPSLTVTPGEQVSISCKSSQSLLYTSSQKNYLAWYLQKPGQSPKLLIYWAST RESGVPDRFSGSGSGTDFTLKISSVEADDVGVYYCQQYYAYPWTFGGGTKLEIK
1462.	ME62C10-LCDR1	artificial	aa	KSSQSLLYTSSQKNYLA
1463.	ME62C10-LCDR2	artificial	aa	WASTRES
1464.	ME62C10-LCDR3	artificial	aa	QQYYAYPWT
1465.	ME62C10-L	artificial	nt	GACATCGTGATGACCCAGACTCCACCCTCCCTAACTGTGACACCTGGAGAGCAGGT TTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAAGAACTA CTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTAAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GATTTCACTCTCAAAATCTCCAGTGTGGAGGCTGACGACGTGGGAGTTTATTACTGT CAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAGTTGGAGATCAA A
1466.	ME62C10-HL	artificial	aa	QVQLVQSGAELKKPGASVKVSCKASGYTFTSYWLHWVKQAPGQRLEWIGMIDPSNSD TRFNPNFKDRVTITVDTSANTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQTPPSLTVTPGEQVSISCKSSQSLLYTSSQKNYL AWYLQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISSVEADDVGVYYCQQY YAYPWTFGGGTKLEIK
1467.	ME62C10-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAACTGAAGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AAACAGGCGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATCACTGTAGACACATC TGCCAACACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCACACCTCCCTAACTGTGACACCT GGAGAGCAGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTAAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGTGTGGAGGCTGACGACGTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAA
1468.	ME62C10 HL x I2C HL	artificial	aa	QVQLVQSGAELKKPGASVKVSCKASGYTFTSYWLHWVKQAPGQRLEWIGMIDPSNSD TRFNPNFKDRVTITVDTSANTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQTPPSLTVTPGEQVSISCKSSQSLLYTSSQKNYL

				AWYLQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISSVEADDVGVYYCQQY YAYPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1469.	ME62C10 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAACTGAAGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAAGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AAACAGGCGCCTGGACAAAGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATCACTGTAGACACATC TGCCAACACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCACACCCTCCCTAACTGTGACACCT GGAGAGCAGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTAAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGTGTGGAGGCTGACGACGTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAG GAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTC ACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGA ATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAA ATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTC TCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCA CACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGG GTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCT CGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCC CTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1470.	ME62A4-H	artificial	aa	QVQLVQSGAEVMKPGASVKVSCRASGYTFTSYWLHWVRQAPGQGLEWIGMIDPSNS DTRFNPNFKDRVTMTVDTSSSTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGT SVTVSS

1471.	ME62A4-HCDR1	artificial	aa	SYWLH
1472.	ME62A4-HCDR2	artificial	aa	MIDPSNSDTRFNPNFKD
1473.	ME62A4-HCDR3	artificial	aa	YGSYVSPLDY
1474.	ME62A4-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGATGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAGGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGGCGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATGACTGTAGACACATC TTCCAGCACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCA
1475.	ME62A4-L	artificial	aa	DIVMTQTPFSLPVTAGETVSISCKSSQSLLYTSSQKNYLAWYLQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYAYPWTFGGGTKLEIK
1476.	ME62A4-LCDR1	artificial	aa	KSSQSLLYTSSQKNYLA
1477.	ME62A4-LCDR2	artificial	aa	WASTRES
1478.	ME62A4-LCDR3	artificial	aa	QQYYAYPWT
1479.	ME62A4-L	artificial	nt	GACATCGTGATGACCCAGACTCCATTCTCCCTACCTGTGACAGCTGGAGAGACGGT TTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAAGAACTA CTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACGTGGGAGTTTATTACTGT CAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAGTTGGAGATCAA A
1480.	ME62A4-HL	artificial	aa	QVQLVQSGAEVMKPGASVKVSCRASGYTFTSYWLHWVRQAPGQGLEWIGMIDPSNS DTRFNPNFKDRVTMTVDTSSSTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGT SVTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTAGETVSISCKSSQSLLYTSSQKN YLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQ QYYAYPWTFGGGTKLEIK
1481.	ME62A4-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGATGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAGGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGGCGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATGACTGTAGACACATC TTCCAGCACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCATTCTCCCTACCTGTGACAGCT GGAGAGACGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT

				CAGAAGAACTACTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACGTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAA
1482.	ME62A4 HL x I2C HL	artificial	aa	QVQLVQSGAEVMKPGASVKVSCRASGYTFTSYWLHWVRQAPGQGLEWIGMIDPSNS DTRFNPNFKDRVTMTVDTSSSTAYMELSSLRSEDTAVYYCATYGSYVSPLDYWGQGT SVTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTAGETVSISCKSSQSLLYTSSQKN YLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQ QYYAYPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1483.	ME62A4 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGGGCTGAAGTGATGAAGCCTGGGGCTTCAGTGA AAGTGTCCTGCAGGGCTTCGGGCTATACCTTCACCAGCTACTGGTTGCACTGGGTT AGACAGGCGCCTGGACAAGGGCTTGAGTGGATAGGCATGATTGATCCTTCCAATAG TGACACTAGGTTTAATCCGAACTTCAAGGACAGGGTCACAATGACTGTAGACACATC TTCCAGCACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCCACATATGGTAGCTACGTTTCCCCTCTGGACTACTGGGGTCAAGGA ACCTCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGACATCGTGATGACCCAGACTCCATCTCCCTACCTGTGACAGCT GGAGAGACGGTTTCTATCAGCTGCAAGTCCAGTCAGTCCCTTTTATATACTAGCAGT CAGAAGAACTACTTGGCCTGGTACCTGCAGAAACCAGGTCAGTCTCCTCAACTGCT GATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTG GATCTGGGACAGATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACGTGGGA GTTTATTACTGTCAGCAATATTATGCCTATCCGTGGACGTTCGGTGGAGGCACAAAG TTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAG GAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTC ACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGA ATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCA GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAA ATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCA CCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTC TCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCA

				CACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGG GTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCT CGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCC CTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATG GTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1484.	ME75H6-H	murine	aa	EVQLLEQSGAELVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG YANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDF WGQGTTVTVSS
1485.	ME75H6-HCDR1	murine	aa	KYWIG
1486.	ME75H6-HCDR2	murine	aa	DIHPGGGYANYNEKFKG
1487.	ME75H6-HCDR3	murine	aa	SGYDYGSSYDYHGMDF
1488.	ME75H6-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTATGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCCGC CATCTATTACTGTGCAAGATCGGGGTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1489.	ME75H6-L	murine	aa	ELQMTQSPASLSASVGEPVTFTCRASENIYSYLAWYQQKQGKSPQLLIYGATNLADGM SSRFSGSGSGRQYSLKISSLHPDDVATYYCQNVLSTPYTFGGGTKLEIK
1490.	ME75H6-LCDR1	murine	aa	RASENIYSYLA
1491.	ME75H6-LCDR2	murine	aa	GATNLAD
1492.	ME75H6-LCDR3	murine	aa	QNVLSTPYT
1493.	ME75H6-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACCTGT CACCTTCACATGTCGAGCAAGTGAGAATATTTACAGTTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGATCTATGGTGCAACCAACTTGGCAGATG GCATGTCATCGAGGTTCAGTGGCAGTGGATCTGGTAGACAGTATTCTCTCAAGATC AGTAGCCTGCATCCTGACGATGTTGCAACGTATTACTGTCAAAATGTGTTAAGTACT CCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1494.	ME75H6-HL	murine	aa	EVQLLEQSGAELVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG YANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDF WGQGTTVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGEPVTFTCRASENIY SYLAWYQQKQGKSPQLLIYGATNLADGMSSRFSGSGSGRQYSLKISSLHPDDVATYYC QNVLSTPYTFGGGTKLEIK
1495.	ME75H6-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTTAGGCCTGGGACTTCAG

				TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTATGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCCGC CATCTATTACTGTGCAAGATCGGGGTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTC CAGCCTCCCTATCTGCATCTGTGGGAGAACCTGTCACCTTCACATGTCGAGCAAGT GAGAATATTTACAGTTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAG CTCCTGATCTATGGTGCAACCAACTTGGCAGATGGCATGTCATCGAGGTTCAGTGG CAGTGGATCTGGTAGACAGTATTCTCTCAAGATCAGTAGCCTGCATCCTGACGATGT TGCAACGTATTACTGTCAAAATGTGTTAAGTACTCCGTACACGTTCGGAGGGGGGA CCAAGCTTGAGATCAAA
1496.	ME75H6 HL x I2C HL	murine	aa	EVQLLEQSGAELVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG YANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDF WGQGTTVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGEPVTFTCRASENIY SYLAWYQQKQGKSPQLLIYGATNLADGMSSRFSGSGSGRQYSLKISSLHPDDVATYYC QNVLSTPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1497.	ME75H6 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTATGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCCGC CATCTATTACTGTGCAAGATCGGGGTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTC CAGCCTCCCTATCTGCATCTGTGGGAGAACCTGTCACCTTCACATGTCGAGCAAGT GAGAATATTTACAGTTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAG CTCCTGATCTATGGTGCAACCAACTTGGCAGATGGCATGTCATCGAGGTTCAGTGG CAGTGGATCTGGTAGACAGTATTCTCTCAAGATCAGTAGCCTGCATCCTGACGATGT TGCAACGTATTACTGTCAAAATGTGTTAAGTACTCCGTACACGTTCGGAGGGGGGA CCAAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTC

				TGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTG
				GATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGT
				TTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG
				ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATC
				TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG
				GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG
				GTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT
				GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC
				AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA
				ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG
				TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC
				TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC
				TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
1498.	ME99B1-H	murine	aa	EVQLLEQSGAELVRPGTSVKISCKATGYTFSNYWISWVKYRPGHGLEWIGDIYPGGSYT NYNEKFKGKVTLTADTSSRTAYMQLSGLTFEDSAIYYCARSGYDYGSDYDYHGMDYW GQGTTVTVSSG
1499.	ME99B1-HCDR1	murine	aa	NYWIS
1500.	ME99B1-HCDR2	murine	aa	DIYPGGSYTNYNEKFKG
1501.	ME99B1-HCDR3	murine	aa	SGYDYGSDYDYHGMDY
1502.	ME99B1-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAG TGAAGATTTCCTGCAAGGCTACTGGGTACACCTTCAGTAATTACTGGATAAGTTGGG TAAAGTATAGGCCTGGACATGGTCTTGAGTGGATTGGAGATATTTACCCTGGAGGC AGTTATACTAATTACAATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACACA TCCTCCAGGACAGCCTACATGCAGCTCAGCGGCCTGACATTTGAGGACTCTGCCAT CTACTACTGTGCAAGATCGGGGTATGACTACGGTAGTGACTACGATTACCATGGTAT GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1503.	ME99B1-L	murine	aa	ELQMTQSPASLSASVGETVTITCRASENIYSNLAWYQQKQGKSPQLLVYAATNLADGVP SRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASYPYTFGGGTKLEIK
1504.	ME99B1-LCDR1	murine	aa	RASENIYSNLA
1505.	ME99B1-LCDR2	murine	aa	AATNLAD
1506.	ME99B1-LCDR3	murine	aa	LQYASYPYT
1507.	ME99B1-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGAGAATATTTACAGTAATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATGCTGCAACAAACTTAGCAGATG GTGTGCCATCAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATC AGCAGCCTTGAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTATC CGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1508.	ME99B1-HL	murine	aa	EVQLLEQSGAELVRPGTSVKISCKATGYTFSNYWISWVKYRPGHGLEWIGDIYPGGSYT NYNEKFKGKVTLTADTSSRTAYMQLSGLTFEDSAIYYCARSGYDYGSDYDYHGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASENIYSN LAWYQQKQGKSPQLLVYAATNLADGVPSRFSGSRSGSDYSLTISSLESEDFVDYYCLQ YASYPYTFGGGTKLEIK
1509.	ME99B1-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAG TGAAGATTTCCTGCAAGGCTACTGGGTACACCTTCAGTAATTACTGGATAAGTTGGG TAAAGTATAGGCCTGGACATGGTCTTGAGTGGATTGGAGATATTTACCCTGGAGGC AGTTATACTAATTACAATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACACA TCCTCCAGGACAGCCTACATGCAGCTCAGCGGCCTGACATTTGAGGACTCTGCCAT CTACTACTGTGCAAGATCGGGGTATGACTACGGTAGTGACTACGATTACCATGGTAT

				GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAG CCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGAG AATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTC CTGGTCTATGCTGCAACAAACTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAG TAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGT AGACTATTACTGTCTACAATATGCTAGTTATCCGTACACGTTCGGAGGGGGGACCAA GCTTGAGATCAAA
1510.	ME99B1 HL x I2C HL	murine	aa	EVQLLEQSGAELVRPGTSVKISCKATGYTFSNYWISWVKYRPGHGLEWIGDIYPGGSYT NYNEKFKGKVTLTADTSSRTAYMQLSGLTFEDSAIYYCARSGYDYGSDYDYHGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASENIYSN LAWYQQKQGKSPQLLVYAATNLADGVPSRFSGSRSGSDYSLTISSLESEDFVDYYCLQ YASYPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1511.	ME99B1 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAG TGAAGATTTCCTGCAAGGCTACTGGGTACACCTTCAGTAATTACTGGATAAGTTGGG TAAAGTATAGGCCTGGACATGGTCTTGAGTGGATTGGAGATATTTACCCTGGAGGC AGTTATACTAATTACAATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACACA TCCTCCAGGACAGCCTACATGCAGCTCAGCGGCCTGACATTTGAGGACTCTGCCAT CTACTACTGTGCAAGATCGGGGTATGACTACGGTAGTGACTACGATTACCATGGTAT GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAG CCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGAG AATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTC CTGGTCTATGCTGCAACAAACTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAG TAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGT AGACTATTACTGTCTACAATATGCTAGTTATCCGTACACGTTCGGAGGGGGGACCAA GCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA

				ACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAAACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGAGGAACCAAACTGACTGTCCTA
1512.	ME05D7-H	murine	aa	EVQLLEQSGAELVRPGTSVKVSCKASGYAFTHYLIEWVKQRPGQGLEWIGMINPENTD TTYNEKFRDKAILTVDKSSNTAYMQLSSLTSDDSAVYFCARQEITSDFDFWGQGTTVTV SS
1513.	ME05D7-HCDR1	murine	aa	HYLIE
1514.	ME05D7-HCDR2	murine	aa	MINPENTDTTYNEKFRD
1515.	ME05D7-HCDR3	murine	aa	QEITSDFDF
1516.	ME06D7-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAG TGAAGGTGTCCTGCAAGGCTTCTGGATACGCCTTCACTCATTACTTAATAGAGTGGG TGAAGCAGAGGCCTGGACAGGGCCTTGAGTGGATTGGAATGATTAATCCTGAAAAT ACTGATACTACCTACAATGAGAAGTTCAGGGACAAGGCAATACTGACTGTAGACAAA TCCTCCAACACTGCCTACATGCAGCTCAGCAGCCTGACTTCTGATGACTCTGCGGT CTATTTCTGTGCAAGACAGGAGATTACGGTCGGACTTTGACTTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCA
1517.	ME05D7-L	murine	aa	ELVLTQSPTTMAASPGEKITITCSASSSISSNYLHWYQQKPGFSPKLLIYRTSNLASGVP ARFSGSGSGTSYSLTIGTMEAEDVATYYCQQGSSIPYTFGGGTKLEIK
1518.	ME05D7-LCDR1	murine	aa	SASSSISSNYLH
1519.	ME05D7-LCDR2	murine	aa	RTSNLAS
1520.	ME05D7-LCDR3	murine	aa	QQGSSIPYT
1521.	ME05D7-L	murine	nt	GAGCTCGTGCTCACCCAGTCTCCAACCACCATGGCTGCATCTCCCGGGGAGAAGA TCACTATCACCTGCAGTGCCAGCTCAAGTATAAGTTCCAATTACTTGCATTGGTATC AGCAGAAGCCAGGATTCTCCCCTAAACTCTTGATTTATAGGACATCCAATCTGGCTT CTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACA ATTGGCACCATGGAGGCTGAAGATGTTGCCACTTACTACTGCCAGCAGGGTAGTAG TATACCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1522.	ME05D7-HL	murine	aa	EVQLLEQSGAELVRPGTSVKVSCKASGYAFTHYLIEWVKQRPGQGLEWIGMINPENTD TTYNEKFRDKAILTVDKSSNTAYMQLSSLTSDDSAVYFCARQEITSDFDFWGQGTTVTV SSGGGGSGGGGSGGGGSELVLTQSPTTMAASPGEKITITCSASSSISSNYLHWYQQKP GFSPKLLIYRTSNLASGVPARFSGSGSGTSYSLTIGTMEAEDVATYYCQQGSSIPYTFG

				GGTKLEIK
1523.	ME05D7-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAG TGAAGGTGTCCTGCAAGGCTTCTGGATACGCCTTCACTCATTACTTAATAGAGTGGG TGAAGCAGAGGCCTGGACAGGGCCTTGAGTGGATTGGAATGATTAATCCTGAAAAT ACTGATACTACCTACAATGAGAAGTTCAGGGACAAGGCAATACTGACTGTAGACAAA TCCTCCAACACTGCCTACATGCAGCTCAGCAGCCTGACTTCTGATGACTCTGCGGT CTATTTCTGTGCAAGACAGGAGATTACGGTCGGACTTTGACTTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGAGCTCGTGCTCACCCAGTCTCCAACCACCATGGCTGCATCTCCC GGGGAGAAGATCACTATCACCTGCAGTGCCAGCTCAAGTATAAGTTCCAATTACTTG CATTGGTATCAGCAGAAGCCAGGATTCTCCCCTAAACTCTTGATTTATAGGACATCC AATCTGGCTTCTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA CTCTCTCACAATTGGCACCATGGAGGCTGAAGATGTTGCCACTTACTACTGCCAGC AGGGTAGTAGTATACCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1524.	ME05D7 HL x I2C HL	murine	aa	EVQLLEQSGAELVRPGTSVKVSCKASGYAFTHYLIEWVKQRPGQGLEWIGMINPENTD TTYNEKFRDKAILTVDKSSNTAYMQLSSLTSDDSAVYFCARQEITSDFDFWGQGTTVTV SSGGGGSGGGGSGGGGSELVLTQSPTTMAASPGEKITITCSASSSISSNYLHWYQQKP GFSPKLLIYRTSNLASGVPARFSGSGSGTSYSLTIGTMEAEDVATYYCQQGSSIPYTFG GGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1525.	ME05D7 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAG TGAAGGTGTCCTGCAAGGCTTCTGGATACGCCTTCACTCATTACTTAATAGAGTGGG TGAAGCAGAGGCCTGGACAGGGCCTTGAGTGGATTGGAATGATTAATCCTGAAAAT ACTGATACTACCTACAATGAGAAGTTCAGGGACAAGGCAATACTGACTGTAGACAAA TCCTCCAACACTGCCTACATGCAGCTCAGCAGCCTGACTTCTGATGACTCTGCGGT CTATTTCTGTGCAAGACAGGAGATTACGGTCGGACTTTGACTTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTG GTGGTGGTTCTGAGCTCGTGCTCACCCAGTCTCCAACCACCATGGCTGCATCTCCC GGGGAGAAGATCACTATCACCTGCAGTGCCAGCTCAAGTATAAGTTCCAATTACTTG CATTGGTATCAGCAGAAGCCAGGATTCTCCCCTAAACTCTTGATTTATAGGACATCC AATCTGGCTTCTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA CTCTCTCACAATTGGCACCATGGAGGCTGAAGATGTTGCCACTTACTACTGCCAGC AGGGTAGTAGTATACCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAATCC

				GGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAG CCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTAC GCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCA TAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTT CACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAA AACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCT ACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGT GGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGA CTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGC TCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACC AGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACT CCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1526.	ME05B7-H	murine	aa	EVQLLEQSGAELVRPGTSVKISCKTTGYTFGYYWISWLKQRPGHGLEWIGDIYPGGGY TNYHEKFKGKVTLTADTSSRTAYMQLSSLTFEDSAIYYCARSGYDYGSDYDYHGMDYW GQGTTVTVSS
1527.	ME05B7-HCDR1	murine	aa	YYWIS
1528.	ME05B7-HCDR2	murine	aa	DIYPGGGYTNYHEKFKG
1529.	ME05B7-HCDR3	murine	aa	SGYDYGSDYDYHGMDY
1530.	ME05B7-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTTAGGCCTGGGACTTCAG TGAAGATTTCCTGCAAGACTACTGGGTACACCTTCGGTTATTACTGGATAAGTTGGT TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT GGTTACACTAACTACCATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACAC ATCCTCCAGGACAGCCTACATGCAGCTCAGCAGCCTGACATTTGAGGACTCTGCCA TCTATTACTGTGCAAGATCGGGATATGACTACGGTAGTGACTACGATTATCATGGTA TGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1531.	ME05B7-L	murine	aa	ELVMTQTPSSLSASLGDRVTISCRASQGISNYLNWYQQKPDGSVKLLIYYTSRLHSGVP SRFSGSGSGTDYSLTISNLDQEDIATYFCQQGNTLPWTFGGGTKLEIK
1532.	ME05B7-LCDR1	murine	aa	RASQGISNYLN
1533.	ME05B7-LCDR2	murine	aa	YTSRLHS
1534.	ME05B7-LCDR3	murine	aa	QQGNTLP
1535.	ME05B7-L	murine	nt	GAGCTCGTGATGACCCAGACTCCATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGT CACCATCAGTTGCAGGGCAAGTCAGGGCATTAGCAATTATTTAAACTGGTATCAGCA GAAACCAGATGGATCTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGG AGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAG

				CAACCTGGATCAAGAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCC GTGGACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1536.	ME05B7-HL	murine	aa	EVQLLEQSGAELVRPGTSVKISCKTTGYTFGYYWISWLKQRPGHGLEWIGDIYPGGGY TNYHEKFKGKVTLTADTSSRTAYMQLSSLTFEDSAIYYCARSGYDYGSDYDYHGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQTPSSLSASLGDRVTISCRASQGISNY LNWYQQKPDGSVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLDQEDIATYFCQQG NTLPWTFGGGTKLEIK
1537.	ME05B7-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTTAGGCCTGGGACTTCAG TGAAGATTTCCTGCAAGACTACTGGGTACACCTTCGGTTATTACTGGATAAGTTGGT TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT GGTTACACTAACTACCATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACAC ATCCTCCAGGACAGCCTACATGCAGCTCAGCAGCCTGACATTTGAGGACTCTGCCA TCTATTACTGTGCAAGATCGGGATATGACTACGGTAGTGACTACGATTATCATGGTA TGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGATGACCCAGACTCCA TCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCA GGGCATTAGCAATTATTTAAACTGGTATCAGCAGAAACCAGATGGATCTGTTAAACT CCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCAGTGGCAG TGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGATCAAGAAGATATTGC CACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGAGGGGGGACCA AGCTTGAGATCAAA
1538.	ME05B7 HL x I2C HL	murine	aa	EVQLLEQSGAELVRPGTSVKISCKTTGYTFGYYWISWLKQRPGHGLEWIGDIYPGGGY TNYHEKFKGKVTLTADTSSRTAYMQLSSLTFEDSAIYYCARSGYDYGSDYDYHGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQTPSSLSASLGDRVTISCRASQGISNY LNWYQQKPDGSVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLDQEDIATYFCQQG NTLPWTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1539.	ME05B7 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGTTAGGCCTGGGACTTCAG TGAAGATTTCCTGCAAGACTACTGGGTACACCTTCGGTTATTACTGGATAAGTTGGT TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT GGTTACACTAACTACCATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACAC ATCCTCCAGGACAGCCTACATGCAGCTCAGCAGCCTGACATTTGAGGACTCTGCCA TCTATTACTGTGCAAGATCGGGATATGACTACGGTAGTGACTACGATTATCATGGTA

				TGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGATGACCCAGACTCCA TCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCA GGGCATTAGCAATTATTTAAACTGGTATCAGCAGAAACCAGATGGATCTGTTAAACT CCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCAGTGGCAG TGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGATCAAGAAGATATTGC CACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGAGGGGGGACCA AGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGG AGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGAT TCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTG GAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATT CAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTAC AAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGG AACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGT CACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGG TTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGT CACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACT GGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTC CTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTG CCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTA TGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1540.	ME05F6-H	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSS
1541.	ME05F6-HCDR1	murine	aa	KYWIG
1542.	ME05F6-HCDR2	murine	aa	DIHPGGGFANYNEKFKG
1543.	ME05F6-HCDR3	murine	aa	SGYDYGSSYDYHGMDY
1544.	ME05F6-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1545.	ME05F6-L	murine	aa	ELVMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASTLDSGVPK RFSGSRSGSDYSLTISSLESEDFADYYCLQYASYPPTFGGGTKLEIK

1546.	ME05F6-LCDR1	murine	aa	RASQEISGYLS
1547.	ME05F6-LCDR2	murine	aa	AASTLDS
1548.	ME05F6-LCDR3	murine	aa	LQYASYPPT
1549.	ME05F6-L	murine	nt	GAGCTCGTGATGACACAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGT CAGTCTCACTTGTCGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGC AGAAACCAGATGGAACTATTAAACGCCTGATCTACGCCGCATCCACTTTAGATTCTG GTGTCCCAAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCA GCAGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTATC CTCCCACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1550.	ME05F6-HL	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASLGERVSLTCRASQEIS GYLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCL QYASYPPTFGGGTKLEIK
1551.	ME05F6-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTC CATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGT CAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACTATTAAA CGCCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAAAGGTTCAGTGG CAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTT TGCAGACTATTACTGTCTACAATATGCTAGTTATCCTCCCACGTTCGGAGGGGGGGA CCAAGCTTGAGATCAAA
1552.	ME05F6 HL x I2C HL	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASLGERVSLTCRASQEIS GYLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCL QYASYPPTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT

				QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1553.	ME05F6 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCC CATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGT CAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACTATTAAA CGCCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAAAGGTTCAGTGG CAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTT TGCAGACTATTACTGTCTACAATATGCTAGTTATCCTCCCACGTTCGGAGGGGGGA CCAAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTC TGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTG GATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGT TTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1554.	ME06C6-H	murine	aa	EVQLLEQSGAELVRPGTSVKIPCKATGYTFSYYWIGWVKQRPGHGLEWIGDIYPGGGY SNYNEKFKGKATLTADTSSSTAYMQLSGLTSEDSAIYYCARSGYDYGSDYDYHGLDYW GQGTTVTVSS
1555.	ME06C6-HCDR1	murine	aa	YYWIG
1556.	ME06C6-HCDR2	murine	aa	DIYPGGGYSNYNEKFKG
1557.	ME06C6-HCDR3	murine	aa	SGYDYGSDYDYHGLDY

1558.	ME06C6-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAACTGGTAAGGCCTGGGACTTCAG TGAAGATTCCCTGCAAGGCTACTGGATACACCTTCAGTTATTACTGGATAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT GGTTATAGTAACTACAATGAGAAATTCAAGGGAAAGGCCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTACATGCAGCTCAGCGGCCTGACATCTGAGGACTCTGCCA TCTATTACTGTGCAAGATCGGGATATGACTACGGTAGTGACTACGATTACCATGGTC TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1559.	ME06C6-L	murine	aa	ELVLTQSPASLAVSLGQRATISCRASESVEYYGTSLMQWYQQKPGQPPKLLIYAASNVE SGVPARFSGSGSGTDFSLNIHPVEEDDIAMYFCQQSRKVPYTFGGGTKLEIK
1560.	ME06C6-LCDR1	murine	aa	RASESVEYYGTSLMQ
1561.	ME06C6-LCDR2	murine	aa	AASNVES
1562.	ME06C6-LCDR3	murine	aa	QQSRKVPYT
1563.	ME06C6-L	murine	nt	GAGCTCGTGCTCACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGAGC CACCATCTCCTGCAGAGCCAGTGAAAGTGTTGAATATTATGGCACAAGTTTAATGCA GTGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCA ACGTAGAATCTGGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTT CAGCCTCAACATCCATCCTGTGGAGGAGGATGATATTGCAATGTATTTCTGTCAGCA AAGTAGGAAGGTTCCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1564.	ME06C6-HL	murine	aa	EVQLLEQSGAELVRPGTSVKIPCKATGYTFSYYWIGWVKQRPGHGLEWIGDIYPGGGY SNYNEKFKGKATLTADTSSSTAYMQLSGLTSEDSAIYYCARSGYDYGSDYDYHGLDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVLTQSPASLAVSLGQRATISCRASESVEYY GTSLMQWYQQKPGQPPKLLIYAASNVESGVPARFSGSGSGTDFSLNIHPVEEDDIAMY FCQQSRKVPYTFGGGTKLEIK
1565.	ME06C6-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAACTGGTAAGGCCTGGGACTTCAG TGAAGATTCCCTGCAAGGCTACTGGATACACCTTCAGTTATTACTGGATAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT GGTTATAGTAACTACAATGAGAAATTCAAGGGAAAGGCCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTACATGCAGCTCAGCGGCCTGACATCTGAGGACTCTGCCA TCTATTACTGTGCAAGATCGGGATATGACTACGGTAGTGACTACGATTACCATGGTC TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGCTCACCCAGTCTCCA GCTTCTTTGGCTGTGTCTCTAGGGCAGAGAGCCACCATCTCCTGCAGAGCCAGTGA AAGTGTTGAATATTATGGCACAAGTTTAATGCAGTGGTACCAACAGAAACCAGGACA GCCACCCAAACTCCTCATCTATGCTGCATCCAACGTAGAATCTGGGGTCCCTGCCA GGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCATCCTGTGGAG GAGGATGATATTGCAATGTATTTCTGTCAGCAAAGTAGGAAGGTTCCGTACACGTTC

				GGAGGGGGGACCAAGCTTGAGATCAAA
1566.	ME06C6 HL x I2C HL	murine	aa	EVQLLEQSGAELVRPGTSVKIPCKATGYTFSYYWIGWVKQRPGHGLEWIGDIYPGGGY SNYNEKFKGKATLTADTSSSTAYMQLSGLTSEDSAIYYCARSGYDYGSDYDYHGLDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVLTQSPASLAVSLGQRATISCRASESVEYY GTSLMQWYQQKPGQPPKLLIYAASNVESGVPARFSGSGSGTDFSLNIHPVEEDDIAMY FCQQSRKVPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1567.	ME06C6 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAACTGGTAAGGCCTGGGACTTCAG TGAAGATTCCCTGCAAGGCTACTGGATACACCTTCAGTTATTACTGGATAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT GGTTATAGTAACTACAATGAGAAATTCAAGGGAAAGGCCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTACATGCAGCTCAGCGGCCTGACATCTGAGGACTCTGCCA TCTATTACTGTGCAAGATCGGGATATGACTACGGTAGTGACTACGATTACCATGGTC TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGTGCTCACCCAGTCTCCA GCTTCTTTGGCTGTGTCTCTAGGGCAGAGAGCCACCATCTCCTGCAGAGCCAGTGA AAGTGTTGAATATTATGGCACAAGTTTAATGCAGTGGTACCAACAGAAACCAGGACA GCCACCCAAACTCCTCATCTATGCTGCATCCAACGTAGAATCTGGGGTCCCTGCCA GGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCATCCTGTGGAG GAGGATGATATTGCAATGTATTTCTGTCAGCAAAGTAGGAAGGTTCCGTACACGTTC GGAGGGGGGACCAAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCAT GTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCT CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCA ACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAA AACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTAC TGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGG CCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATC ACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTG GCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATA GGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCT TGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAA

				TATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACT GACTGTCCTA
1568.	ME06C7-H	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSS
1569.	ME06C7-HCDR1	murine	aa	KYWIG
1570.	ME06C7-HCDR2	murine	aa	DIHPGGGFANYNEKFKG
1571.	ME06C7-HCDR3	murine	aa	SGYDYGSSYDYHGMDY
1572.	ME06C7-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1573.	ME06C7-L	murine	aa	ELQMTQSPTSLAVSLGQRATISCRASQTVYYDGNNYMNWYQHKPGQPPKLLIYATSNL ESGIPARFSGSGSGTDFTLNIHPVEAEDAATYYCQQSYEDPYTFGGGTKLEIK
1574.	ME06C7-LCDR1	murine	aa	RASQTVYYDGNNYMN
1575.	ME06C7-LCDR2	murine	aa	ATSNLES
1576.	ME06C7-LCDR3	murine	aa	QQSYEDPYT
1577.	ME06C7-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAACTTCTTTGGCTGTGTCTCTCGGGCAGAGGGC CACCATCTCCTGCAGGGCCAGCCAAACTGTTTACTATGATGGTAATAATTATATGAA CTGGTATCAACACAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTACATCCAA TCTAGAATCTGGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCA CCCTCAACATCCATCCTGTGGAGGCGGAGGATGCTGCAACCTATTACTGTCAGCAA AGTTATGAGGATCCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1578.	ME06C7-HL	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSSGGGGSGGGGSGGGGSELQMTQSPTSLAVSLGQRATISCRASQTVY YDGNNYMNWYQHKPGQPPKLLIYATSNLESGIPARFSGSGSGTDFTLNIHPVEAEDAAT YYCQQSYEDPYTFGGGTKLEIK
1579.	ME06C7-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC

				ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTC CAACTTCTTTGGCTGTGTCTCTCGGGCAGAGGGCCACCATCTCCTGCAGGGCCAG CCAAACTGTTTACTATGATGGTAATAATTATATGAACTGGTATCAACACAAACCAGGA CAGCCACCCAAACTCCTCATCTATGCTACATCCAATCTAGAATCTGGGATCCCAGCC AGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGA GGCGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTTATGAGGATCCGTACACGT TCGGAGGGGGGACCAAGCTTGAGATCAAA
1580.	ME06C7 HL x I2C HL	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSSGGGGSGGGGSGGGGSELQMTQSPTSLAVSLGQRATISCRASQTVY YDGNNYMNWYQHKPGQPPKLLIYATSNLESGIPARFSGSGSGTDFTLNIHPVEAEDAAT YYCQQSYEDPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTF NKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1581.	ME06C7 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTC CAACTTCTTTGGCTGTGTCTCTCGGGCAGAGGGCCACCATCTCCTGCAGGGCCAG CCAAACTGTTTACTATGATGGTAATAATTATATGAACTGGTATCAACACAAACCAGGA CAGCCACCCAAACTCCTCATCTATGCTACATCCAATCTAGAATCTGGGATCCCAGCC AGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGA GGCGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTTATGAGGATCCGTACACGT TCGGAGGGGGGACCAAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCA GCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGC TCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGC

				AACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAA AAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGG CTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTAT CACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCT GGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAAT AGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGC TTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
1582.	ME06B7-H	murine	aa	EVQLLEQSGAELVRPGTSVKISCKATGYTFTTYWLGWVKQRPGHGLEWIGEIHPGGGY TNYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYYGMDYW GQGTTVTVSS
1583.	ME06B7-HCDR1	murine	aa	TYWLG
1584.	ME06B7-HCDR2	murine	aa	EIHPGGGYTNYNEKFKG
1585.	ME06B7-HCDR3	murine	aa	SGYDYGSSYDYYGMDY
1586.	ME06B7-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAACTGGTAAGGCCTGGGACCTCAG TGAAGATTTCCTGCAAGGCTACTGGATACACCTTCACTACTTACTGGCTAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAGATTCACCCTGGAGG TGGTTATACTAACTACAATGAGAAGTTCAAGGGCCAAGGCCACACTGACTGCAGACA CATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCCGCC ATCTATTACTGTGCAAGATCGGGGTATGACTACGGTAGTAGTTACGATTACTATGGT ATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1587.	ME06B7-L	murine	aa	ELVMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDSGVP KRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGGGTKLEIK
1588.	ME06B7-LCDR1	murine	aa	RASQDIGSSLN
1589.	ME06B7-LCDR2	murine	aa	ATSSLDS
1590.	ME06B7-LCDR3	murine	aa	LQYASSPYT
1591.	ME06B7-L	murine	nt	GAGCTCGTCATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGT CAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGC AGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTG GTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATC AGCAGCCTTGAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTC CGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1592.	ME06B7-HL	murine	aa	EVQLLEQSGAELVRPGTSVKISCKATGYTFTTYWLGWVKQRPGHGLEWIGEIHPGGGY

				TNYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYYGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASLGERVSLTCRASQDIGSS LNWLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYA SSPYTFGGGTKLEIK
1593.	ME06B7-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAACTGGTAAGGCCTGGGACCTCAG TGAAGATTTCCTGCAAGGCTACTGGATACACCTTCACTACTTACTGGCTAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAGATTCACCCTGGAGG TGGTTATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACA CATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCCGCC ATCTATTACTGTGCAAGATCGGGGTATGACTACGGTAGTAGTTACGATTACTATGGT ATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTT CTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCC ATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGTC AGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACTATTAAAC GCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTCAGTGGC AGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTT GTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGGGGGAC CAAGCTTGAGATCAAA
1594.	ME06B7 HL x I2C HL	murine	aa	EVQLLEQSGAELVRPGTSVKISCKATGYTFTTYWLGWVKQRPGHGLEWIGEIHPGGGY TNYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYYGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASLGERVSLTCRASQDIGSS LNWLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYA SSPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNW VRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1595.	ME06B7 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAACTGGTAAGGCCTGGGACCTCAG TGAAGATTTCCTGCAAGGCTACTGGATACACCTTCACTACTTACTGGCTAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAGATTCACCCTGGAGG TGGTTATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACA CATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCCGCC ATCTATTACTGTGCAAGATCGGGGTATGACTACGGTAGTAGTTACGATTACTATGGT ATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTT CTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCC ATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGTC

				AGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACTATTAAAC GCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTCAGTGGC AGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTT GTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGGGGGAC CAAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCT GGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTG GATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGT TTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1596.	ME06D1-H	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSS
1597.	ME06D1-HCDR1	murine	aa	KYWIG
1598.	ME06D1-HCDR2	murine	aa	DIHPGGGFANYNEKFKG
1599.	ME06D1-HCDR3	murine	aa	SGYDYGSSYDYHGMDY
1600.	ME06D1-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1601.	ME06D1-L	murine	aa	ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGAS TRESGVPDRFTGSGSGTDFTLTISSVQAEDLADYFCQQHYSTPYTFGGGTKLEIK
1602.	ME06D1-LCDR1	murine	aa	KSSQSLLNSGNQKNYLA
1603.	ME06D1-LCDR2	murine	aa	GASTRES

1604.	ME06D1-LCDR3	murine	aa	QQHYSTPYT
1605.	ME06D1-L	murine	nt	GAGCTCGTGATGACACAGTCTCCATCCTCCCTGACTGTGACAGCAGGAGAGGAAGGT CACTATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGGCCTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTACGGGG CATCCACTAGGGAATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACA GATTTCACTCTTACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGATTACTTCTGT CAGCAACATTATAGCACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAA A
1606.	ME06D1-HL	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLL NSGNQKNYLAWYQQKPGQPPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAED LADYFCQQHYSTPYTFGGGTKLEIK
1607.	ME06D1-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCC CATCCTCCCTGACTGTGACAGCAGGAGAAGGTCACTATGAGCTGCAAGTCCAGT CAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCCTGGTACCAGCAGAA ACCAGGGCAGCCTCCTAAACTGTTGATCTACGGGGGCATCCACTAGGGAATCTGGAG TCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGC AGTGTGCAGGCTGAAGACCTGGCAGATTACTTCTGTCAGCAACATTATAGCACTCC GTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1608.	ME06D1 HL x I2C HL	murine	aa	EVQLLEQSGAEVVRPGTSVKMSCKAAGYTFTKYWIGWVKQRPGHGLEWIGDIHPGGG FANYNEKFKGKATLTADTSSSTAYMQLSRLTSDDSAIYYCARSGYDYGSSYDYHGMDY WGQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLL NSGNQKNYLAWYQQKPGQPPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAED LADYFCQQHYSTPYTFGGGTKLEIKSGGGGSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGF TFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLA PGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

1609.	ME06D1 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGGTGGTTAGGCCTGGGACTTCAG TGAAGATGTCCTGCAAGGCTGCTGGATACACCTTCACTAAGTACTGGATAGGTTGG GTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTCACCCTGGAG GTGGTTTTGCTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGACTGACATCTGATGACTCTGC CATCTATTACTGTGCAAGATCGGGTTATGACTACGGTAGTAGTTACGATTACCATGG TATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTC CATCCTCCCTGACTGTGACAGCAGGAGAGAAGGTCACTATGAGCTGCAAGTCCAGT CAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCCTGGTACCAGCAGAA ACCAGGGCAGCCTCCTAAACTGTTGATCTACGGGGCATCCACTAGGGAATCTGGAG TCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGC AGTGTGCAGGCTGAAGACCTGGCAGATTACTTCTGTCAGCAACATTATAGCACTCC GTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAATCCGGAGGGTGGTGGATCC GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGGTCATTGA AACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCC GCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAAT AATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT GATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCC GTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCT TACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACT CACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTG TTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGT GGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGG CTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGAT GAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
1610.	ME06D2-H	murine	aa	EVQLLEQSGADLVRPGTSVKLSCKAAGYTFSRYWISWIRQRPGHGLEWIGEIYPGGGY GNYNENFKDKVTLTADTSSSTAYMQLSSLTSEDSAIYYCARSGYDYGSKYDYYGLDYW GQGTTVTVSS
1611.	ME06D2-HCDR1	murine	aa	RYWIS
1612.	ME06D2-HCDR2	murine	aa	EIYPGGGYGNYNENFKD
1613.	ME06D2-HCDR3	murine	aa	SGYDYGSKYDYYGLDY
1614.	ME06D2-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGACCTGGTAAGGCCCTGGGACTTCAG TGAAGCTGTCCTGCAAGGCTGCTGGATACACCTTCAGTAGGTATTGGATAAGTTGG

				ATAAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAAATTTACCCTGGAGG TGGTTATGGTAACTACAATGAGAATTTCAAGGACAAGGTCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCA TCTATTATTGTGCAAGATCGGGGTATGACTACGGCAGTAAGTACGATTATTATGGTT TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1615.	ME06D2-L	murine	aa	ELVMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVP SRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDAFPPTFGAGTKLEIK
1616.	ME06D2-LCDR1	murine	aa	KASQDINSYLS
1617.	ME06D2-LCDR2	murine	aa	RANRLVD
1618.	ME06D2-LCDR3	murine	aa	LQYDAFPPT
1619.	ME06D2-L	murine	nt	GAGCTCGTGATGACACAGTCTCCATCTTCCATGTATGCATCTCTAGGAGAGAGAGT CACTATCACTTGCAAGGCGAGTCAGGACATTAATAGCTATTTAAGCTGGTTCCAGCA GAAACCAGGGAAATCTCCTAAGACCCTGATCTATCGTGCAAACAGATTGGTAGATG GGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGCAAGATTATTCTCTCACCATC AGCAGCCTGGAGTATGAAGATATGGGAATTTATTATTGTCTACAGTATGATGCGTTT CCTCCCACGTTCGGTGCTGGGACCAAGCTTGAGATCAAA
1620.	ME06D2-HL	murine	aa	EVQLLEQSGADLVRPGTSVKLSCKAAGYTFSRYWISWIRQRPGHGLEWIGEIYPGGGY GNYNENFKDKVTLTADTSSSTAYMQLSSLTSEDSAIYYCARSGYDYGSKYDYYGLDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSMYASLGERVTITCKASQDINSY LSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQY DAFPPTFGAGTKLEIK
1621.	ME06D2-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGACCTGGTAAGGCCTGGGACTTCAG TGAAGCTGTCCTGCAAGGCTGCTGGATACACCTTCAGTAGGTATTGGATAAGTTGG ATAAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAAATTTACCCTGGAGG TGGTTATGGTAACTACAATGAGAATTTCAAGGACAAGGTCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCA TCTATTATTGTGCAAGATCGGGGTATGACTACGGCAGTAAGTACGATTATTATGGTT TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCCA TCTTCCATGTATGCATCTCTAGGAGAGAGAGTCACTATCACTTGCAAGGCGAGTCA GGACATTAATAGCTATTTAAGCTGGTTCCAGCAGAAACCAGGGAAATCTCCTAAGAC CCTGATCTATCGTGCAAACAGATTGGTAGATGGGGTCCCATCAAGGTTCAGTGGCA GTGGATCTGGGCAAGATTATTCTCTCACCATCAGCAGCCTGGAGTATGAAGATATG GGAATTTATTATTGTCTACAGTATGATGCGTTTCCTCCCACGTTCGGTGCTGGGACC AAGCTTGAGATCAAA
1622.	ME06D2 HL x I2C	murine	aa	EVQLLEQSGADLVRPGTSVKLSCKAAGYTFSRYWISWIRQRPGHGLEWIGEIYPGGGY

	HL			GNYNENFKDKVTLTADTSSSTAYMQLSSLTSEDSAIYYCARSGYDYYGSKYDYYGLDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSMYASLGERVTITCKASQDINSY LSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQY DAFPPTFGAGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1623.	ME06D2 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGACCTGGTAAGGCCTGGGACTTCAG TGAAGCTGTCCTGCAAGGCTGCTGGATACACCTTCAGTAGGTATTGGATAAGTTGG ATAAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAAATTTACCCTGGAGG TGGTTATGGTAACTACAATGAGAATTTCAAGGACAAGGTCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCA TCTATTATTGTGCAAGATCGGGGTATGACTACGGCAGTAAGTACGATTATTATGGTT TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCCA TCTTCCATGTATGCATCTCTAGGAGAGAGAGTCACTATCACTTGCAAGGCGAGTCA GGACATTAATAGCTATTTAAGCTGGTTCCAGCAGAAACCAGGGAAATCTCCTAAGAC CCTGATCTATCGTGCAAACAGATTGGTAGATGGGGTCCCATCAAGGTTCAGTGGCA GTGGATCTGGGCAAGATTATTCTCTCACCATCAGCAGCCTGGAGTATGAAGATATG GGAATTTATTATTGTCTACAGTATGATGCGTTTCCTCCCACGTTCGGTGCTGGGACC AAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1624.	ME06E10-H	murine	aa	EVQLLEQSGADLVRPGTSVKLSCKAAGYTFSRYWISWIRQRPGHGLEWIGEIYPGGGY

				GNYNENFKDKVTLTADTSSSTAYMQLSSLTSEDSAIYYCARSGYDYGSKYDYYGLDYW GQGTTVTVSS
1625.	ME06E10-HCDR1	murine	aa	RYWIS
1626.	ME06E10-HCDR2	murine	aa	EIYPGGGYGNYNENFKD
1627.	ME06E10-HCDR3	murine	aa	SGYDYGSKYDYYGLDY
1628.	ME06E10-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGACCTGGTAAGGCCTGGGACTTCAG TGAAGCTGTCCTGCAAGGCTGCTGGATACACCTTCAGTAGGTATTGGATAAGTTGG ATAAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAAATTTACCCTGGAGG TGGTTATGGTAACTACAATGAGAATTTCAAGGACAAGGTCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCA TCTATTATTGTGCAAGATCGGGGGTATGACTACGGCAGTAAGTACGATTATTATGGTT TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA	
1629.	ME06E10-L	murine	aa	ELVMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASTLDSGVPK RFSGSRSGSDYSLTISSLESEDFADYYCLQYASSPYTFGGGTKLEIK	
1630.	ME06E10-LCDR1	murine	aa	RASQEISGYLS
1631.	ME06E10-LCDR2	murine	aa	AASTLDS
1632.	ME06E10-LCDR3	murine	aa	LQYASSPYT
1633.	ME06E10-L	murine	nt	GAGCTCGTCATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGT CAGTCTCACTTGTCGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGC AGAACCAGATGGAACTATTAAACGCCTGATCTACGCCGCATCCACTTTAGATTCTG GTGTCCCAAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCA GCAGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTC CGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1634.	ME06E10-HL	murine	aa	EVQLLEQSGADLVRPGTSVKLSCKAAGYTFSRYWISWIRQRPGHGLEWIGEIYPGGGY GNYNENFKDKVTLTADTSSSTAYMQLSSLTSEDSAIYYCARSGYDYGSKYDYYGLDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASLGERVSLTCRASQEISGY LSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCLQYA SSPYTFGGGTKLEIK
1635.	ME06E10-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGACCTGGTAAGGCCTGGGACTTCAG TGAAGCTGTCCTGCAAGGCTGCTGGATACACCTTCAGTAGGTATTGGATAAGTTGG ATAAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAAATTTACCCTGGAGG TGGTTATGGTAACTACAATGAGAATTTCAAGGACAAGGTCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCA TCTATTATTGTGCAAGATCGGGGGTATGACTACGGCAGTAAGTACGATTATTATGGTT TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCCA

				TCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGTCA GGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACTATTAAACG CCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAAAGGTTCAGTGGCA GTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTG CAGACTATTACTGTCTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGGGGGACC AAGCTTGAGATCAAA
1636.	ME06E10 HL x I2C HL	murine	aa	EVQLLEQSGADLVRPGTSVKLSCKAAGYTFSRYWISWIRQRPGHGLEWIGEIYPGGGY GNYNENFKDKVTLTADTSSSTAYMQLSSLTSEDSAIYYCARSGYDYGSKYDYYGLDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASLGERVSLTCRASQEISGY LSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCLQYA SSPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNW VRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1637.	ME06E10 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGACCTGGTAAGGCCCTGGGACTTCAG TGAAGCTGTCCTGCAAGGCTGCTGGATACACCTTCAGTAGGTATTGGATAAGTTGG ATAAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAAATTTACCCTGGAGG TGGTTATGGTAACTACAATGAGAATTTCAAGGACAAGGTCACACTGACTGCAGACAC ATCCTCCAGCACAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCA TCTATTATTGTGCAAGATCGGGGGTATGACTACGGCAGTAAGTACGATTATTATGGTT TGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTC TGGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCCA TCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGTCA GGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACTATTAAACG CCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAAAGGTTCAGTGGCA GTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTG CAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGGGGGACC AAGCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTG GAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTT TGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATG GGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTG GTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGT

				GGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAAC AGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAA ACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAG TTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGC TGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTC TATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1638.	ME06F2-H	murine	aa	EVQLLEQSGAELMKPGASVKISCKATGYTFSNYWIGWVKQRPGHGLEWIGDIYPGGSY TNYNEKFKGKVTLTADTSSRTAYMQLSSLTFEDSAIYYCARSGYDYASDYDYHGMDYW GQGTTVTVSS
1639.	ME06F2-HCDR1	murine	aa	NYWIG
1640.	ME06F2-HCDR2	murine	aa	DIYPGGSYTNYNEKFKG
1641.	ME06F2-HCDR3	murine	aa	SGYDYASDYDYHGMDY
1642.	ME06F2-H	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGATGAAGCCTGGGGCCTCAG TGAAGATATCCTGCAAGGCTACTGGATACACCTTCAGTAATTACTGGATAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT AGTTATACTAACTACAATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACACA TCCTCCAGGACAGCCTACATGCAGCTCAGCAGCCTGACATTTGAGGACTCTGCCAT CTATTACTGTGCAAGATCGGGGGTATGACTACGCTAGTGACTACGATTACCATGGTAT GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1643.	ME06F2-L	murine	aa	ELVLTQSPSSMSASLGDRITITCQATQDIVKNLNWYQQKPGKPPSFLIYYATELAEGVPS RFSGSGSGSDYSLTISNLESEDFADYYCLQFYEFPYTFGGGTKLEIK
1644.	ME06F2-LCDR1	murine	aa	QATQDIVKNLN
1645.	ME06F2-LCDR2	murine	aa	YATELAE
1646.	ME06F2-LCDR3	murine	aa	LQFYEFPYT
1647.	ME06F2-L	murine	nt	GAGCTCGTGCTCACCCAGTCTCCATCTCTATGTCTGCATCTCTGGGAGACAGAAT AACCATCACTTGCCAGGCAACTCAAGACATTGTTAAGAATTTAAACTGGTATCAGCA GAAACCAGGGAAACCCCCTTCATTCCTGATCTATTATGCAACTGAACTGGCAGAAG GGGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGGTCAGACTATTCTCTGACAATC AGCAACCTGGAGTCTGAAGATTTTGCAGACTATTACTGTCTACAGTTTTATGAGTTTC CGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1648.	ME06F2-HL	murine	aa	EVQLLEQSGAELMKPGASVKISCKATGYTFSNYWIGWVKQRPGHGLEWIGDIYPGGSY TNYNEKFKGKVTLTADTSSRTAYMQLSSLTFEDSAIYYCARSGYDYASDYDYHGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVLTQSPSSMSASLGDRITITCQATQDIVKNL NWYQQKPGKPPSFLIYYATELAEGVPSRFSGSGSGSDYSLTISNLESEDFADYYCLQFY EFPYTFGGGTKLEIK
1649.	ME06F2-HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGATGAAGCCTGGGGCCTCAG

				TGAAGATATCCTGCAAGGCTACTGGATACACCTTCAGTAATTACTGGATAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT AGTTATACTAACTACAATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACACA TCCTCCAGGACAGCCTACATGCAGCTCAGCAGCCTGACATTTGAGGACTCTGCCAT CTATTACTGTGCAAGATCGGGGTATGACTACGCTAGTGACTACGATTACCATGGTAT GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGCTCACCCAGTCTCCAT CCTCTATGTCTGCATCTCTGGGAGACAGAATAACCATCACTTGCCAGGCAACTCAA GACATTGTTAAGAATTTAAACTGGTATCAGCAGAAACCAGGGAAACCCCCTTCATTC CTGATCTATTATGCAACTGAACTGGCAGAAGGGGTCCCATCAAGGTTCAGTGGCAG TGGGTCTGGGTCAGACTATTCTCTGACAATCAGCAACCTGGAGTCTGAAGATTTTGC AGACTATTACTGTCTACAGTTTTATGAGTTTCCGTACACGTTCGGAGGGGGGACCAA GCTTGAGATCAAA
1650.	ME06F2 HL x I2C HL	murine	aa	EVQLLEQSGAELMKPGASVKISCKATGYTFSNYWIGWVKQRPGHGLEWIGDIYPGGSY TNYNEKFKGKVTLTADTSSRTAYMQLSSLTFEDSAIYYCARSGYDYASDYDYHGMDYW GQGTTVTVSSGGGGSGGGGSGGGGSELVLTQSPSSMSASLGDRITITCQATQDIVKNL NWYQQKPGKPPSFLIYYATELAEGVPSRFSGSGSGSDYSLTISNLESEDFADYYCLQFY EFPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNW VRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1651.	ME06F2 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGATGAAGCCTGGGGCCTCAG TGAAGATATCCTGCAAGGCTACTGGATACACCTTCAGTAATTACTGGATAGGTTGGG TAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGT AGTTATACTAACTACAATGAGAAATTCAAGGGCAAGGTCACACTGACTGCAGACACA TCCTCCAGGACAGCCTACATGCAGCTCAGCAGCCTGACATTTGAGGACTCTGCCAT CTATTACTGTGCAAGATCGGGGTATGACTACGCTAGTGACTACGATTACCATGGTAT GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCT GGCGGCGGCGGCTCCGGTGGTGGTTCTGAGCTCGTGCTCACCCAGTCTCCAT CCTCTATGTCTGCATCTCTGGGAGACAGAATAACCATCACTTGCCAGGCAACTCAA GACATTGTTAAGAATTTAAACTGGTATCAGCAGAAACCAGGGAAACCCCCTTCATTC CTGATCTATTATGCAACTGAACTGGCAGAAGGGGTCCCATCAAGGTTCAGTGGCAG TGGGTCTGGGTCAGACTATTCTCTGACAATCAGCAACCTGGAGTCTGAAGATTTTGC AGACTATTACTGTCTACAGTTTTATGAGTTTCCGTACACGTTCGGAGGGGGGACCAA GCTTGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA

1652.	EN00B12-H	artificial	aa	GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA ACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
				QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWVKQAPGQRLEWMGYINPYDDD TTYNQKFKGRVTITVDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSS
1653.	EN00B12-HCDR1	artificial	aa	DYVIH
1654.	EN00B12-HCDR2	artificial	aa	YINPYDDDTTYNQKFKG
1655.	EN00B12-HCDR3	artificial	aa	RGNSYDGYFDYSMDY
1656.	EN00B12-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA AGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACAAATC CGCCAGCACAGCCTACATGGAGCTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1657.	EN00B12-L	artificial	aa	DIQLTQSPSFLSASVGDRVTITCRASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVP SRFSGSGSGTEFTLTISSLQPEDFATYYCQQYTNYPMYTFGQGTKLEIK
1658.	EN00B12-LCDR1	artificial	aa	RASQNVGTAVA
1659.	EN00B12-LCDR2	artificial	aa	SASNRYT
1660.	EN00B12-LCDR3	artificial	aa	QQYTNYPMYT
1661.	EN00B12-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAGCTTCCTGTCCGCATCAGTAGGAGACAGAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGAAAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATC

				AGCAGTCTGCAGCCTGAAGACTTCGCAACTTATTACTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAAA
1662.	EN00B12-HL	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWVKQAPGQRLEWMGYINPYDDD TTYNQKFKGRVTITVDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQNVGTA VAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQY TNYPMYTFGQGTKLEIK
1663.	EN00B12-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA AGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACACATC CGCCAGCACAGCCTACATGGAGCTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTC CTGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGACTTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAA
1664.	EN00B12 HL x I2C HL	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWVKQAPGQRLEWMGYINPYDDD TTYNQKFKGRVTITVDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQNVGTA VAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQY TNYPMYTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1665.	EN00B12 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA AGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACACATC CGCCAGCACAGCCTACATGGAGCTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT

				ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTC CTGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGACTTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA ACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1666.	EN00C3-H	artificial	aa	QVQLVQSGPEVKKPGASVKMSCKASGYTFTDYVIHWVRQGPGQRLEWMGYINPYDD DTTYNQKFKGRVTMTLDKSASTAYMQLNSLRSEDTAVYYCARRGNSYDGYFDYSMDY WGQGTLVTVSS
1667.	EN00C3-HCDR1	artificial	aa	DYVIH
1668.	EN00C3-HCDR2	artificial	aa	YINPYDDDTTYNQKFKG
1669.	EN00C3-HCDR3	artificial	aa	RGNSYDGYFDYSMDY
1670.	EN00C3-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGGGACCTGGACAGCGTCTTGAGTGGATAGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATGACTCTAGACAAATC CGCCAGCACAGCCTACATGCAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1671.	EN00C3-L	artificial	aa	DIQLTQSPNFLSASVGDRVTITCRASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTNYPMYTFGQGTKLEIK

1672.	EN00C3-LCDR1	artificial	aa	RASQNVGTAVA
1673.	EN00C3-LCDR2	artificial	aa	SASNRYT
1674.	EN00C3-LCDR3	artificial	aa	QQYTNYPMYT
1675.	EN00C3-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAACTTCCTGTCCGCATCAGTAGGAGACAGAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGAAAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC AGCAGTCTGCAGCCTGAAGACTTCGCAACTTATTACTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAAA
1676.	EN00C3-HL	artificial	aa	QVQLVQSGPEVKKPGASVKMSCKASGYTFTDYVIHWVRQGPGQRLEWMGYINPYDD DTTYNQKFKGRVTMTLDKSASTAYMQLNSLRSEDTAVYYCARRGNSYDGYFDYSMDY WGQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPNFLSASVGDRVTITCRASQNVGT AVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ YTNYPMYTFGQGTKLEIK
1677.	EN00C3-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGGGACCTGGACAGCGTCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATGACTCTAGACAAATC CGCCAGCACACAGCCTACATGCAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAACTTC CTGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGACTTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAA
1678.	EN00C3 HL x I2C HL	artificial	aa	QVQLVQSGPEVKKPGASVKMSCKASGYTFTDYVIHWVRQGPGQRLEWMGYINPYDD DTTYNQKFKGRVTMTLDKSASTAYMQLNSLRSEDTAVYYCARRGNSYDGYFDYSMDY WGQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPNFLSASVGDRVTITCRASQNVGT AVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ YTNYPMYTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA

				RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1679.	EN00C3 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGGGACCTGGACAGCGTCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATGACTCTAGACAAATC CGCCAGCACAGCCTACATGCAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAACTTC CTGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGACTTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA ACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAAACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1680.	EN01D5-H	artificial	aa	QVQLVQSGPEVMKPGASVKMSCKASGYTFTDYVIHWVRQAPGKRLEWMGYINPYDDD TTYNQKFKGRVTITVDKSASTAYMELNSLTSEDTAVYYCARRGNSYDGYFDYSMDYWG QGTLVTVSS
1681.	EN01D5-HCDR1	artificial	aa	DYVIH
1682.	EN01D5-HCDR2	artificial	aa	YINPYDDDTTYNQKFKG
1683.	EN01D5-HCDR3	artificial	aa	RGNSYDGYFDYSMDY
1684.	EN01D5-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA

				GGCAGGCACCTGGAAAGCGCCTTGAGTGGATGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACAAATC CGCCAGCACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1685.	EN01D5-L	artificial	aa	DIQLTQSPSFMSASVGDRVTITCRASQNVGTAVAWYQQKPGQAPKLLIYSASNRYTGV PSRFSGSGSGTEFTLTISSLQSEDFATYYCQQYTNYPMYTFGQGTKLEIK
1686.	EN01D5-LCDR1	artificial	aa	RASQNVGTAVA
1687.	EN01D5-LCDR2	artificial	aa	SASNRYT
1688.	EN01D5-LCDR3	artificial	aa	QQYTNYPMYT
1689.	EN01D5-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAGCTTCATGTCCGCATCAGTAGGAGACAGAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGACAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATC AGCAGTCTGCAGTCTGAAGACTTCGCAACTTATTACTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAAA
1690.	EN01D5-HL	artificial	aa	QVQLVQSGPEVMKPGASVKMSCKASGYTFTDYVIHWVRQAPGKRLEWMGYINPYDDD TTYNQKFKGRVTITVDKSASTAYMELNSLTSEDTAVYYCARRGNSYDGYFDYSMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFMSASVGDRVTITCRASQNVGTAV AWYQQKPGQAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQSEDFATYYCQQYT NYPMYTFGQGTKLEIK
1691.	EN01D5-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGATGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGGCACCTGGAAAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACAAATC CGCCAGCACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTC ATGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGACAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGTCTGAAGACTTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAA
1692.	EN01D5 HL x I2C	artificial	aa	QVQLVQSGPEVMKPGASVKMSCKASGYTFTDYVIHWVRQAPGKRLEWMGYINPYDDD

	HL			TTYNQKFKGRVTITVDKSASTAYMELNSLTSEDTAVYYCARRGNSYDGYFDYSMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFMSASVGDRVTITCRASQNVGTAV AWYQQKPGQAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQSEDFATYYCQQYT NYPMYTFGQGTKLEIK SGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVAR IRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1693.	EN01D5 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGATGAAGCCTGGGGCTTCAGTGA AGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGGCACCTGGAAAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGTAGACAAATC CGCCAGCACACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTC ATGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGACAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGTCTGAAGACTTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA ACTTCGGTAATAGCTACATATCCTACTGGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA

1694.	EN00E4-H	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWMRQAPGQRLEWMGYINPYDDD TTYNQKFKGRVTITLDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYWG QGTLVTVSS
1695.	EN00E4-HCDR1	artificial	aa	DYVIH
1696.	EN00E4-HCDR2	artificial	aa	YINPYDDDTTYNQKFKG
1697.	EN00E4-HCDR3	artificial	aa	RGNSYDGYFDYSMDY
1698.	EN00E4-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGATGA GGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTCTAGACACATC CGCCAGCACAGCCTACATGGAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1699.	EN00E4-L	artificial	aa	DIQLTQSPKFMSTSVGDKVTITCRASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVP SRFSGSGSGTEFTLTISSLQPEDFANYFCQQYTNYPMYTFGQGTKLEIK
1700.	EN00E4-LCDR1	artificial	aa	RASQNVGTAVA
1701.	EN00E4-LCDR2	artificial	aa	SASNRYT
1702.	EN00E4-LCDR3	artificial	aa	QQYTNYPMYT
1703.	EN00E4-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAAATTCATGTCCACATCAGTAGGAGACAAAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGAAAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATC AGCAGTCTGCAGCCTGAAGACTTCGCAAATTATTTCTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAAA
1704.	EN00E4-HL	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWMRQAPGQRLEWMGYINPYDDD TTYNQKFKGRVTITLDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPKFMSTSVGDKVTITCRASQNVGTAV AWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQPEDFANYFCQQYT NYPMYTFGQGTKLEIK
1705.	EN00E4-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGATGA GGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTCTAGACACATC CGCCAGCACAGCCTACATGGAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGG

				CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAAATTCA TGTCCACATCAGTAGGAGACAAAGTCACCATCACCTGCAGGGCCAGTCAGAATGTG GGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGATT TACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGATC TGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGACTTCGCAAATT ATTTCTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAAGC TGGAAATAAAA
1706.	EN00E4 HL x I2C HL	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWMRQAPGQRLEWMGYINPYDDD TTYNQKFKGRVTITLDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPKFMSTSVGDKVTITCRASQNVGTAV AWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQPEDFANYFCQQYT NYPMYTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1707.	EN00E4 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGATGA GGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTCTAGACACATC CGCCAGCACAGCCTACATGGAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAAATTCA TGTCCACATCAGTAGGAGACAAAGTCACCATCACCTGCAGGGCCAGTCAGAATGTG GGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGATT TACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGATC TGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGACTTCGCAAATT ATTTCTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAAGC TGGAAATAAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGG AGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCA CCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAA TGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAG TGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAA TGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAAC TTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCAC

				CGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCT CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCAC ACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTC GCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCC TCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGG TACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1708.	EN00F7-H	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWVKQAPGQRLEWMGYINPYDDD TTYNQKFKGQVTITVDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSS
1709.	EN00F7-HCDR1	artificial	aa	DYVIH
1710.	EN00F7-HCDR2	artificial	aa	YINPYDDDTTYNQKFKG
1711.	EN00F7-HCDR3	artificial	aa	RGNSYDGYFDYSMDY
1712.	EN00F7-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA AGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCAGGTCACAATTACTGTAGACAAATCC GCCAGCACAGCCTACATGGAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCTA TTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACTA CTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1713.	EN00F7-L	artificial	aa	DIQLTQSPSFLSASVGDRVTITCRASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVP SRFSGSGSGTEFTLTISSMQPEDLATYFCQQYTNYPMYTFGQGTKLEIK
1714.	EN00F7-LCDR1	artificial	aa	RASQNVGTAVA
1715.	EN00F7-LCDR2	artificial	aa	SASNRYT
1716.	EN00F7-LCDR3	artificial	aa	QQYTNYPMYT
1717.	EN00F7-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAGCTTCCTGTCCGCATCAGTAGGAGACAGAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGAAAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATC AGCAGTATGCAGCCTGAAGACCTCGCAACTTATTTCTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAA
1718.	EN00F7-HL	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWVKQAPGQRLEWMGYINPYDDD TTYNQKFKGQVTITVDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQNVGTA VAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSMQPEDLATYFCQQ YTNYPMYTFGQGTKLEIK

1719.	EN00F7-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA AGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCAGGTCACAATTACTGTAGACACATCC GCCAGCACAGCCTACATGGAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCTA TTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACTA CTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGC GGCGGCTCCGGTGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTCC TGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGTG GGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGATT TACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGATC TGGGACAGAGTTCACTCTCACCATCAGCAGTATGCAGCCTGAAGACCTCGCAACTT ATTTCTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAAGC TGGAAATAAAA
1720.	En00F7 HL x I2C HL	artificial	aa	QVQLVQSGPEVKKPGASVKLSCKASGYTFTDYVIHWVKQAPGQRLEWMGYINPYDDD TTYNQKFKGQVTITVDTSASTAYMELNSLRSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQNVGTA VAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSMQPEDLATYFCQQ YTNYPMYTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1721.	En00F7 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGACCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA AGCAGGCACCTGGACAGCGCCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCAGGTCACAATTACTGTAGACACATCC GCCAGCACAGCCTACATGGAACTCAACAGCCTGAGATCTGAGGACACTGCAGTCTA TTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACTA CTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGC GGCGGCTCCGGTGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTCC TGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGTG GGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGATT TACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGATC TGGGACAGAGTTCACTCTCACCATCAGCAGTATGCAGCCTGAAGACCTCGCAACTT ATTTCTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAAGC

1722.	EN00H6-H	artificial	aa	TGGAAATAAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGG AGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCA CCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAA TGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAG TGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATCTACAAA TGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAAC TTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCAC CGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCT CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGAACAGTCAC ACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGG TCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTC GCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCC TCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGG TACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
				QVQLVQSGAEVKKPGASVKLSCKASGYTFTDYVIHWVRQTPGQRLEWMGYINPYDDD TTYNQKFKGRVTITGDTSANTAYMELNSLTSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSS
1723.	EN00H6-HCDR1	artificial	aa	DYVIH
1724.	EN00H6-HCDR2	artificial	aa	YINPYDDDTTYNQKFKG
1725.	EN00H6-HCDR3	artificial	aa	RGNSYDGYFDYSMDY
1726.	EN00H6-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGACACCTGGACAGCGTCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGGAGACACATC CGCCAACACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCA
1727.	EN00H6-L	artificial	aa	DIQLTQSPSFLSASVGDRVTITCRASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVP SRFSGSGSGTEFTLTISSLQSEDLATYYCQQYTNYPMYTFGQGTKLEIK
1728.	EN00H6-LCDR1	artificial	aa	RASQNVGTAVA
1729.	EN00H6-LCDR2	artificial	aa	SASNRYT
1730.	EN00H6-LCDR3	artificial	aa	QQYTNYPMYT
1731.	EN00H6-L	artificial	nt	GACATCCAGCTGACCCAGTCTCCAAGCTTCCTGTCCGCATCAGTAGGAGACAGAGT CACCATCACCTGCAGGGCCAGTCAGAATGTGGGTACTGCTGTAGCCTGGTATCAAC AGAAACCAGGAAAAGCCCCTAAATTACTGATTTACTCGGCATCGAATCGGTACACTG GAGTCCCTAGTCGCTTCTCAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATC

				AGCAGTCTGCAGTCTGAAGACCTCGCAACTTATTACTGCCAGCAATATACCAACTAT CCCATGTATACGTTTGGACAGGGGACCAAGCTGGAAATAAAA
1732.	EN00H6-HL	artificial	aa	QVQLVQSGAEVKKPGASVKLSCKASGYTFTDYVIHWVRQTPGQRLEWMGYINPYDDD TTYNQKFKGRVTITGDTSANTAYMELNSLTSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQNVGTA VAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQSEDLATYYCQQY TNYPMYTFGQGTKLEIK
1733.	EN00H6-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGACACCTGGACAGCGTCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGGAGACACATC CGCCAACACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTC CTGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGTCTGAAGACCTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAA
1734.	EN00H6 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKLSCKASGYTFTDYVIHWVRQTPGQRLEWMGYINPYDDD TTYNQKFKGRVTITGDTSANTAYMELNSLTSEDTAVYYCARRGNSYDGYFDYSMDYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQNVGTA VAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQSEDLATYYCQQY TNYPMYTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1735.	EN00H6 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCAGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTGA AGTTGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTATACACTGGGTGA GGCAGACACCTGGACAGCGTCTTGAGTGGATGGGATATATTAATCCTTATGATGAT GATACTACCTACAACCAGAAGTTCAAGGGCCGGGTCACAATTACTGGAGACACATC CGCCAACACAGCCTACATGGAACTCAACAGCCTGACATCTGAGGACACTGCAGTCT ATTACTGTGCAAGAAGGGGGAACTCCTATGATGGTTACTTCGACTATTCTATGGACT

				ACTGGGGTCAAGGAACCTTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCCAGCTGACCCAGTCTCCAAGCTTC CTGTCCGCATCAGTAGGAGACAGAGTCACCATCACCTGCAGGGCCAGTCAGAATGT GGGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCTAAATTACTGA TTTACTCGGCATCGAATCGGTACACTGGAGTCCCTAGTCGCTTCTCAGGCAGTGGA TCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGTCTGAAGACCTCGCAAC TTATTACTGCCAGCAATATACCAACTATCCCATGTATACGTTTGGACAGGGGACCAA GCTGGAAATAAAATCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGA GGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATT CACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGG AATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTC AGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACA AATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGA ACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTC ACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTT CTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTC ACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTG GGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCC TCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGC CCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTAT GGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1736.	HEP14G6-H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSG NIHYNEKFKGRATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTT VTVSS
1737.	HEP14G6-HCDR1	artificial	aa	NYWLG
1738.	HEP14G6-HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1739.	HEP14G6-HCDR3	artificial	aa	LRNWDEPMDY
1740.	HEP14G6-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGA AGGTATCCTGCAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAA GGCAGGCGCCTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGG TAATATCCACTACAATGAGAAGTTCAAGGGCAGAGCCACAATCACTGCAGACAAATC TACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCT ATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGG GACCACGGTCACCGTCTCCTCC
1741.	HEP14G6-L	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCQNDYSYPLTFGQGTKLEIK

1742.	HEP14G6-LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1743.	HEP14G6-LCDR2	artificial	aa	WASTRES
1744.	HEP14G6-LCDR3	artificial	aa	QNDYSYPLT
1745.	HEP14G6-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGT CTCTATCAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCTGCAGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAAAATCAGCCGTGTGCAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA
1746.	HEP14G6-LH	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGG SGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQG LEWMGDIFPGSGNIHYNEKFKGRATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWD EPMDYWGQGTTVTVSS
1747.	HEP14G6-LH	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGT CTCTATCAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCTGCAGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAAAATCAGCCGTGTGCAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA GGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG CTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGC CTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCAC TACAATGAGAAGTTCAAGGGCAGAGCCACACAATCACTGCAGACAAATCTACGAGCAC AGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCTATTACTGTGC AAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCC
1748.	hEp14G6 LH x I2C HL	artificial	aa	DIVMTQTPLSLTVTPGEPVSISCKSSQSLLNSGNQKNYLTWYLQKPGQPPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGG SGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQG LEWMGDIFPGSGNIHYNEKFKGRATITADKSTSTAYMELSSLTSEDTAVYYCARLRNWD EPMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG

				SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1749.	hEp14G6 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGACTGTGACACCAGGAGAGCCGGT CTCTATCAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAGAACTA CTTGACCTGGTACCTGCAGAAACCAGGGCAGCCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAAAATCAGCCGTGTGCAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA GGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG CTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGC CTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCAC TACAATGAGAAGTTCAAGGGCAGAGCCACAATCACTGCAGACAAATCTACGAGCAC AGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCTATTACTGTGC AAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAG GATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACC TTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATG GGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTG AAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATG AACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTT CGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCG TCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCA GACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACACAGTCACAC TCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTC CAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGC CCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTC ACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTA CAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1750.	HEP14D2-H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQGLEWMGDIFPGSG NIHYNEKFKGRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTT VTVSS
1751.	HEP14D2-HCDR1	artificial	aa	NYWLG
1752.	HEP14D2-HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1753.	HEP14D2-HCDR3	artificial	aa	LRNWDEPMDY
1754.	HEP14D2-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGA AGGTATCCTGCAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAA

				GGCAGGCGCCTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGG TAATATCCACTACAATGAGAAGTTCAAGGGCAGAGTCACAATCACTGCAGACAAATC TACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCT ATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGG GACCACGGTCACCGTCTCCTCC
1755.	HEP14D2-L	artificial	aa	DIVMTQTPLSLPVTPGEQVSISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1756.	HEP14D2-LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1757.	HEP14D2-LCDR2	artificial	aa	WASTRES
1758.	HEP14D2-LCDR3	artificial	aa	QNDYSYPLT
1759.	HEP14D2-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGT CTCTATCAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCAGCAGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA
1760.	HEP14D2-LH	artificial	aa	DIVMTQTPLSLPVTPGEQVSISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGGG SGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQG LEWMGDIFPGSGNIHYNEKFKGRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWD EPMDYWGQGTTVTVSS
1761.	HEP14D2-LH	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGT CTCTATCAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCAGCAGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA GGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG CTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGC CTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCAC TACAATGAGAAGTTCAAGGGCAGAGTCACAATCACTGCAGACAAATCTACGAGCAC AGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCTATTACTGTGC AAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCC
1762.	hEp14D2 LH x I2C	artificial	aa	DIVMTQTPLSLPVTPGEQVSISCKSSQSLLNSGNQKNYLTWYQQKPGQSPQLLIYWAST

	HL			RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGG SGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQAPGQG LEWMGDIFPGSGNIHYNEKFKGRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWD EPMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1763.	hEp14D2 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGT CTCTATCAGCTGCAAGTCCAGTCAGAGTCTGTTAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCAGCAGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAAAATCAGCCGTGTGGAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA GGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG CTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGGCGC CTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCAC TACAATGAGAAGTTCAAGGGCAGAGTCACAATCACTGCAGACAAATCTACGAGCAC AGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCTATTACTGTGC AAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAG GATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACC TTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATG GGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTG AAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATG AACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTT CGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCG TCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCA GACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACAC TCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTC CAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGC CCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTC ACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTA CAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1764.	HEP18A6-H	artificial	aa	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQGLEWMGDIFPGSG

				NIHYNEKFKGRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNWDEPMDYWGQGTT VTVSS
1765.	HEP18A6-HCDR1	artificial	aa	NYWLG
1766.	HEP18A6-HCDR2	artificial	aa	DIFPGSGNIHYNEKFKG
1767.	HEP18A6-HCDR3	artificial	aa	LRNWDEPMDY
1768.	HEP18A6-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGA AGGTATCCTGCAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAA GGCAGACGCCTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGG TAATATCCACTACAATGAGAAGTTCAAGGGCAGAGTCACAATCACTGCAGACAAATC TACGAGCACAGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCT ATTACTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGG GACCACGGTCACCGTCTCCTCC
1769.	HEP18A6-L	artificial	aa	DIVMTQTPLSLPVTPGEQVSMSCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWAS TRESGVPDRFSGSGSGTDFTLNISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIK
1770.	HEP18A6-LCDR1	artificial	aa	KSSQSLLNSGNQKNYLT
1771.	HEP18A6-LCDR2	artificial	aa	WASTRES
1772.	HEP18A6-LCDR3	artificial	aa	QNDYSYPLT
1773.	HEP18A6-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGT CTCTATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCTGCAGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAACATCAGCAGTGTGGAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA
1774.	HEP18A6-LH	artificial	aa	DIVMTQTPLSLPVTPGEQVSMSCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWAS TRESGVPDRFSGSGSGTDFTLNISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGG GSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQ GLEWMGDIFPGSGNIHYNEKFKGRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNW DEPMDYWGQGTTVTVSS
1775.	HEP18A6-LH	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTGACACCAGGAGAGCAGGT CTCTATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCTGCAGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAACATCAGCAGTGTGGAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA GGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG CTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG

				CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGC CTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCAC TACAATGAGAAGTTCAAGGGCAGAGTCACAATCACTGCAGACAAATCTACGAGCAC AGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCTATTACTGTGC AAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCC
1776.	hEp18A6 LH x I2C HL	artificial	aa	DIVMTQTPLSLPVTPGEQVSMSCKSSQSLLNSGNQKNYLTWYLQKPGQSPQLLIYWAS TRESGVPDRFSGSGSGTDFTLNISSVEAEDVGVYYCQNDYSYPLTFGQGTKLEIKGGG GSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGYTFSNYWLGWVRQTPGQ GLEWMGDIFPGSGNIHYNEKFKGRVTITADKSTSTAYMELSSLTSEDTAVYYCARLRNW DEPMDYWGQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1777.	hEp18A6 LH x I2C HL	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTGCCTGTCACACCAGGAGAGCAGGT CTCTATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA CTTGACCTGGTACCTGCAGAAACCAGGGCAGTCTCCTCAACTGTTGATCTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGAACA GATTTCACTCTCAACATCAGCAGTGTGGAGGCTGAAGACGTGGGAGTTTATTACTGT CAGAATGATTATAGTTATCCGCTCACGTTCGGTCAAGGGACCAAGCTTGAGATCAAA GGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAG CTGGTCCAGTCTGGAGCTGAGGTGAAAAAGCCTGGGTCTTCAGTGAAGGTATCCTG CAAGGCTTCTGGATACACCTTCTCTAACTACTGGCTAGGTTGGGTAAGGCAGACGC CTGGACAGGGACTTGAGTGGATGGGAGATATTTTCCCTGGAAGTGGTAATATCCAC TACAATGAGAAGTTCAAGGGCAGAGTCACAATCACTGCAGACAAATCTACGAGCAC AGCCTATATGGAACTCAGTAGCCTGACATCTGAGGACACTGCTGTCTATTACTGTGC AAGACTGAGGAACTGGGACGAGCCTATGGACTACTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAG GATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACC TTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATG GGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTG AAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATG AACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTT CGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCG TCTCCTCAGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCA

				GACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACAC TCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTC CAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGC CCCCGGTACTCCTGCCAGATTCTCAGGCTCCCCTGCTTGGAGGCAAGGCTGCCCTC ACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTA CAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1778.	FA22A9-H	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRVTITIDTSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSS
1779.	FA22A9-HCDR1	artificial	aa	EYTIH
1780.	FA22A9-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1781.	FA22A9-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1782.	FA22A9-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTATAGACACGTCC TCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCTA TTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGACT ACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA
1783.	FA22A9-L	artificial	aa	DIVMTQTPLSLAVTVGETASMSCKSSQSLLYSRNQKNYLAWYLQKPGQSPQLLIYWAS TRESGVPDRFSGSGSGTDFTLTISRVEAEDVGVYYCQQYFSYPLTFGGGTKVEIK
1784.	FA22A9-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1785.	FA22A9-LCDR2	artificial	aa	WASTRES
1786.	FA22A9-LCDR3	artificial	aa	QQYFSYPLT
1787.	FA22A9-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTAGCTGTGACAGTTGGAGAGACGGC TTCTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAAGAACTA CTTGGCCTGGTACCTGCAGAAGCCAGGGCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGAC GGATTTCACTCTCACGATCAGCAGAGTGGAGGCTGAGGACGTGGGAGTTTATTACT GTCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATC AAA
1788.	FA22A9-HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRVTITIDTSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLAVTVGETASMSCKSSQSLLYSR NQKNYLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLTISRVEAEDVGV

				YYCQQYFSYPLTFGGGTKVEIK
1789.	FA22A9-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTATAGACACGTCC TCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCTA TTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGACT ACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTCC CTAGCTGTGACAGTTGGAGAGACGGCTTCTATGAGCTGCAAGTCCAGTCAGAGCCT TTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGGCA GTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATC GCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCACGATCAGCAGAGTGGAG GCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTC GGTGGTGGGACCAAGGTGGAGATCAAA
1790.	FA22A9 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRVTITIDTSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLAVTVGETASMSCKSSQSLLYSR NQKNYLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLTISRVEAEDVGV YYCQQYFSYPLTFGGGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1791.	FA22A9 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTATAGACACGTCC TCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCTA TTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGACT ACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTCC CTAGCTGTGACAGTTGGAGAGACGGCTTCTATGAGCTGCAAGTCCAGTCAGAGCCT TTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGGCA GTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATC GCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCACGATCAGCAGAGTGGAG

1792.	FA22C11-H	artificial	aa	GCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTC GGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCAT GTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCT CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCA ACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAA AACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTAC TGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGG CCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATC ACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTG GCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATA GGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCT TGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAA TATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACT GACTGTCCTA
				QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQSPGQRLEWMGGINPNNGI PNYNQKFKGRVTITRDKSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSS
1793.	FA22C11-HCDR1	artificial	aa	EYTIH
1794.	FA22C11-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1795.	FA22C11-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1796.	FA22C11-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGTCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTAGAGACAAGTCC TCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCTA TTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGACT ACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA
1797.	FA22C11-L	artificial	aa	DIVMTQTPLSLPVTVGEPASISCKSSQSLLYSRNQKNYLAWYLQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCQQYFSYPLTFGGGTKVEIK
1798.	FA22C11-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1799.	FA22C11-LCDR2	artificial	aa	WASTRES
1800.	FA22C11-LCDR3	artificial	aa	QQYFSYPLT
1801.	FA22C11-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTACCTGTGACAGTTGGAGAGCCGGC

				TTCTATCAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAAGAACTA CTTGGCCTGGTACCTGCAGAAGCCAGGGCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GACTTCACCCTCAAGATCTCTCGTGTGGAGGCGGAGGATGTTGGAATCTATTACTG TCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATCA AA
1802.	FA22C11-HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQSPGQRLEWMGGINPNNGI PNYNQKFKGRVTITRDKSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTVGEPASISCKSSQSLLYSRN QKNYLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGIYY CQQYFSYPLTFGGGTKVEIK
1803.	FA22C11-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGTCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTAGAGACAAGTCC TCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCTA TTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGACT ACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTCC CTACCTGTGACAGTTGGAGAGCCGGCTTCTATCAGCTGCAAGTCCAGTCAGAGCCT TTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGGCA GTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATC GCTTCTCAGGCAGTGGATCTGGGACAGACTTCACCCTCAAGATCTCTCGTGTGGAG GCGGAGGATGTTGGAATCTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTC GGTGGTGGGACCAAGGTGGAGATCAAA
1804.	FA22C11 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQSPGQRLEWMGGINPNNGI PNYNQKFKGRVTITRDKSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTVGEPASISCKSSQSLLYSRN QKNYLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGIYY CQQYFSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLK TEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1805.	FA22C11 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA

				GACAGTCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTAGAGACAAGTCC TCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCTA TTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGACT ACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGG CGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTCC CTACCTGTGACAGTTGGAGAGCCGGCTTCTATCAGCTGCAAGTCCAGTCAGAGCCT TTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGGCA GTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATC GCTTCTCAGGCAGTGGATCTGGGACAGACTTCACCCTCAAGATCTCTCGTGTGGAG GCGGAGGATGTTGGAATCTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTTC GGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCAT GTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCT CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCA ACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAA AACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTAC TGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGG CCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATC ACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTG GCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATA GGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCT TGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAA TATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACT GACTGTCCTA
1806.	FA22D8-H	artificial	aa	QVQLVQSGAEVEKPGASVKVSCKASGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATITIDTSSSTAYMELSSLTSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSS
1807.	FA22D8-HCDR1	artificial	aa	EYTIH
1808.	FA22D8-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1809.	FA22D8-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1810.	FA22D8-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGGAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTATAGACACGTC

				CTCCAGCACCGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA
1811.	FA22D8-L	artificial	aa	DIVMTQTPLSLPVTVGEQASISCKSSQSLLYSRNQKNYLAWYLQKPGQSPKLLIYWAST RESGVPDRFSGSGSGTDFTLKISSVEAEDVGVYYCQQYFSYPLTFGGGTKVEIK
1812.	FA22D8-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1813.	FA22D8-LCDR2	artificial	aa	WASTRES
1814.	FA22D8-LCDR3	artificial	aa	QQYFSYPLT
1815.	FA22D8-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTACCTGTGACAGTTGGAGAGCAGGC TTCTATCAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAAGAACTA CTTGGCCTGGTACCTGCAGAAGCCAGGGCAGTCTCCTAAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGAC GGATTTCACTCTCAAGATCAGCAGTGTGGAGGCTGAGGATGTTGGAGTCTATTACT GTCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATC AAA
1816.	FA22D8-HL	artificial	aa	QVQLVQSGAEVEKPGASVKVSCKASGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATITIDTSSSTAYMELSSLTSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTVGEQASISCKSSQSLLYSR NQKNYLAWYLQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISSVEAEDVGV YYCQQYFSYPLTFGGGTKVEIK
1817.	FA22D8-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGGAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTATAGACACGTC CTCCAGCACCGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTC CCTACCTGTGACAGTTGGAGAGCAGGCTTCTATCAGCTGCAAGTCCAGAGCC TTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGGC AGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCAAGATCAGCAGTGTGGA GGCTGAGGATGTTGGAGTCTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTT CGGTGGTGGGACCAAGGTGGAGATCAAA
1818.	FA22D8 HL x I2C HL	artificial	aa	QVQLVQSGAEVEKPGASVKVSCKASGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATITIDTSSSTAYMELSSLTSEDTAVYYCARRRIAYGYDEGHAMDYWG

				QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTVGEQASISCKSSQSLLYSR NQKNYLAWYLQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISSVEAEDVGV YYCQQYFSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1819.	FA22D8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGGAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACACAATAACTATAGACACCGTC CTCCAGCACCGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTC CCTACCTGTGACAGTTGGAGAGCAGGCTTCTATCAGCTGCAAGTCCAGTCAGAGCC TTTTATATAGTCGTAATCAAAAGAACTACTTGTCAGCAATATTTTAGCTATCCGCTCACGTT AGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCAAGATCAGCAGTGTGGA GGCTGAGGATGTTGGAGTCTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTT CGGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCA GCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGC TCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGC AACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAA AAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGG CTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTAT CACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCT GGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGGTGGTCTAAT AGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGC TTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
1820.	FA22E8-H	artificial	aa	QVQLVQSGAELVKPGASVKVSCKASGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGIP

				NYNQKFKGRATITIDTSASTAYMELRSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQ GTLVTVSS
1821.	FA22E8-HCDR1	artificial	aa	EYTIH
1822.	FA22E8-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1823.	FA22E8-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1824.	FA22E8-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGGTGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTATAGACACGTC CGCCAGCACCGCCTACATGGAGCTCCGCAGCCTGAGATCTGAGGATACTGCGGTC TATTACTGTGCAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGA CTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA
1825.	FA22E8-L	artificial	aa	DIVMTQTPLSLAVTPGEQASISCKSSQSLLYSRNQKNYLAWYLQKPGQSPQLLIYWAST RESGVPDRFSGSGFGTDFTLKISGVEAEDVGVYYCQQYFSYPLTFGGGTKVEIK
1826.	FA22E8-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1827.	FA22E8-LCDR2	artificial	aa	WASTRES
1828.	FA22E8-LCDR3	artificial	aa	QQYFSYPLT
1829.	FA22E8-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTAGCTGTGACACCTGGAGAGCCAGGC TTCTATCAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAAGAACTA CTTGGCCTGGTACCTGCAGAAGCCAGGGCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATTTGGGACG GATTTCACTCTCAAGATCAGCGGAGTGGAGGCTGAGGACGTGGGAGTTTATTACTG TCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATCA AA
1830.	FA22E8-HL	artificial	aa	QVQLVQSGAELVKPGASVKVSCKASGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGIP NYNQKFKGRATITIDTSASTAYMELRSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQ GTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLAVTPGEQASISCKSSQSLLYSRN QKNYLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGFGTDFTLKISGVEAEDVGVY YCQQYFSYPLTFGGGTKVEIK
1831.	FA22E8-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGGTGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTATAGACACGTC CGCCAGCACCGCCTACATGGAGCTCCGCAGCCTGAGATCTGAGGATACTGCGGTC TATTACTGTGCAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGA CTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGC

				GGCGGCGGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCT CCCTAGCTGTGACACCTGGAGAGCAGGCTTCTATCAGCTGCAAGTCCAGTCAGAGC CTTTTATATAGTCGTAATCAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGG CAGTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGA TCGCTTCTCAGGCAGTGGATTTGGGACGGATTTCACTCTCAAGATCAGCGGAGTGG AGGCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGT TCGGTGGTGGGACCAAGGTGGAGATCAAA
1832.	FA22E8 HL x I2C HL	artificial	aa	QVQLVQSGAELVKPGASVKVSCKASGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGIP NYNQKFKGRATITIDTSASTAYMELRSLRSEDTAVYYCARRRIAYGYDEGHAMDYWGQ GTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLAVTPGEQASISCKSSQSLLYSRN QKNYLAWYLQKPGQSPQLLIYWASTRESGVPDRFSGSGFGTDFTLKISGVEAEDVGVY YCQQYFSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1833.	FA22E8 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGCTGGTGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTATAGACACGTC CGCCAGCACCGCCTACATGGAGCTCCGCAGCCTGAGATCTGAGGATACTGCGGTC TATTACTGTGCAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGA CTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGC GGCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCT CCCTAGCTGTGACACCTGGAGAGCAGGCTTCTATCAGCTGCAAGTCCAGTCAGAGC CTTTTATATAGTCGTAATCAAAGAACTACTTGGCCTGGTACCTGCAGAAGCCAGGG CAGTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGA TCGCTTCTCAGGCAGTGGATTTGGGACGGATTTCACTCTCAAGATCAGCGGAGTGG AGGCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGT TCGGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCA GCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGC TCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGC AACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAA AAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG

				GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGG CTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTAT CACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCT GGCAACTACCCAAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAAT AGGTGGGACTAAGTTCCTCGCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGC TTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
1834.	FA20H3-H	artificial	aa	QVQLVQSGAEVKKPGASVKMSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATITRDTSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSS
1835.	FA20H3-HCDR1	artificial	aa	EYTIH
1836.	FA20H3-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1837.	FA20H3-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1838.	FA20H3-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGATGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTAGAGACACGTC CTCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA
1839.	FA20H3-L	artificial	aa	DIVMTQTPFSLPVTPGEPASISCKSSQSLLYSRNQKNYLAWYQQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLNISRVEAEDVGVYYCQQYFSYPLTFGGGTKVEIK
1840.	FA20H3-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1841.	FA20H3-LCDR2	artificial	aa	WASTRES
1842.	FA20H3-LCDR3	artificial	aa	QQYFSYPLT
1843.	FA20H3-L	artificial	nt	GACATCGTGATGACACAGACTCCATTCTCCCTACCTGTGACACCTGGAGAGCCGGC TTCTATCAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAAGAACTA CTTGGCCTGGTACCAGCAGAAGCCAGGGCAGTCTCCTCAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACA GACTTCACCCTCAATATCTCTCGTGTGGAGGCGGAGGATGTTGGAGTCTATTACTG TCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATCA AA
1844.	FA20H3-HL	artificial	aa	QVQLVQSGAEVKKPGASVKMSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATITRDTSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG

				QGTLVTVSSGGGGSGGGGSGGGSDIVMTQTPFSLPVTPGEPASISCKSSQSLLYSRN QKNYLAWYQQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLNISRVEAEDVGVY YCQQYFSYPLTFGGGTKVEIK
1845.	FA20H3-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGATGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTAGAGACACGTC CTCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCATTCTC CCTACCTGTGACACCTGGAGAGCCGGCTTCTATCAGCTGCAAGTCCAGTCAGAGCC TTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCAGCAGAAGCCAGGGC AGTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCTCAGGCAGTGGATCTGGGACAGACTTCACCCTCAATATCTCTCGTGTGGA GGCGGAGGATGTTGGAGTCTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTT CGGTGGTGGGACCAAGGTGGAGATCAAA
1846.	FA20H3 HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKMSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATITRDTSSSTAYMELSSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTPGEPASISCKSSQSLLYSRN QKNYLAWYQQKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLNISRVEAEDVGVY YCQQYFSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1847.	FA20H3 HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGATGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACAATAACTAGAGACACGTC CTCCAGCACCGCCTACATGGAGCTCAGCAGCCTGAGATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCATTCTC CCTACCTGTGACACCTGGAGAGCCGGCTTCTATCAGCTGCAAGTCCAGTCAGAGCC TTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCAGCAGAAGCCAGGGC

1848.	FA19D12-H	artificial	aa	AGTCTCCTCAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCTCAGGCAGTGGATCTGGGACAGACTTCACCCTCAATATCTCTCGTGTGGA GGCGGAGGATGTTGGAGTCTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTT CGGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCA GCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGC TCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGC AACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAA AAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGG CTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTAT CACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCT GGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAAT AGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGC TTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
				QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTIHWVRQAHGQSLEWMGGINPNNGI PNYNQKFKGRVTITVDTSASTAYMELRSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSS
1849.	FA19D12-HCDR1	artificial	aa	EYTIH
1850.	FA19D12-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1851.	FA19D12-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1852.	FA19D12-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCATGGACAGAGCCTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTGTAGACACGTC CGCCAGCACCGCCTACATGGAGCTCCGCAGCCTGAGATCTGAGGATACTGCGGTC TATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGA CTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGC GGCGGCGCTCCGGTGGTGGTGGTTCT
1853.	FA19D12-L	artificial	aa	DIVMTQTPFSLPVTPGEPASISCKSSQSLLYSRNQKNYLAWYQQKPGQSPKLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYFSYPLTFGGGTKVEIK
1854.	FA19D12-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1855.	FA19D12-LCDR2	artificial	aa	WASTRES

1856.	FA19D12-LCDR3	artificial	aa	QQYFSYPLT
1857.	FA19D12-L	artificial	nt	GACATCGTGATGACACAGACTCCATTCTCCCTACCTGTGACACCTGGAGAGCCGGC TTCTATCAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAAGAACTA CTTGGCCTGGTACCAGCAGAAGCCAGGGCAGTCTCCTAAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGAC GGATTTCACTCTCAAAATCTCCAGAGTGGAGGCTGAGGACGTGGGAGTTTATTACT GTCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATC AAA
1858.	FA19D12-HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTIHWVRQAHGQSLEWMGGINPNNGI PNYNQKFKGRVTITVDTSASTAYMELRSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTPGEPASISCKSSQSLLYSRN QKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVY YCQQYFSYPLTFGGGTKVEIK
1859.	FA19D12-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCATGGACAGAGCCTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTGTAGACACGTC CGCCAGCACCGCCTACATGGAGCTCCGCAGCCTGAGATCTGAGGATACTGCGGTC TATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGA CTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGC GGCGGCGGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGACTCCATTCT CCCTACCTGTGACACCTGGAGAGCCGGCTTCTATCAGCTGCAAGTCCAGTCAGAGC CTTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCAGCAGAAGCCAGGG CAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGA TCGCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCAAAATCTCCAGAGTGG AGGCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGT TCGGTGGTGGGACCAAGGTGGAGATCAAA
1860.	FA19D12HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTIHWVRQAHGQSLEWMGGINPNNGI PNYNQKFKGRVTITVDTSASTAYMELRSLRSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPFSLPVTPGEPASISCKSSQSLLYSRN QKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVY YCQQYFSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPA RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

1861.	FA19D12HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGGCTTCTGGATACACATTCACTGAATACACCATACACTGGGTG AGACAGGCCCATGGACAGAGCCTTGAGTGGATGGGAGGTATTAATCCTAACAATGG TATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGTCACAATAACTGTAGACACGTC CGCCAGCACCGCCTACATGGAGCTCCGCAGCCTGAGATCTGAGGATACTGCGGTC TATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGA CTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGC GGCGGCGGCTCCGGTGGTGGTGGTTCTGACATCGTGATGACACAGACTCCATTCT CCCTACCTGTGACACCTGGAGAGCCGGCTTCTATCAGCTGCAAGTCCAGTCAGAGC CTTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTACCAGCAGAAGCCAGGG CAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGA TCGCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCAAAATCTCCAGAGTGG AGGCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGT TCGGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCA GCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGC TCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGC AACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAA AAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGG CTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTAT CACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCT GGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGGTGGTCTAAT AGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGC TTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC TGACTGTCCTA
1862.	FA19D9-H	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATLTIDTSASTAYMELSSLTSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSS
1863.	FA19D9-HCDR1	artificial	aa	EYTIH
1864.	FA19D9-HCDR2	artificial	aa	GINPNNGIPNYNQKFKG
1865.	FA19D9-HCDR3	artificial	aa	RRIAYGYDEGHAMDY
1866.	FA19D9-H	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA

				GACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACATTAACTATAGACACGTCC GCCAGCACCGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA
1867.	FA19D9-L	artificial	aa	DIVMTQTPLSLPVTPGEPASMSCKSSQSLLYSRNQKNYLAWFLQKPGQSPKLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYFSYPLTFGGGTKVEIK
1868.	FA19D9-LCDR1	artificial	aa	KSSQSLLYSRNQKNYLA
1869.	FA19D9-LCDR2	artificial	aa	WASTRES
1870.	FA19D9-LCDR3	artificial	aa	QQYFSYPLT
1871.	FA19D9-L	artificial	nt	GACATCGTGATGACACAGACTCCACTCTCCCTACCTGTGACACCTGGAGAGCCGGC TTCTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGTAATCAAAGAACTA CTTGGCCTGGTTCCTGCAGAAGCCAGGGCAGTCTCCTAAACTGCTGATTTACTGGG CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGAC GGATTTCACTCTCAAGATCAGCAGAGTGGAGGCTGAGGACGTGGGAGTTTATTACT GTCAGCAATATTTTAGCTATCCGCTCACGTTCGGTGGTGGGACCAAGGTGGAGATC AAA
1872.	FA19D9-HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATLTIDTSASTAYMELSSLTSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASMSCKSSQSLLYSR NQKNYLAWFLQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGV YYCQQYFSYPLTFGGGTKVEIK
1873.	FA19D9-HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACATTAACTATAGACACGTCC GCCAGCACCGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTC CCTACCTGTGACACCTGGAGAGCCGGCTTCTATGAGCTGCAAGTCCAGTCAGAGCC TTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTTCCTGCAGAAGCCAGGGC AGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCAAGATCAGCAGAGTGGA GGCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTT CGGTGGTGGGACCAAGGTGGAGATCAAA

1874.	FA19D9HL x I2C HL	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQRLEWMGGINPNNGI PNYNQKFKGRATLTIDTSASTAYMELSSLTSEDTAVYYCARRRIAYGYDEGHAMDYWG QGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASMSCKSSQSLLYSR NQKNYLAWFLQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGV YYCQQYFSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1875.	FA19D9HL x I2C HL	artificial	nt	CAGGTGCAGCTGGTCCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCTTCAGTAA AGGTGTCCTGCAAGACTTCTGGATACACATTCACTGAATACACCATACACTGGGTGA GACAGGCCCCTGGACAGAGACTTGAGTGGATGGGAGGTATTAATCCTAACAATGGT ATTCCTAACTACAATCAGAAGTTCAAGGGCAGGGCCACATTAACTATAGACACGTCC GCCAGCACCGCCTACATGGAGCTCAGCAGCCTGACATCTGAGGATACTGCGGTCT ATTACTGTGCAAGAAGAAGAATCGCCTATGGTTACGACGAGGGCCATGCTATGGAC TACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTGACATCGTGATGACACAGACTCCACTCTC CCTACCTGTGACACCTGGAGAGCCGGCTTCTATGAGCTGCAAGTCCAGTCAGAGCC TTTTATATAGTCGTAATCAAAAGAACTACTTGGCCTGGTTCCTGCAGAAGCCAGGGC AGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCTCAGGCAGTGGATCTGGGACGGATTTCACTCTCAAGATCAGCAGAGTGGA GGCTGAGGACGTGGGAGTTTATTACTGTCAGCAATATTTTAGCTATCCGCTCACGTT CGGTGGTGGGACCAAGGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCA GCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCA TGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGC TCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGC AACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAA AAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTA CTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGG GCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGG CTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTAT CACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCT GGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAAT AGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGC TTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGA ATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAAC

				TGACTGTCCTA
1876.	FA87G9-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSS
1877.	FA87G9-HCDR1	murine	aa	RYWMS
1878.	FA87G9-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1879.	FA87G9-HCDR3	murine	aa	GYYRYPYYYTMDY
1880.	FA87G9-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1881.	FA87G9-L	murine	aa	ELVMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGV PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1882.	FA87G9-LCDR1	murine	aa	RASGNIHNYLA
1883.	FA87G9-LCDR2	murine	aa	NAKTLAD
1884.	FA87G9-LCDR3	murine	aa	QHFWSTPYT
1885.	FA87G9-L	murine	nt	GAGCTCGTGATGACACAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACATATTCTCTCAAGATCAA CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1886.	FA87G9-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIK
1887.	FA87G9-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTTACTATACTATGGACTACTGGGGC

				CAAGGGACCACCGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1888.	FA87G9 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1889.	FA87G9 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAAT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG

				TGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1890.	FA86C12-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRSWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYYTMDYWGQGT TVTVSS
1891.	FA86C12-HCDR1	murine	aa	RSWMS
1892.	FA86C12-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1893.	FA86C12-HCDR3	murine	aa	GYYRYPYYYYTMDY
1894.	FA86C12-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATCCTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTTGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1895.	FA86C12-L	murine	aa	ELQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGV PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1896.	FA86C12-LCDR1	murine	aa	RASGNIHNYLA
1897.	FA86C12-LCDR2	murine	aa	NAKTLAD
1898.	FA86C12-LCDR3	murine	aa	QHFWSTPYT
1899.	FA86C12-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTGGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCCTCAGCTCCTAGTCTATAATGCAAAAACCTTAGCGGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAA CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1900.	FA86C12-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRSWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIK

1901.	FA86C12-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATCCTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTTGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTGGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTAGTCTATAATGCA AAAACCTTAGCGGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1902.	FA86C12 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRSWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1903.	FA86C12 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATCCTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTTGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTGGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTAGTCTATAATGCA AAAACCTTAGCGGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAAT

				CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATGCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1904.	FA86D2-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSS
1905.	FA86D2-HCDR1	murine	aa	TYWMS
1906.	FA86D2-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1907.	FA86D2-HCDR3	murine	aa	GYYRYPYYYTMDY
1908.	FA86D2-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1909.	FA86D2-L	murine	aa	ELVMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGV PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1910.	FA86D2-LCDR1	murine	aa	RASGNIHNYLA
1911.	FA86D2-LCDR2	murine	aa	NAKTLAD
1912.	FA86D2-LCDR3	murine	aa	QHFWSTPYT
1913.	FA86D2-L	murine	nt	GAGCTCGTCATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAA

				CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1914.	FA86D2-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIK
1915.	FA86D2-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1916.	FA86D2 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIKSGGGGSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1917.	FA86D2 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT

				CCGGTGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAAT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1918.	FA86D6-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMTKVRPEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSS
1919.	FA86D6-HCDR1	murine	aa	TYWMS
1920.	FA86D6-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1921.	FA86D6-HCDR3	murine	aa	GYYRYPYYYTMDY
1922.	FA86D6-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGACCAAAGTGAGACCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1923.	FA86D6-L	murine	aa	ELVMTQSPASLSASVGETVTITCRASGSIHNYLAWYQQKQGKSPQLLVYNAKTLADGVP SRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1924.	FA86D6-LCDR1	murine	aa	RASGSIHNYLA

1925.	FA86D6-LCDR2	murine	aa	NAKTLAD
1926.	FA86D6-LCDR3	murine	aa	QHFWSTPYT
1927.	FA86D6-L	murine	nt	GAGCTCGTCATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAGTATTCACAATTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAA CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1928.	FA86D6-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMTKVRPEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPASLSASVGETVTITCRASGSIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIK
1929.	FA86D6-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGACCAAAGTGAGACCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAGTATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1930.	FA86D6 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMTKVRPEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPASLSASVGETVTITCRASGSIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1931.	FA86D6 HL x I2C	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA

	HL			
				AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGACCAAAGTGAGACCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTCATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAGTATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAAT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATCCTACTGGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1932.	FA86E5-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRSWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSS
1933.	FA86E5-HCDR1	murine	aa	RSWMS
1934.	FA86E5-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1935.	FA86E5-HCDR3	murine	aa	GYYRYPYYYTMDY
1936.	FA86E5-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATCCTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTTGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC

				AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1937.	FA86E5-L	murine	aa	ELQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQLLVYNAKTLAEGVP SRFSGSGSRTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1938.	FA86E5-LCDR1	murine	aa	RASENIYSYLA
1939.	FA86E5-LCDR2	murine	aa	NAKTLAE
1940.	FA86E5-LCDR3	murine	aa	QHFWSTPYT
1941.	FA86E5-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGAGAATATTTACAGTTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGAAG GTGTGCCATCAAGGTTCAGTGGCAGTGGATCAAGAACACAATATTCTCTCAAGATCA ACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTC CGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1942.	FA86E5-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRSWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASENIYSYLAWY QQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSRTQYSLKINSLQPEDFGSYYCQHFWST PYTFGGGTKLEIK
1943.	FA86E5-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATCCTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTTGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGAGAATATTTACAGTTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGAAGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAAGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1944.	FA86E5 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSRSWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASENIYSYLAWY QQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSRTQYSLKINSLQPEDFGSYYCQHFWST

				PYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1945.	FA86E5 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATCCTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTTGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGAGAATATTTACAGTTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAACCTTAGCAGAAGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAAGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAAT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1946.	FA86F10-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSDDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSS
1947.	FA86F10-HCDR1	murine	aa	TYWMS

1948.	FA86F10-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1949.	FA86F10-HCDR3	murine	aa	GYYRYPYYYYTMDY
1950.	FA86F10-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGACGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1951.	FA86F10-L	murine	aa	ELVMTQSPSSLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGV PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1952.	FA86F10-LCDR1	murine	aa	RASGNIHNYLA
1953.	FA86F10-LCDR2	murine	aa	NAKTLAD
1954.	FA86F10-LCDR3	murine	aa	QHFWSTPYT
1955.	FA86F10-L	murine	nt	GAGCTCGTGATGACACAGTCTCCATCCTCCTTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAA CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1956.	FA86F10-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSDDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIK
1957.	FA86F10-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGACGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCCATCCTCCTTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA

				ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1958.	FA86F10 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSDDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELVMTQSPSSLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1959.	FA86F10 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGACGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCGTGATGACACAGTCTCCACTCCCTCCTTATCTGCA TCTGTGGGAGAAACTGTCACCCATCACATGTCGAGCAAGTGGGAATATTCACACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAAT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCCTCACCCTCTCAG

				GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1960.	FA86F12-H	murine	aa	EVQLLESGGGLVQPGGSLNLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSDDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSS
1961.	FA86F12-HCDR1	murine	aa	TYWMS
1962.	FA86F12-HCDR2	murine	aa	EINPDSSTINYTPSLKD
1963.	FA86F12-HCDR3	murine	aa	GYYRYPYYYTMDY
1964.	FA86F12-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA ATCTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAGTGAGATCTGACGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1965.	FA86F12-L	murine	aa	ELQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGV PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1966.	FA86F12-LCDR1	murine	aa	RASGNIHNYLA
1967.	FA86F12-LCDR2	murine	aa	NAKTLAD
1968.	FA86F12-LCDR3	murine	aa	QHFWSTPYT
1969.	FA86F12-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAA CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1970.	FA86F12-HL	murine	aa	EVQLLESGGGLVQPGGSLNLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSDDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIK
1971.	FA86F12-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA ATCTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGACGACACAGCCCTTTAT

				TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1972.	FA86F12 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLNLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSSTI NYTPSLKDKFIISRDNAKNTLYLQMNKVRSDDTALYYCAGGYYRYPYYYTMDYWGQGT TVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWS TPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1973.	FA86F12 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA ATCTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGATAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGAACAAAGTGAGATCTGACGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAAT CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC

				TACATATCCTACTGGCTTACTGGGCCAAGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1974.	FA86F2-H	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSST VNYTPSLKDKFIISRDNAKNTLYLQMTKVRSEDTALYYCAGGYYRYPYYYTMDYWGQG TTVTVSS
1975.	FA86F2-HCDR1	murine	aa	TYWMS
1976.	FA86F2-HCDR2	murine	aa	EINPDSSTVNYTPSLKD
1977.	FA86F2-HCDR3	murine	aa	GYYRYPYYYTMDY
1978.	FA86F2-H	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGGTAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGACCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
1979.	FA86F2-L	murine	aa	ELQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGV PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIK
1980.	FA86F2-LCDR1	murine	aa	RASGNIHNYLA
1981.	FA86F2-LCDR2	murine	aa	NAKTLAD
1982.	FA86F2-LCDR3	murine	aa	QHFWSTPYT
1983.	FA86F2-L	murine	nt	GAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT CACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTATCAGCA GAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGG TGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAA CAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCC GTACACGTTCGGAGGGGGGACCAAGCTTGAGATCAAA
1984.	FA86F2-HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSST VNYTPSLKDKFIISRDNAKNTLYLQMTKVRSEDTALYYCAGGYYRYPYYYTMDYWGQG TTVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAW YQQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFW

				STPYTFGGGTKLEIK
1985.	FA86F2-HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGGTAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGACCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGC CAAGGGACCACGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAA
1986.	FA86F2 HL x I2C HL	murine	aa	EVQLLESGGGLVQPGGSLKLSCAASGFDFSTYWMSWVRQAPGKGLEWIGEINPDSST VNYTPSLKDKFIISRDNAKNTLYLQMTKVRSEDTALYYCAGGYYRYPYYYTMDYWGQG TTVTVSSGGGGSGGGGSGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAW YQQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFW STPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNW VRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1987.	FA86F2 HL x I2C HL	murine	nt	GAGGTGCAGCTGCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGA AACTCTCCTGTGCAGCCTCAGGATTCGATTTTAGTACATACTGGATGAGTTGGGTCC GGCAGGCTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGT ACGGTAAACTATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCC AAAAATACGCTGTACCTGCAAATGACCAAAGTGAGATCTGAGGACACAGCCCTTTAT TACTGTGCAGGAGGATACTATAGGTACCCATATTACTATGGACTACTGGGGCGGCGCT CCGGTGGTGGTGGTTCTGAGCTCCAGATGACCCAGTCTCCAGCCTCCCTATCTGCA TCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTAT TTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCA AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACA ATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTTGGGAGTTATTACTGTCA ACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAGCTTGAGATCAAAT

				CCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGC AGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGT ACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCG CATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGG TTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGA AAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGC TACATATGCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGG TGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGTTGTG ACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGG CTCCTCGACTGGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAAC CAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTAC TCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAG GGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGC TGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
1988.	human IGF-R1 construct	artificial	nt	ATGAAGTCTGGCTCCGGCGGAGGGTCCCCGACCTCGCTGTGGGGGCTCCTGTTTCTCTCCGCCGC GCTCTCGCTCTGGCCCGACGAGTGGAGAAATCTGCGGGCCAGGCATCGACATCCGCAACGACTATC AGCAGCTGAAGCGCCTGGCAGAACTGCACGGTGATCGAGGGCTACCTCCACATCCTGCTCATCTCC AAGGCCGAGGACTACCGCAGCTACCGCTTCCCCAAGCTCACGGTCATCACCGAGTACTTGCTGCT GTTCCGAGTGGCTGGCCICGAGAGCCTCTTCCCCAACCICACGGTCATCCGCGGCT GGAAACTCTTCTACAACTACGCCCTGGTCAICTTCGAGATGACCAATCTCAAGGATATTGGGCTT TACAACCTGAGGAACATTACTCGGGGGGCCATCAGGATTGAGAAAAACTGCTGACCTCTGTTACCT CTCCACTGTGGACTGGTCCCTGATCCTGGATGCGGTGTCCAATAACTACATTGTGGGGAATAAGC CCCCAAAGGAATGTGGGCACCTGTGTCCAGGGACCATGGAGGAGAAGCCGATGTGTGAGAAGACC ACCATCAACAATGAGTACAACTACCGCTGCTGGACCACACAACCGCTGCCAGAAAATGTGCCCAAG CACGTGTGGGAAGCGGGCGTGCACCGAGAACAATGAGTGCTGCCACCCCGAGTGCCTGGGCAGCT GCAGCGCGCCTGACAACGACACGGCCTGTGTAGCTTGCCGCCACTACTACTATGCCGGTGTCTGT GTGCCTGCCTGCCCGCCCAACACCTACAGGTTTGAGGGCTGGCGCTGTGTGGACCGTGACTTCTG CGCCAACATCCTCAGCGCCGAGAGCAGCGACTCCGAGGGGTTTGTGACTCCACGACGGCGAGTGCA TGCAGGAGTGCCCCTCGGGCTTCATCCGCAACGGCAGCCAGAGCATGTCACTGCATCCCTTGTGAA GGTCCTTGCCCGAAGGTCTGTGAGGAAGAAAGAAACACAAGACCATTGATTCTGTTACTTCTGC TCAGATGCTCCAAGGATGCCACCATCTTCAAGGGCAATTTGCTCATTAACATCCGACGGGGGAATA ACATTGCTTCAGAGCTGGAGAACTTCATGGGGCTCATCGAGGTGGTGACGGGCTACGTGAAGATC CGCCATTCTCATGCCTTCGTCCTCTTCCTTAAAAAACCTTCGCCTCATCCTAGGAGAGGA GCAGCTAGAAGGGAATTACTCCTTCTACGTCCTCGACAACCAGAACTTGCAGCAACTGTGGGACT GGGACCACCGCAACCTGACCATCAAAGCAGGGAAAATGTACTTTGCTTTCAATCCCAAATTATGT GTTTCCGAAATTACCGCATGGAGGAAGTGACGGGACTAAAGGCGCCAAAGCAAAGGGACAT AAACACCAGGAACAACGGGGAGAGAGCCTCCTGTGAAAGTGACGTCCTGCATTTCACCTCCACCA

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1989.	human IGF-R1 construct	artificial	aa	MKSGSGGGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLENCTVIEGYLHILLIS KAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGL YNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKT TINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVC VPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCE GPCPKVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKI RHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLC VSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLHFTSTTTSKNRIIITWHRYRPPDYRDL ISFTVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVT LTMVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQR QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEKGPCCACPKTEAEKQAEKEE AEYRKVFENFLHNSIFVPRPERKRDVMQVANTTMSSRSRNTTAADTYNITDPEELETEYPFFES RVDNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPE NSIFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQFYRKYGGAKLNRLNPGNYTARIQATSL SGNGSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHRKRNNSRLGNGVLYAS VNPEYFSAADVYVPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAAS MRERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLA PPSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGG KGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPD NCPDMLFELMRMCWQYNPKMRPSFLEIISSIKEEMEPGFREVSFYYSEENKLPEPEELDLEPENM ESVPLDPSASSSSLPLPDRHSGHKAENGPGPGVLVLRASFDERQPYAHMNGGRKNERALPLPQSS TC
1990.	soluble fusion protein of h IGF-R1 and m IgG1 Fc	artificial	nt	ATGAAGTCTGGCTCCGGCGGAGGGTCCCCGACCTCGCTGTGGGGGCTCCTGTTTCTCTCCGCCGC GCTCTCGCTCTGGCCCGACGAGTGGAGAAATCTGCGGGCCAGGCATCGACATCCGCAACGACTATC AGCAGCTGAAGCGCCTGGAGAACTGCACGGTGATCGAGGGCTACCTCCACATCCTGCTCATCTCC AAGGCCGAGGACTACCGCAGCTACCGCTTCCTCCAAGCTCACGGTCATCTACCGAGTACTTGCTGCT GTTCCGAGTGGTGGCCTCGAGAGCCTCGGAGACCTCTTCCCCAACCTCACGGTCATCCGCGGCT GGAAACTCTTCTACAACTACGCCCTGGTCATCTTCGAGATGACCAATCTCAAGGATATTGGGCTT TACAACCTGAGGAACATTACTCGGGGGGGCCATCAGGATTGAGAAAAACTGCTGACCTCTGTTACCT CTCCACTGTGGACTGGTCCCTGATCCTGGATGCGGTGTCCAATAACTACATTGTGGGGAATAAGC CCCCAAAGGAATGTGGGGACCTGTGTCCAGGGACCATGGAGGAGAAGCCGATGTGTGAGAAGACC ACCATCAACAATGAGTACAACTACCGCTGCTGGACCACACAAACCGCTGCCAGAAAATGTGCCCAAG CACGTGTGGGAAGCGGCGTGCACCGAGAACAATGAGTGCTGCCACCCCGAGTGCCTGGGCAGCT

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1991.	soluble fusion protein of h IGF-R1 and m IgG1 Fc	artificial	aa	MKSGSGGGGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLENCTVIEGYLHILLIS KAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGL YNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKT TINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVC VPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCE GPCPKVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKI RHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLC VSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLHFTSTTTSKNRIIITWHRYRPPDYRDL ISFTVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVT LTMVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQR QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEKGPCCACPKTEAESQAEKEE AEYRKVFENFLHNSIFVPRPERKRRDVMQVANTTMSSRSRNTTAADTYNITDPEELETEYPFFES RVDNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPE NSIFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSL SGNGSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHRKRNNSRLGNGVLYA LTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQINSTFRSVSELPIMHQDWLNGKEF KCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITNFFPEDITVEWQWN GQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGKSG HHHHHH
1992.	murine IGF-R1 construct	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGATTACAA GGACGACGATGACAAGGAAATCTGTGGGCCCGGCATTGACATCCGCAACGACTATCAGCAGCTGA AGCGCCTGGAAAACTGCACGGTGATCGAGGGCTTCCTCCACATCCTGCTCATCTCCAAGGCCGAG GACTACCGAAGCTACCGCTTCCCCAAGCTCACCGTCATCACTGAGTACTTGCTGCTCTTCCGAGT CGCTGGCCTCGAGAGCCIGGGAGACCTCTTCCCCAACCTCACAGTCATCCGTGGCTGGAAACTCT TCTACAACTACGCACTGGTCATCTTCGAGAIGACCAATCTCAAGGATATTGGGCTTTATAATCTG AGGAACATTACTCGGGGGGCCATCAGGATTGAGAAGAACGCCGACCTCTGTTACCTCTCCACCAT AGACTGGTCTCTCATCTTGGATGCGGTGTCCAATAACTACATTGTGGGGAACAAGCCCCCGAAGG AATGTGGGGACCTGTGTCCAGGGACATTGGAGGAGAAGCCCATGTGTGAGAAGACCACCATCAAC AATGAGTACAACTACCGCTGCTGGACCACACAAATCGCTGCCAGAAAATGTGCCCAAGTGTGCGG GAAGCGAGCCTGCACCGAGAACAACGAGTGCTGCCACCCGGAGTGCCTGGGCAGCTGCCACACAC

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CACCATGAACCGGGAGCTCGGACAAGGGTCCTTTGGGATGGTCTATGAAGGAGTGGCCAAGGGTG
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				GAAAGAATCGAGTTTCTCAACGAGGCCTCGGTGATGAAGGAGTTCAACATGTCACCATGTGGTCCG GTTGCTGGGTGTGGTATCCCAAGGCCAGCCCACCCTGGTCATCATGGAACTAATGACACGCGGTG ATCTCAAAAGTTATCTCCGGTCTCTGAGGCCAGAAGTGGAGCAGAATAATCTAGTCCTCATTCCT CCCAGCTTAAGCAAGATCATCCAGATGGCCTGCAGACATTGCACATGCCATGGCCCTACCTCAATGC CAACAAGTTCGTCCACACAGACCTTGCTGCTAGGAACTGCATGGTAGCCGAAGATTTCACAGTCA AAATTGGAGATTTCGGTATGACACGAGACATCTACGAGACGGACTACTACCGGAAAGGCGGGAAG GGGTTGCTGCCTGTGCGCTGGATGTCTCCCGAGTCCCTCAAGGATGGCGTGTCTTCACTACTCATTC TGATGTCTGGTCCTTCGGGGTCGTCCTCTGGGAGATCGCCACGCTGGCTGAGCAGCCCTACCAGG GCTTGTCCAACGAGCAAGTTCTTCGTTTCGTCATGGAGGGTGGCCTTCTGGACAAGCCGGACAAC TGCCCTGATATGCTGTTTGAACTTATGCGCATGTGCTGGCAGTATAACCCCAAGATGCGGCCCTC CTTCCTGGAGATCATCGGCAGCATCAAGGAIGAGATGGAGCCCAGCTTCCAGGAGGTCTCCTTCT ACTACAGCGAGGAGAACAAGCCTCCCGAGCCAGAGGAGCTGGAGATGGAGCCTGAGAACATGGAG AGCGTCCCACTGGACCCTTCGGCCTCCTCAGCCTCCCTGCCTCTGCCTGAAAGACACTCAGGACA CAAGGCTGAGAATGGCCCGGGCCCTGGCGTGCTCGTTCTCCGCGCCAGTTTTGATGAGACAGC CTTACGCTCACATGAACGGGGGACGCGCCAACGAGAGGGCCTTGCCTCTGCCCCAGTCCTCGACC TGCTGA
1993.	murine IGF-R1 construct	artificial	aa	MGWSCIILFLVATATGVHSDYKDDDDKEICGPGIDIRNDYQQLKRLENCTVIEGFLHILLISKAE DYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNL RNITRGAIRIEKNADLCYLSTIDWSLILDAVSNNYIVGNKPPKECGDLCPGTLEEKPMCEKTTIN NEYNYRCWTTNRCQKMCPSVCGKRACTENNECCHPECLGSCHTPDDNTCVACRHYYYKGVCVPA CPPGTYRFEGWRCVDRDFCANIPNAESSDSDGFVIHDDECMQECPSGFIRNSTQSMYCIPCEGPC PKVCGDEEKKTKTIDSVTSAQMLQGCTILKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRH SHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWNHRNLTVRSGKMYFAFNPKLCVS EIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLRFTSTTTWKNRIITWHRYRPPDYRDLIS FTVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKEGEPGILLHGLKPWTQYAVYVKAVTLT MVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPTLPNGNLSYYIVRWQRQP QDGYLYRHNYCSKDKIPIRKYADGTIDVEEVTENPKTEVCGGDKGPCCACPKTEAEKQAEKEEAE YRKVFENFLHNSIFVPRERRRRDVMQVANTTMSSRSRNTTVADTYNITDPEELETEYPFFESRV DNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPENS IFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSLSG NGSWTDPVFFYVPAKTTYENPMHLIIALPVAILLIVGGLVIMLYVFHRKRNNSRLGNGVLYASVN PEYFSAADVYVPDEWEVAREKITMNRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAASMR ERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEVENNPVLAP PSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGK GLLPVRWMSPESLKDGVFTTHSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDN CPDMLFELMRMCWQYNPKMRPSFLEIISSIKDEMEPSFQEVSFYYSEENKPPEPELEMEPENME SVPLDPSASSASLPLPERHSGHKAENGPGSVLVLRASFDERQPYAHMNGGRANERALPLPQSST

				C
1994.	mutated human IGF-R1 antigen	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGATTACAA GGACGACGATGACAAGGAAATCTGTGGGCCCGGCATTGACATCCGCAACGACTATCAGCAGCTGA AGCGCCTGGAAAACTGCACGGTGATCGAGGGCTTCCTCCACATCCTGCTCATCTCCAAGGCCGAG GACTACCGAAGCTACCGCTTCCCCAAGCTCACCGTCATCACTGAGTACTTGCTGCTCTTCCGAGT CGCTGGCCTCGAGAGCCTGGGAGACCTCTTCCCCAACCTCACAGTCATCCGTGGCTGGCTGAAACTCT TCTACAACTACGCACTGGTCATCTTCGAGATGACCAATCTCAAGGATATTGGGCTTTATAATCTG AGGAACATTACTCGGGGGGCCATCAGGATTGAGAAGACGCCGACCTCTGTTACCTCTCCACCAT AGACTGGTCTCTCATCTTGGATGCGGTGTCCAATAACTACATTGTGGGGAACAAGCCCCCGAAGG AATGTGGGACCTGTGTCCAGGGACATTGAGGAGAAGCCCATGTGTGAGAAGACCACCATCAAC AATGAGTACAACTACCGCTGCTGGACCACACAAATCGCTGCCAGAAAATGTGCCCAAGTGTGTGCGG GAAGCGAGCCTGCACCGAGAACAACGAGTGCTGCCACCCGGAGTGCCTGGGCAGCTGCCACACAC CGGACGACAACACAACCTGCGTGGCCTGCAGACACTACTACAAAGGCGTGTGTGCCTGCC TGCCCGCCTGGCACCTACAGGTTCGAGGGCTGGCGCTGTGTGGATCGCCGATTTCTGCGCCAACAT CCCCAACGCTGAGAGCAGTGACTCGGATGGCTTCGTTATCCACGACGATGAGTGCATGCAGGAGT GTCCCTCAGGCTTCATCCGCAACAGCACCCAGAGCATGTACTGTATCCCCTGCGAAGGCCCCTGC CCCAAGGTCTGTGAGGAAGAAAGAAACACAAAGACCATTGATTCTGTTACTTCTGCTCAGATGCT CCAAGGATGCACCATCTTCAAGGGCAATTTGCTCATTAACATCCGACGGGGGAATAACATTGCTT CAGAGCTGGAGAACTTCATGGGGCTCATCGAGGTGGTGACGGGCTACGTGAAGATCCGCCATTCT CATGCCTTGGTCTCCTTGTCCTTCCTAAAAAACCTTCGCCTCATCCTAGGAGAGGAGCAGCTAGA AGGGAATTACTCCTTCTACGTCCTCGACAACCAGAACTTGCAGCAACTGTGGGACCACC GCAACCTGACCATCAAAGCAGGGAAAATGTACTTTGCTTTCAATCCCAAATTATGTGTTTCCGAA ATTTACCGCATGGAGGAAGTGACGGGGACTAAAGGGCGCCAAAGCAAAGGGACATAAACACCAG GAACAACGGGGAGAGAGCCTCCTGTGAAAGTGACGTCCTGCATTTCACCTCCACCACACGTCGA AGAATCGCATCATCATAACCTGGCACCGGTACCGGCCCCCTGACTACAGGGATCTCATCAGCTTC ACCGTTTACTACAAGGAAGCACCCCTTTAAGAATGTCACAGAGTATGATGGGCAGGATGCCTGCGG CTCCAACAGCTGGAACATGGTGGACGTGGACCTCCCGCCCAACACAAGGACGTGGAGCCCGGCATCT TACTACATGGGCTGAAGCCCCTGGACTCAGTACGCCGTTTACGTCAAGGCTGTGACCCTCACCATG GTGGAGAACGACCATATCCGTGGGGCCAAGAGTGAGATCTTGTACATCTCGCACCAATGCTTCAGT TCCTTCCATTCCCTTGGACGTTCTTTCAGCATCGAACTCCTCTTCAGTTAATCGTGAAGTGGA ACCCTCCCTCTCTGCCCAACGGCAACCTGAGTTACTACATTGTGCGCTGGCAGCGGCAGCCTCAG GACGGCTACCTTTACCGGCACAATTACTGCTCCAAAGACAAAATCCCCATCAGGAAGTATGCCGA CGGCACCATCGACATTGAGGAGGTCACAGAGAACCCCAAGACTGAGGTGTGTGGGGAGAAAG GGCCTTGCTGCGCCTGCCCCAAAACTGAAGCCAGGCCGAGAAGCAGGCCGAGAAGGAGGCTGAATAC CGCAAAGTCTTTGAGAATTTCCTGCACACAACICCATCTTCGTGCCCAGACCTGAAGGAAGCGGAG AGATGTCATGCAAGTGGCCAACACCACCATGTCCAGCCGAAGCAGGAACACCACGGCCGCAGACA CCTACAACATCACCGACCCGGAAGAGCTGGAGACAGAGTACCCTTCTTGAGAGCAGAGTGGAT

				AACAAGGAGAGAACTGTCATTTCTAACCTTCGGCCTTTCACATTGTACCGCATCGATATCCACAG
				CTGCAACCACGAGGCTGAGAAGCTGGGCTGCAGCGCCTCCAACTTCGTCTTGCAAGGACTATGC
				CCGCAGAAGGAGCAGATCACATTCCTGGGCCAGTGACCTGGGAGCCAAGGCCTGAAAACTCCATC
				TTTTTAAACTGCCCCGCAACCTGACAATCCCAATGCATTCATTCTAATGTATCAAATAAAATACGG
				ATCACAAGTTGAGGATCAGCGAGAATGTGTCTCCAGACAGGAATACAGGAAGTATGGAGGGCCA
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				TCTGATCATCGCTCTGCCCGTCGCTGTCCTGTTGATCGTGGGAGGGTTGGTGATTATGCTGTACG
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				GAGTACTTCAGCGCTGCTGATGTGTACGTTCCTGATGAGTGGGAGGTGGCTCGGGAGAAGATCAC
				CATGAGCCGGGAACTTGGGCAGGGTCGTTTGGGATGGTCTATGAAGGAGTTGCCAAGGGTGTGG
				TGAAAGATGAACCTGAAACCAGAGTGGCCAITAAAACAGTGAACGAGGCCGCAAGCATGCGTGAG
				AGGATTGAGTTTCTCAACGAAGCTTCTGTGATGAAGGAGTTCAATTGTCACCATGTGGTGCGATT
				GCTGGGTGTGGTGTCCCAAGGCCAGCCAACACTGGTCATCATGGAACTGATGACACGGGGCGATC
				TCAAAAGTTATCTCCGGTCTCTGAGGCCAGAAATGGAGAATAATCCAGTCCTAGCACCTCCAAGC
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				CTGGTCCTTCGGGGTCGTCCTCTGGGAGATCGCCACACTGGCCGAGCAGCCCTACCAGGGCTTGT
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				CCCCTGGACCCCCTCGGCCTCCTCGTCCCCTGCCACTGCCCCGACAGACACTCAGGACACAAGGC
				CGAGAACGGCCCCGGCCCTGGGGTGCTGGTCCTCCGCGCCAGCTTCGACGAGAGACAGCCTTACG
				CCCACATGAACGGGGGCCCGCAAGAACGAGCCGGGCCTTGCCGCTGCCCCAGTCTTCGACCTGCTGA
1995.	mutated human IGF-R1 antigen	artificial	aa	MGWSCIILFLVATATGVHSDYKDDDDKEICGPGIDIRNDYQQLKRLENCTVIEGFLHILLISKAE
				DYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNL
				RNITWGALRLRNLADLCYLSIIDWSLILDAVSNNYIVGNKPPKECGDLCPGTLEEKPMCEKTTIN
				NEYNYRCWTTNRCQKMCPSVCGKRACTENNECCHPECLGSCHTPDDNTCVACRHYYYKGVCVPA
				CPPGTYRFEGWRCVDRDFCANIPNAESSDSDGFVIHDDECMQECPSGFIRNSTQSMYCIPCEGPC
				PKVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHS
				HALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLCVSE
				IYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLHFTSTTTSKNRIIITWHRYRPPDYRDLISF
				TVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVTLTM
				VENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQRQPQ

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				NKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPENSI
				FLKWPEPENPNGLIILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSLSGN
				GSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHRKRNNSRLGNGVLYASVNP
				EYFSAADVYVPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAASMRE
				RIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLAPPS
				LSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGKGL
				LPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCP
				DMLFELMRMCWQYNPKMRPSFLEIISSIKEEMEPGFREVSFYYSEENKLPEPEELDLEPENMESV
				PLDPSASSSSLPLPDRHSGHKAENGPGPGVLVLRASFDERQPYAHMNGGRKNERALPLPQSSTC
1996.	mutated murine IGF-R1 antigen	artificial	nt	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTACACTCCGATTACAA
				GGACGACGATGACAAGGAAATCTGCGGGCCAGGCATCGACATCCGCAACGACTATCAGCAGCTGA
				AGCGCCTGGAGAACTGCACGGTGATCGAGGGCTACCTCCACATCCTGCTCATCTCCAAGGCCGAG
				GACTACCGCAGCTACCGCTTCCCCAAGCTCACGGTCATTACCGAGTACTTGCTGTTCCGAGT
				GGCTGGCCTCGAGAGCCTCGGAGACCTCTTCCCCAACCTCACGGTCATCCGCGGCTGGAAACTCT
				TCTACAACTACGCCCTGGTCATCTTCGAGATGACCAATCTCAAGGATATTGGGCTTTACAACCTG
				AGGAACATTACTCGGGGGCCATCAGGATTGAGAAAAATGCTGACCTCTGTTACCTCCACTGT
				GGACTGGTCCCTGATCCIGGATGCGGTGTCCAATAACTACATTGTGGGGAATAAGCCCCCAAAGG
				AATGTGGGGACCTGTGTCCAGGGACCATGGAGAGGAAGCCGATGTGTGAGAAGACCACCATCAAC
				AATGAGTACAACTACCGCTGCTGGACCACACAAACCGCTGCCAGAAAATGTGCCCAAGCACGTGTGG
				GAAGCGGGCGTGCACCGAGAACAATGAGTGCTGCCACCCCGAGTGCCTGGGCAGCTGCAGCGCGC
				CTGACAACGACACGGCCIGTGTAGCTTGCCGCCACTACTATGCCGGTGTCTGTGTGCCTGCC
				TGCCCGCCCAACACCTACAGGTTTGAGGGCTGGCGCTGTGTGGACCGCTGACTTCTGCGCCAACAT
				CCTCAGCGCCGAGAGCACCGACTCCGAGGGCTTTGTGATCCACGACGGCGAGTGCATGCAGGAGT
				GCCCCTCGGGCTTCATCCGCAACGGCAGCCAGAGCATGTACTGCATCCCTTGTGAAGGTCCTTGC
				CCGAAAGTCTGCGGCGATGAAGAGAAGAAAACGAAAACCATCGATTCGGTGACTTCTGCTCAAAT
				GCTCCAAGGATGCACCATCCCTGAAGGGCAATCTGCTTATTAACATCCGGAGAGGCAATAACATTG
				CCTCGGAGTTGGAGAACTTCATCATGGGGCTCATCGAGGTGGTGACCGGCTACGTGAAGATCCGCCAT
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				GGAAGGGAACTACTCCTTCTATGTCCTAGACAACCAGAACTTGCAGCAGCTGTGGGACTGGAACC
				ACCGGAACCTGACCGTCAGGTCCGGAAGAIGTACTTTGCTTTCAATCCCAAGCTGTGTCTCC
				GAAATTTACCGCATGGAGGAAGTGACCGGAACCAAGGGACGCCAGAGCAAAGGGACATAAACAC
				CAGGAACAACGGAGAGCGAGCTTCCTGTGAAAGTGATGTTCTCCGTTTCACCTCCACCACGACCT
				GGAAGAACCGAATCATCATAACGTGGCACCGGTACCGGCCGCGGACCACCGGGATCTCATCAGC
				TTCACAGTTTACTACAAGGAGGCACCATTTAAAAACGTTACGGAATACGACGGGCAGGATGCCTG
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CTTACGCTCACATGAACGGGGGACGCGCCAACGAGAGGGCCTTGCCTCTGCCCCAGTCCTCGACC

				TGCTGA
1997.	mutated murine IGF-R1 antigen	artificial	aa	MGWSCIILFLVATATGVHSDYKDDDDKEICGPGIDIRNDYQQLKRLENCTVIEGYLHILLISKAE DYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNL RNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKTTIN NEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVCVPA CPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCEGPC PKVCGDEEKKTKTIDSVTSAQMLQGCTILKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRH SHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWNHRNLTVRSGKMYFAFNPKLCVS ETYRMEVTGTKGRQSKGDINTRNNGERASCESDVLRFTSTTTWKNRIITWHRYRPPDYRDLIS FTVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKESGEPGILLHGLKPWTQYAVYVKAVTLT MVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPTLPNGNLSYYIVRWQRQP QDGYLYRHNYCSKDKIPIRKYADGTIDVEEVTENPKTEVCGGDKGPCCACPKTEAEKQAEKEEAE YRKVFENFLHNSIFVPRPERRRRDVMQVANTTMSSRSRNTTVADTYNITDPEELETEYPFFESRV DNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPENS IFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSLSG NGSWTDPVFFYVPAKTTYENFMHLITALPVAILLIVGGLVIMLYVFHRKRNNSRLGNGVLYASVN PEYFSAADVYVPDEWEVAREKITMNRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAASMR ERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEVENNPVLAP PSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGK GLLPVRWMSPESLKDGVFTTHSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDN CPDMLFELMRMCWQYNPKMRPSFLEIISSIKDEMEPSFQEVSFYYSEENKPPEPELEMEPENME SVPLDPSASSASLPLPERHSGHKAENGPGSVLVLRASFDERQPYAHMNGGRANERALPLPQSST C
1998.	macaque IGF-R1	artificial	nt	ATGAAGTCTGGCTCTGGAGAAGGGTCCCCGACCTCGCTGTGGGGGCTCCTGTTCTCTCCGCCGC GCTCTCGCTCTGGCCGACGAGTGGAGAAATCTGTGGCCGGGCATCGACATCCGCAACGACTATC AGCAGCTGAAGCGCCTGCAGAACTGCACGGTGATCGAGGGCTACCTCCACATCCTGCTCATCTCC AAGGCCGAGGACTACCGCAGCTACCGCTTCCCCAAGCTCACGGTCATCACCGAGTACTTGCTGTT GTTCCGAGTGGCTGGCCTAGAGAGCCTCGGAGACCTGTTCCCCAACCTCACGGTAATCCGCGGCT GGAAACTCTTCTACAACTACGCCCTGGTCATCTTTGAGATGACCAATCTCAAGGATATTGGGCTT TACAACCTGAGGAACATTACTCTGGGGGGCCATCAGGATTGAGAAAAATGCTGACCTCTGTTACCT CTCCACTGTGGACTGGTCCCTGATCCTGGAIGCAGTGTCCAATAACTACATTGTGGGGAATAAGC CCCCAAAGGAATGCCGGGCACCTGTGTCCGGGACCATGGAGGAGAAGCCGATGTGCGAGAAGACC ACCATCAACAATGAGTACAACTACCGCTGCTGGACCACAAACCGCTGCCAGAAAATGTGCCCGAG TGCCTGTGGGAAGAGGCATGCACCGAGAACAACGAGTGCTGCCACCCCGAGTGCCTGGGCAGCT GCAGCGCGCCTGACAACGACACGGCCTGTGTAGCTTGCCGCCACTACTACTACGCCGGTGTCTGC GTGCCTGCCTGCCCGCCCAACACCTACAGGTTTGAGGGCTGGCGCTGTGTGGACCGTGACTTCTG CGCCAACATCCTCAGCGCCGAGAGCAGCGACTCCGAGGGTTTCGTGACTCCACGACGGCGAGTGCA

TGCAGGAGTGCCCCTCAGGCTTCATCCGCAACGGCAGCCAGAGCATGTACTGCATCCCTTGTGAA
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AGAGTGGATAATAAGGACAGAACTGTCATTTCTAACCTTCGGCCTTTCACATTGTACCGCATTGA
TATCCACACGCTGCCAACCACCAGGCTGACAAACTGGCGCTCCAGCGCCTCCAACTTTGTCTTTGCCAA
GGACTATGCCTGCAGAACGAGATGACATTCCTGGGCCCAGTGACCTGGGAGCCCAAGGCCTGAA
AACTCCATCTTTTTAAAGTGGCCCAGAACCTGAGAATCCCAATGGATTGATTCTAATGTATGAAAT
AAAATACGGATCACACAAGTTGAGGATCAGCGAGAATGTGTGTCCAGACAGGAATACAGGAAGTATG
GAGGGGCCAAGCTAAACCGGCTAAACCCAGGAACTACACAGCCCGGATTCAGGCTACATCTCTC
TCTGGGAATGGGTCGTGGCACAGATCCTGTGTTCTTCTATGTCCAGGCCAAAACAGGATATGAAAA
CTTCATCCATCTGATCATCGCTCTGCCCGTCGCTGTTGATCGTGGGAGGGTTGGTGATCA
TGCTGTACGTCTTCCATAGAAAGAGAATAACAGCAGGCTGGGGAATGGAGTGCTGTACGCGTCT
GTGAACCCGGAGTACTTCAGCGCTGCGGATGTGTACGTTCCTGATGAGTGGGAGGTGGCTCGGGA
GAAGATCACCATGAGCCCGGAACTTGGGCAGGGTCGTTTGGGATGGCTCTATGAAGGAGTTGCCA
AGGGTGTGGTGAAAGACGAACCTGAAACCAGAGTGGCCATTAAAACAGTGAACGAGGCCGCGAGC
ATGCGTGAAAGGATCGAGTTTCTCAACGAGGCTTCTGTGATGAAGGAGTTCAATTGTCACCATGT
GGTGCGGTTGCTGGGTGTGGTCCCAGGGCCAGCCAACGCTGGTCATCATGGAACTGATGACGC
GGGGCGATCTCAAAAGTTATCTCCGGTCTCTGAGGCCAGAAATGGAGAATAATCCAGTCCTAGCA

				CCTCCAAGCCTAAGCAGATGATTCAGATGGCTGGAGAGATTGCAGACGGCATGGCATACCTCAA CGCCAACAAGTTCGTCCACAGAGACCTTGCTGCCCGGAATTGCATGGTAGCCGAGGATTTCACAG TCAAAATTGGAGATTTTCGGATGACGCGAGATATCTATGAGACAGACTATTACCGGAAAGGAGGG AAAGGGCTGTTCCCCCTCCCTGGATGTCTCTCCGACTCCCTCAAGCATCGACTCTTCACCACTTA CTCGGACGTCTGGTCCTTCGGGGTTGTCCTCTGGGAGATCGCCACACTGGCCGAGCAGCCCTACC AGGGCTTGTCCAACGAGCAAGTCCTTCGCTTCGTCATGGAGGGCGGCCTTCTGGACAAGCCAGAC AACTGCCCCGACATGCTGTTTGAATTGATGCGCATGTGCTGGCAGTACAACCCCAAGATGAGGCC TTCCTTCCTGGAGATCATCAGCAGCATCAAAGACGAGATGGAGCCTGGCTTCCGGGAGGTCTCCT TCTACTACAGTGAGGAGAACACAAGCTGCCCGAGCCGGAGGAGCTGGACCTGGAGCCAGAGAACATG GAGAGCGTCCCCCTGGACCCCTCGGCCTCCTCGTCCTCCCTGCCACTGCCCGACAGACACTCAGG ACACAAGGCCGAGAACGGCCCCGGCCCTGGAGTGCTGGTGCTCCGCGCCAGCTTCGATGAGAGAC AGCCTTACGCACACATGAACGGTGGCCGCAAGAACGAGCGGGCCTTGCCGCTGCCCCAGTCTTCG ACCTGCTGA
1999.	macaque IGF-R1	artificial	aa	MKSGSGEGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLENCTVIEGYLHILLIS KAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGL YNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKT TINNEYNYRCWTTNRCQKMCPSACGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVC VPACPPNTYRFEGWRCVDRDFCANILSAESSDSFGFVIHDGFCMQFCPSGFIRNGSQSMYCIPCE GPCPKVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKI RHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLC VSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLHFTSTTTWKNRIIITWHRYRPPDYRDL ISFTVYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVT LTMVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQR QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEKGPCCACPKTEAEKQAEKEE AEYRKVFENFLHNSIFVPRPERKRRDVMQVANTTMSSRSRNTTVADTYNITDLEELETEYPFFES RVDNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPE NSIFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSL SGNGSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHRKRNNSRLGNGVLYAS VNPEYFSAADVYVPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAAS MRERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLA PPSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGG KGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPD NCPDMLFELMRMCWQYNPKMRPSFLEIISSIKDEMEPGFREVSFYYSEENKLPEPEELDLEPENM ESVPLDPSASSSSLPLPDRHSGHKAENGPGPGVLVLRASFDERQPYAHMNGGRKNERALPLPQSS TC
2000.	human c-MET extracellular four Ig	human	aa	PAIYKVFPNSAPLEGGTRLTICGWDFGFRRNNKFDLKKTRVLLGNESCTLTLSESTMNTLKCTVG PAMNKHFNMSIIISNGHGTTQYSTFSYVDPVITSISPKYGPMAGGTLLTLTGNYLNSGNSRHISI

	domains			
2001.	human c-MET extracellular cystein-rich domain	human	aa	GGKTCTLKSVSNSILECYTPAQTISTEFAVKLKIDLANRETSIFSYREDPIVYEIHPTKSFISGG STITGVGKNLNSVSVPRMVINVHEAGRNFTVACQHRSNSEIICCTTPSLQQLNLQLPLKTKAFFM LDGILSKYFDLIYVHNPVFKPFEKPVMISMGNENVLEIKGNDIDPEAVKGEVLKVGNKSCENIHL HSEAVLCTVPNDLLKLNSELNIEWKQAISSTVLGKVI
2002.	human c-MET extracellular beta-chain of a sema domain	human	aa	CRHFQSCSQCLSAPPFVQCGWCHDKCVRSEECLSGTWTQQIC STKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQSKPDSAEPMDRSAMCAFPIKYVND FFNKIVNKNNVRCLQHFYGPNHEHCFNRTLLRNSSGCEARRDEYRTEFTTALQRVDLFMGQFSEV LLTSISTFIKGDLTIANLGTSEGRFMQVVVSRSGPSTPHVNFLLDSHPVSPEVIVEHTLNQNGYT LVITGKKITKIPLNGLG
2003.	human c-MET extracellular domain	human	aa	ECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPV LEHPDCFPCQDCSSKANLSGGVWKDNINMALVVDTYYDDQLISCGSVNRGTCQRHVFPHNHTADI QSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGNTINSSYFPDHPLHISVRRL KETKDGFMFLTDQSYIDVLPEFRDSYPIKYVHAFESNNFIYFLTVQRETLDAQTFHTRIIRFCSI NSGLHSYMEMPLECILTEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQS KPDSAEPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFYGPNHEHCFNRTLLRNSSGCEARRD EYRTEFTTALQRVDLFMCQFSEVLLTSISTFIKGDLTIANLGTSEGRFMQVVVSRSGPSTPHVNF LLDSHPVSPEVIVEHTLNQNGYTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDK CVRSEECLSGTWTQQICLPAIYKVFPNSAPLEGGTRLTICGWDFGFRRNNKFDLKKTRVLLGNES CTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTTQYSTFSYVDPVITSISPKYGPMAGGTL LTLTGNYLNSGNSRHISIGGKTCTLKSVSNSILECYTPAQTISTEFAVKLKIDLANRETSIFSYR EDPIVYEIHPTKSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNFTVACQHRSNSEIICCTTP SLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPFEKPVMISMGNENVLEIKGNDIDPEA VKGEVLKVGNKSCENIHLHSEAVLCTVPNDLLKLNSELNIEWKQAISSTVLGKVIVQPDQNF
2004.	human Endosialin extracellular mucin domain	human	aa	ASQDLGDELLDDGEDEEDEDEAWKAFNGGWTEMPGILWMEPTQPPDPALAYRPSFPEDREPQIPY PEPTWPPPLSAPKVPYHSSVLSVTRPVVVSATHPTLPSAHQPPVIPAPHPALSRDHQIPVIAANY PDLPSAYQPGILSVSHSAQPPAHQPPMISTKYPELPPAHQSPMFPDTRVAGTQTTTHLPGIPPNH APLVTTLGAQLPPQAPDALVLRTQATQLPIIPTAQPSLTTTSRSPVSPAHQISVPAATQPAALPT LLPSQSPTNQTSPISPTHPHSKAPQIPREDGPSPKLALWLPSPAPTAAPTALGEAGLAEHSQRDD R
2005.	human Endosialin extracellular three EGF-like domains	human	aa	CSPDNGGCEHECVEEVDGHVSCRCTEGFRLAADGRSCEDPCAQAPCEQQCEPGGPQGYSCHCRLG FRPAEDDPHRCVDTDECQIAGVCQQMCVNYVGGFECYCSEGHELEADGISC
2006.	human Endosialin extracellular Sushi/SCR/CCP	human	aa	PAVYTTPFHLVSTEFEWLPFGSVAAVQCQAGRGASLLCVKQPEGGVGWSRAGPLC

	domain			
2007.	human Endosialin extracellular domain	human	aa	WAAEPRAACGPSSCYALFPRRRTFLEAWRACRELGGDLATPRTPEEAQRVDSLVGAGPASRLLWI GLQRQARQCQLQRPLRGFTWTTGDQDTAFTNWAQPASGGPCPAQRCVALEASGEHRWLEGSCTLA VDGYLCQFGFEGACPALQDEAGQAGPAVYTTPFHLVSTEFEWLPFGSVAAVQCQAGRGASLLCVK QPEGGVGWSRAGPLCLGTGCSPDNGGCEHECVEEVDGHVSCRCTEGFRLAADGRSCEDPCAQAPC EQQCEPGGPQGYSCHCRLGFRPAEDDPHRCVDTDECQIAGVCQQMCVNYVGGFECYCSEGHELEA DGISCSPACAMCAQASQDLCDELLDDGEDEEDEDEAWKAFNGCWTEMPCILWMEPTQPPDFALAY RPSFPEDREPQIPYPEPTWPPPLSAPRVPYHSSVLSVTRPVVVSATHPTLPSAHQPPVIPATHPA LSRDHQIPVIAANYPDLPSAYQPGILSVSHSAQPPAHQPPMISTKYPELFPAHQSPMFPDTRVAG TQTTTHLPGIPPNHAPLVTTLGAQLPPQAPDALVLRTQATQLPIIPTAQPSLTTTSRSPVSPAHQ ISVPAATQPAALPTLLPSQSPTNQTSPISPTHPHSKAPQIPREDGPSPKLALWLPSPAPTAAPTA LGEAGLAEHSQRDDR
2008.	human IGF-R1 extracellular three fibronectin type III domains	human	aa	SDVLHFTSTTTSKNRIIITWHRYRPPDYRDLISFTVYYKEAPFKNVTEYDGQDACGSNSWNMVDV DLPPNKDVEPGILLHGLKPWTQYAVYVKAVTLTMVENDHIRGAKSEILYIRTNASVPSIPLDVLS ASNSSSQLIVKWNPPSLPNGNLSYYIVRWQRQPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVT ENPKTEVCGGEKGPCCACPKTEAEKQAEKEEAEYRKVFENFLHNSIFVPRPERKRRDVMQVANTT MSSRSRNTTAADTYNITDPEELETEYPFFESRVDNKERTVISNLRPFTLYRIDIHSCNHEAEKLG CSASNFVFARTMPAEGADDIPGPVTWEPRPENSIFLKWPEPENPNGLILMYEIKYGSQVEDQREC VSRQEYRKYGGAKLNRLNPGNYTARIQATSLSGNGSWTDPVFFYVQAKTGYENFIHL
2009.	human IGF-R1 extracellular L2 domain	human	aa	KVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSH ALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLCVSEI YRMEEVTGTKGRQSKGDINTRNNGERASCE
2010.	human IGF-R1 extracellular domain	human	aa	EICGPGIDIRNDYQQLKRLENCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGLES LGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLI LDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPSTCGKRACT ENNECCHPECLGSCSAPDNDTACVACRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAES SDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCEGPCPKVCEEEKKTKTIDSVTSAQMLQGCTI FKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSHALVSLSFLKNLRLILGEEQLEGNYSF YVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLCVSEIYRMEEVTGTKGRQSKGDINTRNNGER ASCESDVLHFTSTTTSKNRIIITWHRYRPPDYRDLISFTVYYKEAPFKNVTEYDGQDACGSNSWN MVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVTLTMVENDHIRGAKSEILYIRTNASVPSIPL DVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQRQPQDGYLYRHNYCSKDKIPIRKYADGTIDI EEVTENPKTEVCGGEKGPCCACPKTEAEKQAEKEEAEYRKVFENFLHNSIFVPRPERKRRDVMQV ANTTMSSRSRNTTAADTYNITDPEELETEYPFFESRVDNKERTVISNLRPFTLYRIDIHSCNHEA EKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPENSIFLKWPEPENPNGLILMYEIKYGSQVED QRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSLSGNGSWTDPVFFYVQAKTGYENFIHL
2011.	IGF-1R-1	artificial	nt	ATGAAGTCTGGCTCCGGCGGAGGGTCCCCGACCTCGCTGTGGGGGCTCCTGTTTCTCTCCGCCGC

GCTCTCGCTCTGGCCGACGAGTGGAGAAATCTGCGGGCCAGGCATCGACATCCGCAACGACTATC
AGCAGCTGAAGCGCCTGGAGAACTGCACGGTGATCGAGGGCTACCTCCACATCCTGCTCATCTCC
AAGGCCGAGGACTACCGCAGCTACCGCTTCCCCAAGCTCACGGTCATCTACCGAGTACTTGCTGCT
GTTCCGAGTGGCTGGCCICCAGAGCCTCGGAGACCTCTTCCCCAACCTCACGGTCATCCCCGGCT
GGAAACTCTTCTACAACTACGCCCTGGTCATCTTCGAGATGACCAATCTCAAGGATATTGGGCTT
TACAACCTGAGGAACATIACTCGGGGGGCCATCAGGATTGAGAAAAA-GCTGACCTCTGTTACCT
CTCCACTGTGGACTGGTCCCTGATCCTGGAIGCGGTGTCCAATAACTACATTGTGGGGAATAAGC
CCCCAAAGGAATGTGGGGACCTGTGTCCAGGGACCATGGAGGAGAAGCCGATGTGTGAGAAGACC
ACCATCAACACAATGAGTACAACTACCGCTGCIGGACCACACAACCGCTGCCAGAAAATGTGCCCAAG
CACGTGTGGGAAGCGGGCGTGCACCGAGAACAATGAGTGCTGCCACCCCGAGTGCCTGGGCAGCT
GCAGCGCGCCTGACAACGACACGGCCTGTGTAGCTTGCCGCCACTACTACTATGCCGGTGTCTGT
GTGCCTGCCTGCCCGCCCAACACCTACAGGTTTGAGGGCTGGCGCTGTGTGGACCGTGACTTCTG
CGCCAACATCCTCAGCGCCGAGAGCAGCGACTCCGAGGGGTTTGTGATCCACGACGGCGAGTGCA
TGCAGGAGTGCCCCTCGCGCTTCATCCGCAACGGCAGCCAGAGCATGTACTGCATCCCTTGTGAA
GGTCCTTGCCCGAAGGTCTGTGAGGAAGAAAGAAACACAAAGACCATTGATTCTGTTACTTCTGC
TCAGATGCTCCAAGGATGCCACCATCTTCAAGGCAATTTGCTCATTAACATCCGACGGGGGAATA
ACATTGCTTCAGAGCTGCAGAACTTCATGGGGCTCATCGAGGTGGTGACGGGCTACGTGAAGATC
CGCCATTCTCATGCCTTCGTCTCCTTGTCCTTCCTAAAAAACCTTCGCCTCATCCTAGGAGAGGA
GCAGCTAGAAGGGAATTACTCCTTCTACGTCCTCGACAACCAGAACTTGCAGCAACTGTGGGACT
GGGACCACCGCAACCTGACCATCAAGCAGGGAAAATGTACTTTGCTTTCAATCCCAAATTATGT
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AAACACCAGGAACAACGCGGAGAGAGCCTCCTGTGAAAGTGACGTCCTGCATTTCACCTCCACCA
CCACGTCGAAGAATCGCATCATCATAACCTGGCACCGGTACCGGCCCCCTGACTACAGGGATCTC
ATCAGCTTCACCGTTTACTACAAGCAAGCACACCCTTTAACAATGTCACACAGTATGATGGCCAGGA
TGCCTGCGGCTCCAACACCTGGAACATGGTGGACGTGGACCTCCCGCCCAACAAGGACGTGGAGC
CCGGCATCTTACTACATGGGCTGAAGCCCTGGACTCAGTACGCCGTTTACGTCAAGGCTGTGACC
CTCACCATGGTGGAGAACGACCATATCCGTGGGGCCAAGAGTGAGATCTTGTACATTCGCACCAA
TGCTTCAGTTCCTTCCATTCCCTTGGACGTTCTTTCAGCATCGAACTCCTCTTCTCAGTTAATCG
TGAAGTGGAACCCTCCCICTCTGCCCAACGGCAACCTGAGTTACTACATTGTGCGCTGGCAGCGG
CAGCCTCAGGACGGCTACCTTTACCGGCACAATTACTGCTCCAAAGACAAAATCCCCATCAGGAA
GTATGCCGACGGCACCATCGACATTGAGGAGGTCACAGAGAACCCCAAGACTGAGGTGTGTGGTG
GGGAGAAAGGGCCTTGCIGCGCCTGCCCCAAAACTGAAGCCGAGAAGCAGGCCGAGAAGGAGAG
GCTGAATACCGCAAAGTCTTTGAGAATTTCCTGCACAACTCCATCTTCGTGCCCAGACCTGAAAG
GAAGCGGAGAGATGTCAIGCAAGTGGCCAACACCACCATGTCCAGCCGAAGCAGGAACACCACGG
CCGCAGACACCTACAACATCACCGACCCGGAAGAGCTGGAGACAGAGACTACCCTTTCTTTGAGAGC
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				GGACTATGCCCGCAGAAGGAGCAGATGACATTCCTGGGCCAGTGACCTGGGAGCCAAGGCCTGAA
				AACTCCATCTTTTTAAAGTGGCCGGAACCTGAGAATCCCAATGGATTGATTCTAATGTATGAAAT
				AAAATACGGATCACAAGTTGAGGATCAGCGAGAATGTGTGTCCAGACAGGAATACAGGAAGTATG
				GAGGGCCCAAGCTAAACCGGCTAAACCCGCGCGAACTACACAGCCCCGCATTCAGGCCACATCTCTC
				TCTGGGAATGGGTCGTGCACAGATCCTGTGTTCTTCTATGTCCAGGCCAAAACAGGATATGAAAA
				CTTCATCCATCTGATCATCGCTCTCGCCGTGCTGTCCTGTTGATCGTGGGAGGGTTGGTGATTA
				TGCTGTACGTCTTCCATAGAAAGAGAAATAACAGCAGGCTGGGGAATGGAGTGCTGTATGCCTCT
				GTGAACCCGGAGTACTTCAGCGCTGCTGATGTGTACGTTCCTGATGAGTGGGAGGTGGCTCGGGA
				GAAGATCACCATGAGCCCGGAACTTGGGCAGGGGTCGTTTGGGATGGTCTATGAAGGAGTTGCCA
				AGGGTGTGGTGAAAGATGAACCTGAAACCACAGAGTGGCCATTAAAACAGTGAACGAGGCCGCAAGC
				ATGCGTGAGAGGATTGAGTTTCTCAACGAAGCTTCTGTGATGAAGGAGTTCAATTGTCACCATGT
				GGTGCGATTGCTGGGTGTGGTCCCAAGGCCAGCCAACACTGGTCATCATGGAACTGATGACAC
				GGGGCGATCTCAAAAGTTATCTCCGGTCTCTGAGGCCAGAAATGGAGAATAATCCAGTCCTAGCA
				CCTCCAAGCCTGAGCAACATGATTCAGATGGCCGGAGAGATTGCAGACGGCATGGCATACCTCAA
				CGCCAATAAGTTCGTCCACAGAGACCTTGCTGCCCGGAATTGCATGGTAGCCGAAGATTTCACAG
				TCAAAATCGGAGATTTTGGTATGACGCGAGATATCTATGAGACAGACTATTACCGGAAAGGAGGG
				AAAGGGCTGCTGCCCGTGCGCTGGATGTCTCCTGAGTCCCTCAAGGATGGAGTCTTCACCACTTA
				CTCGGACGTCTGGTCCTTCGGGGTCGTCCTCTGGGAGATCGCCACACTGGCCGAGCAGCCCTACC
				AGGGCTTGTCCAACGAGCAAGTCCTTCGCTTCGTCATGGAGGGCGGCCTTCTGGACAAGCCAGAC
				AACTGTCCTGACATGCTGTTTGAACTGATGCGCATGTGCTGGCAGTATAACCCCAAGATGAGGCC
				TTCCTTCCTGGAGATCATCAGCAGCATCAAAGAGGAGATGGAGCCTGGCTTCCGGGAGGTCTCCT
				TCTACTACAGCGAGGAGAACAAGCTGCCCGAGCCGGAGGAGCTGGACCTGGAGCCAGAGAACATG
				GAGAGCGTCCCCCTGGACCCCTCGGCCTCCICGTCCTCCCTGCCACTGCCCGACAGACACTCAGG
				ACACAAGGCCGAGAACGCCCCCGGCCCTGGCGTGCTGCTCCTCCGCGCCCAGCTTCGACGAGACAC
				AGCCTTACGCCCACATGAACGGGGGCCGCAAGAACGAGCGGCCTTGCCGCTGCCCCAGTCTTCG
				ACCTGCTGA
2012.	IGF-1R-2	artificial	aa	MKSGSGGGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLENCTVIEGYLHILLIS
				KAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGL
				YNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKT
				TINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVC
				VPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCE
				GPCPKVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKI
				RHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLC
				VSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLHFTSTTTSKNRIIITWHRYRPPDYRDL
				ISFTVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVT
				LTMVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQR
				QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEKGPCCACPKTEAEKQAEKEE

				AEYRKVFENFLHNSIFVPRPERKRRDVMQVANTTMSSRSRNTTAADTYNITDPEELETEYPFFES RVDNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPE NSIFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSL SCNGSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHRKRNNSRLGNGVLYAS VNPEYFSAADVYVPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAAS MRERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLA PPSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGG KGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPD NCPDMLFELMRMCWQYNPKMRPSFLEIISSIKEEMEPGFREVSFYYSEENKLPEPEELDLEPENM ESVPLDPSASSSSLPLPDRHSGHKAENGPGPGVLVLRASFDERQPYAHMNGGRKNERALPLPQSS TC
2013.	IGF-1R-3	artificial	nt	ATGAAGTCTGGCTCTGGAGAAGGGTCCCCGACCTCGCTGTGGGGGCTCCTGTTTCTCTCCGCCGC GCTCTCGCTCTGGCCGACGAGTGGAGAAATCTGTGGGCCGGCATCGACACATCCGCAACGACTATC AGCAGCTGAAGCGCCTGGAGAACTGCACGGIGATCGAGGGCTACCTCCACATCCTGCTCATCTCC AAGGCCGAGGACTACCGCAGCTACCGCTTCCCCAAGCTCACGGTCATCACCGAGTACTTGCTGTT GTTCCGAGTGGCTGGCCTAGAGAGCCTCGGAGACCTGTTCCCCAACCTCACGGTAATCCGCGGCT GGAAACTCTTCTACAACTACGCACTAGTCATCTTTGAGATGACCAATCTCAAGGATATTGGGCTT TACAACCTGAGGAACATTACTCGGGGGGCCATCAGGATTGAGAAAAATGCTGACCTCTGTTACCT CTCCACTGTGGACTGGTCCCTGATCCTGGAIGCAGTGTCCAATAACTACATTGTGGGGAATAAGC CCCCAAAGGAATGCGGGGGACCTGTGTCCGGGACCATGGAGGAGAAGCCGATGTGCGAGAAGACC ACCATCAACAATGAGTACAACTACCGCTGCTGGACCACACAACCGCTGCCAGAAAATGTGCCCGAG TGCCTGTGGGAAGAGGGCATGCACCGAGAACAACGAGTGCTGCCACCCCGAGTGCCTGGGCAGCT GCAGCGCGCCTGACAACGACACGGCCTGTGTAGCTTGCCGCCACTACTACTACGCCGGTGTCTGC GTGCCTGCCTGCCCGCCCAACACCTACAGGTTTGAGGGCTGGCGCTGTGTGGACCGTGACTTCTG CGCCAACATCCTCAGCGCCGAGAGCAGCGACTCCGAGGGTTTCGTGATCCACGACGGCGAGTGCA TGCAGGAGTGCCCCTCAGGCTTCATCCGCAACGGCAGCCAGAGCATGTACTGCATCCCTTGTGAA GGTCCTTGCCCCAAGGTCTGTGAGGAAGAAAAGAAAACACAAAGACCATTGATTCTGTTACTTCTGC TCAGATGCTCCAAGGATGCACCATCTTCAAGGGCAATTTGCTCATTAACATCCGACGGGGGAATA ACATTGCTTCAGAACTTGAGAACTTCATTGGGGCTTCATTCGAGGTTGGTGACGGGCTTACGTGAAGATC CGCCATTCCCATGCCTTGGTCTCCTTCTGTCCTTCCTAAAAAACCTTCGCCTCATCTTAGGAGAGGA GCAGCTAGAAGGGAATTACTCCTTCTACGTCCTCGACAACCAGAACTTGCAGCAACTATGGGACT GGGACCACCGCAACCTGACCATCAAAGCAGGAAATGTACTTTGCTTCAATCCCAAATTGTGT GTTTCGGAAATTTACCGCATGGAGGAAGTGACGGGGACTAAAGGGCGCCAAAGCAAGGGACAT AAACACCAGGAACAACGGGGAAAGAGCCTCCTGTGAAAGTGACGTCCTGCATTTCACCTCCACCA CCACGTGGAAGAATCGCATCATCATAACCTGGCACCGGTACCGGCCCCCTGACTACAGGGATCTC ATCAGCTTCACCGTTTACTACAAGGAAGCACCTTTTAAGAATGTCACGGAGTATGATGGGCAGGA

TGCCTGCGGCTCCAACAGCTGGAACATGGTGGATGTGGACCTCCCGCCCAACAAGGACGTGGAGC
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CTCACCATGGTGGAGAACGACCATATCCGTGGGGCCAAGAGTGAGATCTTGTACATTCGCACCAA
TCCTTCAGTTCCTTCCATTCCCTTCGCACGTTCTTTCAGCATCCAACTCCTCTTCTCAGTTAATCG
TGAAGTGGAACCCTCCCTCTCTGCCCAACGGCAACCTGAGTTACTACATTGTGCCGCTGGCAGCGG
CAGCCTCAGGACGGCTACCTTTACCGGCACAATTACTGCTCCAAAGACAAAATCCCCATCAGGAA
GTATGCCGACGGCACCATTGACATTGAGGAGGTCACAGAGAACCCGAAGACTGAGGTGTGGTG
GAGAGAAAGGGCCTTGCTGCGCCTGCCCCAAAACTGAAGCTGAAGCAGGCCGAGAAGGAGGAG
GCTGAGTACCGCAAAGTCTTTGAGAATTCCTGCACAACTCCATCTTTGTGCCCAGACCTGAAAG
GAAGCGGAGAGATGTCATGCAAGTGGCCAACACCACCATGTCCAGCCGAAGCAGGAACACCACGG
TGGCAGACACCTACAACATCACAGATCTGGAAGAGCTAGAGACAGAGTACCCTTCTTTGAGAGC
AGAGTGGATAATAAGGAGAGAACTGTCATTCTAACCTTCGGCCTTTCACATTGTACCGCATTGA
TATCCACAGCTGCAACCACGAGGCTGAGAAACTGGGCTGCAGCGCCTCCAACTTTGTCTTTGCAA
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GAGGGGCCAAGCTAAACCGGCTAAACCCCGGGAACTACACAGCCCGGATTCAGGCTACATCTCTC
TCTGGGAATGGGTCGTGGACAGATCCTGTGTTCTTCTATGTCCAGGCCAAAACAGGATATGAAAA
CTTCATCCATCTGATCATCGCTCTCGCCGTCGCTGTCCTGTTGATCGTGGGAGGGTTGGTGATCA
TGCTGTACGTCTTCCATAGAAAGAGAAATAACAGCAGGCTGGGGAATGGAGTGCTGTACGCGTCT
GTGAACCCGGAGTACTTCAGCGCTGCGGATGTGTACGTTCCTGATGAGTGGGAGGTGGCTCGGGA
GAAGATCACCATGAGCCCGGAACTTGGGCAGGGTCGTTTGGGATGGCTCTATGAAGGAGTTGCCA
AGGGTGTGGTGAAAGACCAACCTGAAACCAGAGTGGCCATTAAAACAGTGAACGAGGCCGCGAGC
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GGTGCGGTTGCTGGGTGTGGTGTCCCAGGGCCAGCCAACGCTGGTCATGGAACTGATGACGGC
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CCTCCAAGCCTAAGCAAGATGATTCAGATGGCTGGAGAGATTGCAGACGGCATGGCATACCTCAA
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TCTACTACAGTGAGGAGAACAAGCTGCCCGAGCCGGAGGAGCTGGACCTGGAGCCAGAGAACATG
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				AGCCTTACGCACACATGAACGGTGGCCGCAAGAACGAGCGGGCCTTGCCGCTGCCCCAGTCTTCG ACCTGCTGA
2014.	IGF-1R-4	artificial	aa	MKSGSGEGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLENCTVIEGYLHILLIS KAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGL YNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECGDLCPGTMEEKPMCEKT TINNEYNYRCWTTNRCQKMCPSACGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVC VPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCE GPCPKVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKI RHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLC VSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVLHFTSTTTSWKNSILIVWHRYRPPDYRDL ISFTVYYKEAPFKNVTEYDGQDACGSNSWNMVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAVT LTMVENDHIRGAKSEILYIRTNASVPSIPLDVLSASNSSSQLIVKWNPPSLPNGNLSYYIVRWQR QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEKGPCCACPKTEAEKQAEKEE AEYRKVFENFLHNSIFVPRPERKRRDVMQVANTTMSSRSRNTTVADTYNITDLEELETEYPFFES RVDNKERTVISNLRPFTLYRIDIHSCNHEAEKLGCSASNFVFARTMPAEGADDIPGPVTWEPRPE NSIFLKWPEPENPNGLILMYEIKYGSQVEDQRECVSRQEYRKYGGAKLNRLNPGNYTARIQATSL SGNGSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHRKRNNSRLGNGVLYAS VNPEYFSAADVYVPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAVKTVNESAS MRERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLA PPSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGG KGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPD NCPDMLFELMRMCWQYNPKMRPSFLEIISSIKDEMEPGFREVSFYYSEENKLPEPEELDLEPENM ESVPLDPSASSSSLPLPDRHSGHKAENGPGPGVLVLRASFDERQPYAHMNGGRKNERALPLPQSS TC
2015.	IGF1R2-H	artificial	aa	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTA NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARAPLRFLEWSTQDHYYYYY MDVWGKGTTVTVSS
2016.	IGF1R2-HCDR1	artificial	aa	SYAIS
2017.	IGF1R2-HCDR2	artificial	aa	GIIPIFGTANYAQKFQG
2018.	IGF1R2-HCDR3	artificial	aa	APLRFLEWSTQDHYYYYYMDV
2019.	IGF1R2-H	artificial	nt	GAGGTGCAACTAGTCCAGAGCGGAGCGGGAGGTGAAGAAACCTGGATCCAGCGTGA AAGTGAGCTGTAAGGCTAGCGGAGGCACATTCTCCTCGTATGCCATTAGCTGGGTT AGACAAGCACCTGGACAAGGACTGGAGTGGATGGGAGGGATAATCCCAATCTTCG GAACTGCCAACTACGCACAGAAGTTCCAAGGACGGGTCACCATCACTGCGGATAAG TCCACCTCGACTGCCTACATGGAGCTCAGTAGCTTACGGAGCGAAGACACAGCCGT ATACTATTGCGCACGAGCACCCCTAAGATTCCTGGAGTGGAGCACGCAGGATCACT ATTACTATTACTACATGGACGTGTGGGGAAAGGGAACGACTGTCACCGTTTCAAGC

2020.	IGF1R2-L	artificial	aa	SSELTQDPAVSVALGQTVRITCQGDSLRSYYATWYQQKPGQAPILVIYGENKRPSGIPD RFSGSSSGNTASLTITGAQAEDEADYYCKSRDGSGQHLVFGGGTKLTVL
2021.	IGF1R2-LCDR1	artificial	aa	QGDSLRSYYAT
2022.	IGF1R2-LCDR2	artificial	aa	GENKRPS
2023.	IGF1R2-LCDR3	artificial	aa	KSRDGSGQHLV
2024.	IGF1R2-L	artificial	nt	AGCTCGGAATTGACCCAGGATCCTGCTGTATCCGTCGCTCTCGGACAAACCGTGCG CATAACATGTCAAGGGGACTCCCTGAGGAGCTACTACGCCACATGGTACCAGCAAA AACCCGGACAAGCTCCAATCCTGGTGATTTATGGCGAAAACAAGCGTCCCTCAGGG ATCCCAGACAGGTTTAGCGGAAGTTCGAGCGGCAATACTGCCAGTCTGACGATTAC CGGAGCTCAAGCTGAGGATGAAGCCGACTACTATTGCAAATCACCGCGACGGAAGC GGCCAGCACCTGGTGTTTGGTGGCGGGACAAAGCTGACCGTTTTG
2025.	IGF1R2-HL	artificial	aa	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTA NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARAPLRFLEWSTQDHYYYY MDVWGKGTTVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVALGQTVRITCQGDSL RSYYATWYQQKPGQAPILVIYGENKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY CKSRDGSGQHLVFGGGTKLTVL
2026.	IGF1R2-HL	artificial	nt	GAGGTGCAACTAGTCCAGAGCGGAGCGGAGGTGAAGAAACCTGGATCCAGCGTGA AAGTGAGCTGTAAGGCTAGCGGAGGCACATTCTCCTCGTATGCCATTAGCTGGGTT AGACAAGCACCTGGACAAGGACTGGAGTGGATGGGAGGGATAATCCCAATCTTCG GAACTGCCAACTACGCACAGAAGTTCCAGGACGGGTCACCATCACTGCGGATAAG TCCACCTCGACTGCCTACATGGAGCTCAGTAGCTTACGGAGCGAAGACACAGCCGT ATACTATTGCGCACGAGCACCCCTAAGATTCCTGGAGTGGAGCACGCAGGATCACT ATTACTATTACTACATGGACGTGTGGGGAAAGGGAACGACTGTCACCGTTTCAAGC GGTGGAGGTGGAAGTGGTGGAGGAGGGAGCGGTGGGGGAGGATCAAGCTCGGAA TTGACCCAGGATCCTGCTGTATCCGTCGCTCTCGGACAAACCGTGCGCATAACATG TCAAGGGGACTCCCTGAGGAGCTACTACGCCACATGGTACCAGCAAAAACCCGGA CAAGCTCCAATCCTGGTGATTTATGGCGAAAACAAGCGTCCCTCAGGGATCCCAGA CAGGTTTAGCGGAAGTTCGAGCGGCAATACTGCCAGTCTGACGATTACCGGAGCTC AAGCTGAGGATGAAGCCGACTACTATTGCAAATCACCGCGACGGAAGCGGCCAGCA CCTGGTGTTTGGTGGCGGGACAAAGCTGACCGTTTTG
2027.	IGF1R2HLxl2CHL	artificial	aa	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTA NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARAPLRFLEWSTQDHYYYY MDVWGKGTTVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVALGQTVRITCQGDSL RSYYATWYQQKPGQAPILVIYGENKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY CKSRDGSGQHLVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTF NKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN

				NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2028.	IGF1R2HLxl2CHL	artificial	nt	GAGGTGCAACTAGTCCAGAGCGGAGCGGGAGGTGAAGAAACCTGGATCCAGCGTGA AAGTGAGCTGTAAGGCTAGCGGAGGCACATTCTCCTCGTATGCCATTAGCTGGGTT AGACAAGCACCTGGACAAGGACTGGAGTGGGAGGGGATAATCCCAATCTTCG GAACTGCCAACTACGCACAGAAGTTCCAAGGACGGGTCACCATCACTGCGGATAAG TCCACCTCGACTGCCTACATGGAGCTCAGTAGCTTACGGAGCGAAGACACAGCCGT ATACTATTGCGCACGAGCACCCCTAAGATTCCTGGAGTGGAGCACGCAGGATCACT ATTACTATTACTACATGGACGTGTGGGGAAAGGGAACGACTGTCACCGTTTCAAGC GGTGGAGGTGGAAGTGGTGGAGGAGGGAGCGGTGGGGGAGGATCAAGCTCGGAA TTGACCCAGGATCCTGCTGTATCCGTCGCTCTCGGACAAACCGTGCGCATAACATG TCAAGGGGACTCCCTGAGGAGCTACTACGCCACACATGGTACCAGCAAAAACCCGGA CAAGCTCCAATCCTGGTGATTTATGGCGAAAACAAGCGTCCCTCAGGGATCCCAGA CAGGTTTAGCGGGAAGTTCGAGCGGCAATACTGCCAGTCTGACGATTACCGGAGCTC AAGCTGAGGATGAAGCCGACTACTATTGCAAATCACGCGACGGAAGCGGCCAGCA CCTGGTGTTTGGTGGCGGGACAAAGCTGACCGTTTTGTCCGGAGGTGGTGGATCC GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGA AACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCC GCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAAT AATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT GATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAGACTGAGGACACTGCC GTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCT TACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCG GCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACT CACCGTATCACCTGGTGGAACAGTCACACACTCACTTGTGGCTCCTCGACTGGGGCTG TTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGT GGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGG CTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGAT GAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
2029.	IGF1R7-H	artificial	aa	QVELVESGGGVVQPGRSQRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWFDGS STYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYFCARELGRRYFDLWGRGTLV SVSS
2030.	IGF1R7-HCDR1	artificial	aa	SYGMH
2031.	IGF1R7-HCDR2	artificial	aa	IIWFDGSSTYYADSVRG

2032.	IGF1R7-HCDR3	artificial	aa	ELGRRYFDL
2033.	IGF1R7-H	artificial	nt	CAGGTCGAATTGGTGGAAAGCGGGGGAGGCGTCGTTCAGCCTGGTAGGAGCCAGA GGCTTAGCTGTGCTGCCTCCGGTTTCACCTTCTCTAGCTACGGAATGCACTGGGTG AGACAGGCACCCGGAAAAGGACTGGAATGGGTGGCCATCATCTGGTTCGACGGCT CTTCCACCTACTATGCCGATAGCGTGAGAGGACGCTTCACCATCTCCCGTGACAAC TCCAAGAACACCCTGTACCTCCAGATGAATAGCCTGCGAGCTGAGGACACTGCCGT GTACTTTTGTGCACGGGAGCTGGGACGTAGGTACTTTGATCTGTGGGGAAGAGGCA CACTGGTTAGCGTTAGCTCC
2034.	IGF1R7-L	artificial	aa	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRAYGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPWTFGQGTKVESK
2035.	IGF1R7-LCDR1	artificial	aa	RASQSVSSYLA
2036.	IGF1R7-LCDR2	artificial	aa	DASKRAY
2037.	IGF1R7-LCDR3	artificial	aa	QQRSKWPP
2038.	IGF1R7-L	artificial	nt	GAAATCGTGCTCACCCAGAGCCCTGCCACATTGAGCCTTTCACCTGGCGAGCGAG CTACATTGTCATGCCGAGCTAGCCAGAGCGTGAGCTCTTACCTGGCATGGTATCAG CAGAAACCTGGGCAGGCTCCACGACTGCTCATCTATGACGCCTCCAAGCGAGCCTA TGGGATTCCTGCAAGGTTTAGCGGAAGCGGAACCGATTTCACCCTGACTA TCTCCTCACTCGAGCCTGAGGACTTTGCCGTGTATTACTGCCAGCAGCGGAGCAAG TGGCCTCCATGGACATTCGGCCAGGGTACCAAAGTGGAGAGCAAG
2039.	IGF1R7-HL	artificial	aa	QVELVESGGGVVQPGRSQRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWFDGS STYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYFCARELGRRYFDLWGRGTLV SVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLLIYDASKRAYGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPW TFGQGTKVESK
2040.	IGF1R7-HL	artificial	nt	CAGGTCGAATTGGTGGAAAGCGGGGGAGGCGTCGTTCAGCCTGGTAGGAGCCAGA GGCTTAGCTGTGCTGCCTCCGGTTTCACCTTCTCTAGCTACGGAATGCACTGGGTG AGACAGGCACCCGGAAAAGGACTGGAATGGGTGGCCATCATCTGGTTCGACGGCT CTTCCACCTACTATGCCGATAGCGTGAGAGGACGCTTCACCATCTCCCGTGACAAC TCCAAGAACACCCTGTACCTCCAGATGAATAGCCTGCGAGCTGAGGACACTGCCGT GTACTTTTGTGCACGGGAGCTGGGACGTAGGTACTTTGATCTGTGGGGAAGAGGCA CACTGGTTAGCGTTAGCTCCGGCGGAGGGGGAAGCGGAGGCGGAGGTAGCGGGG GAGGTGGAAGCGAAATCGTGCTCACCCAGAGCCCTGCCACATTGAGCCTTTCACCT GGCGAGCGAGCTACATTGTCATGCCGAGCTAGCCAGAGCGTGAGCTCTTACCTGG CATGGTATCAGCAGAAACCTGGGCAGGCTCCACGACTGCTCATCTATGACGCCTCC AAGCGAGCCTATGGGATTCCTGCAAGGTTTAGCGGAAGCGGAAGCCGGAACCGATT TCACCCTGACTATCTCCTCACTCGAGCCTGAGGACTTTGCCGTGTATTACTGCCAG

				CAGCGGAGCAAGTGGCCTCCATGGACATTCGGCCAGGGTACCAAAGTGGAGAGCA AG
2041.	IGF1R7HLxl2CHL	artificial	aa	QVELVESGGGVVQPGRSQRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWFDGS STYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYFCARELGRRYFDLWGRGTLV SVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLLIYDASKRAYGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPW TFGQGTKVESKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2042.	IGF1R7HLxl2CHL	artificial	nt	CAGGTCGAATTGGTGGAAAGCGGGGGAGGCGTCGTTCAGCCTGGTAGGAGCCAGA GGCTTAGCTGTGCTGCCTCCGGTTTCACCTTCTCTAGCTACGGAATGCACTGGGTG AGACAGGCACCCGGAAAAGGACTGGAATGGGTGGCCATCATCTGGTTCGACGGCT CTTCCACCTACTATGCCGATAGCGTGAGAGGACGCTTCACCATCTCCCGTGACAAC TCCAAGAACACCCTGTACCTCCAGATGAATAGCCTGCGAGCTGAGGACACTGCCGT GTACTTTTGTGCACGGGAGCTGGGACGTAGGTACTTTGATCTGTGGGAAGAGGCA CACTGGTTAGCGTTAGCTCCGGCGAGGGGAAGCGGGAGGCGGAGGTAGCGGGG GAGGTGGAAGCGAAATCGTGCTCACCCAGAGCCCTGCCACATTGAGCCTTTCACCT GGCGAGCGAGCTACATTGTCATGCCGAGCTAGCCAGAGCGTGAGCTCTTACCTGG CATGGTATCAGCAGAAACCTGGGCAGGCTCCCACCGACTGCTCATCTATGACGCCTCC AAGCGAGCCTATGGGATTCCTGCAAGGTTTAGCGGAAGCGGAAGCGGAACCGATT TCACCCTGACTATCTCCTCACTCGAGCCTGAGGACTTTGCCGTGTATTACTGCCAG CAGCGGAGCAAGTGGCCTCCATGGACATTCGGCCAGGGTACCAAAGTGGAGAGCA AGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGT GCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATA AGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGC TCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAAAGAC AGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAAC TTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAA TAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCT CAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGT TGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTT GTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAA AACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCG GTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC

				TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAA CCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2043.	IGF1R9-H	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYRMQWVRQAPGKGLEWVSGISPSGGT TWYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWSGGSGYAFDIWGQGT MVTVSS
2044.	IGF1R9-HCDR1	artificial	aa	IYRMQ
2045.	IGF1R9-HCDR2	artificial	aa	GISPSGGTTWYADSVKG
2046.	IGF1R9-HCDR3	artificial	aa	WSGGSGYAFDI
2047.	IGF1R9-H	artificial	nt	GAAGTTCAGCTGCTCGAGAGCGGAGGTGGACTTGTGCAGCCTGGGGGATCACTGA GATTGTCATGCGCAGCTAGCGGCTTTACCTTCTCCATCTATCGCATGCAGTGGGTT CGACAGGCACCCGGAAAGGGATTGGAATGGGTCTCCGGCATTAGCCCTAGCGGGG GAACAACCTGGTATGCCGATAGCGTGAAGGGCAGGTTCACCATCTCTAGGGACAAC AGCAAAAATACTCTGTACCTGCAGATGAACTCCCTGCGTGCCGAGGATACTGCCGT CTACTACTGTGCTCGATGGTCCGGTGGCTCCGGCTATGCCTTCGATATCTGGGGAC AGGGTACAATGGTGACTGTGAGTAGC
2048.	IGF1R9-L	artificial	aa	DIQMTQSPLSLSASVGDRVTITCQASRDIRNYLNWYQQKPGKAPKLLIYDASSLQTGVP SRFGGSGSGTDFSFTIGSLQPEDIATYYCQQFDSLPHTFGQGTKLEIK
2049.	IGF1R9-LCDR1	artificial	aa	QASRDIRNYLN
2050.	IGF1R9-LCDR2	artificial	aa	DASSLQT
2051.	IGF1R9-LCDR3	artificial	aa	QQFDSLPHT
2052.	IGF1R9-L	artificial	nt	GACATTCAGATGACCCAGAGCCCATTGTCACTGTCAGCTTCCGTGGGCGATCGGGT GACCATTACATGCCAGGCTTCACGCGACATCAGGAACTACCTGAACTGGTATCAGC AGAAGCCTGGCAAAGCCCCCCAAGCTCCTTATCTACCGACGCAAGCTCACTGCAGACT GGTGTTCCCTCAAGATTCGGTGGAAGCGGGAGTGGCACCGACTTTAGCTTTACCAT CGGCTCTCTGCAGCCTGAGGACATCGCCACATATTACTGCCAGCAGTTTGACTCCC TGCCACACACATTTGGCCAGGGCACCAAACTGGAGATCAAG
2053.	IGF1R9-HL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYRMQWVRQAPGKGLEWVSGISPSGGT TWYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWSGGSGYAFDIWGQGT MVTVSSGGGGSGGGGSGGGGSDIQMTQSPLSLSASVGDRVTITCQASRDIRNYLNWY QQKPGKAPKLLIYDASSLQTGVPSRFGGSGSGTDFSFTIGSLQPEDIATYYCQQFDSLP HTFGQGTKLEIK
2054.	IGF1R9-HL	artificial	nt	GAAGTTCAGCTGCTCGAGAGCGGAGGTGGACTTGTGCAGCCTGGGGGATCACTGA GATTGTCATGCGCAGCTAGCGGCTTTACCTTCTCCATCTATCGCATGCAGTGGGTT CGACAGGCACCCGGAAAGGGATTGGAATGGGTCTCCGGCATTAGCCCTAGCGGGG GAACAACCTGGTATGCCGATAGCGTGAAGGGCAGGTTCACCATCTCTAGGGACAAC AGCAAAAATACTCTGTACCTGCAGATGAACTCCCTGCGTGCCGAGGATACTGCCGT

				CTACTACTGTGCTCGATGGTCCGGTGGCTCCGGCTATGCCTTCGATATCTGGGGAC AGGGTACAATGGTGACTGTGAGTAGCGGAGGGGGAGGTAGCGGAGGAGGTGGAA GTGGCGGAGGTGGAAGCGACATTCAGATGACCCAGAGCCCATTGTCACTGTCAGC TTCCGTGGGCGATCGGGTGACCATTACATGCCAGGCTTCACCGCGACATCAGGAACT ACCTGAACTGGTATCAGCAGAAGCCTGGCAAAGCCCCCAAGCTCCTTATCTACGAC GCAAGCTCACTGCAGACTGGTGTTCCCTCAAGATTCGGTGGAAGCGGGAGTGGCA CCGACTTTAGCTTTACCATCGGCTCTCTGCAGCCTGAGGACATCGCCACATATTACT GCCAGCAGTTTGACTCCCTGCCACACACATTTGGCCAGGGCACCAAACTGGAGATC AAG
2055.	IGF1R9HLxl2CHL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYRMQWVRQAPGKGLEWVSGISPSGGT TWYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWSGGSGYAFDIWGQGT MVTVSSGGGGSGGGGSGGGGSDIQMTQSPLSLSASVGDRVTITCQASRDIRNYLNWY QQKPGKAPKLLIYDASSLQTGVPSRFGGSGSGTDFSFTIGSLQPEDIATYYCQQFDSLP HTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2056.	IGF1R9HLxl2CHL	artificial	nt	GAAGTTCAGCTGCTCGAGAGCGGAGGTGGACTTGTGCAGCCTGGGGGATCACTGA GATTGTCATGCGCAGCTAGCGGCTTTACCTTCTCCATCTATCGCATGCAGTGGGTT CGACAGGCACCCGGAAAGGGATTGGAATGGGTCTCCGGCATTAGCCCTAGCGGGG GAACAACCTGGTATGCCGATAGCGTGAAGGGCAGGTTCACCATCTCTAGGGACAAC AGCAAAAATACTCTGTACCTGCAGATGAACTCCCTGCGTGCCGAGGATACTGCCGT CTACTACTGTGCTCGATGGTCCGGTGGCTCCGGCTATGCCTTCGATATCTGGGGAC AGGGTACAATGGTGACTGTGAGTAGCGGAGGGGGAGGTAGCGGAGGAGGTGGAA GTGGCGGAGGTGGAAGCGACATTCAGATGACCCAGAGCCCATTGTCACTGTCAGC TTCCGTGGGCGATCGGGTGACCATTACATGCCAGGCTTCACCGCGACATCAGGAACT ACCTGAACTGGTATCAGCAGAAGCCTGGCAAAGCCCCCAAGCTCCTTATCTACGAC GCAAGCTCACTGCAGACTGGTGTTCCCTCAAGATTCGGTGGAAGCGGGAGTGGCA CCGACTTTAGCTTTACCATCGGCTCTCTGCAGCCTGAGGACATCGCCACATATTACT GCCAGCAGTTTGACTCCCTGCCACACACATTTGGCCAGGGCACCAAACTGGAGATC AAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGG TGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATA AGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGC TCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGAC AGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAAC

				TTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAA TAGCTACATATCCTACTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCT CAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACTGT TGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTT GTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAA AAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCG GTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAA CCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2057.	IGF1R10-H	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYHMAWVRQAPGKGLEWVSVISPTGGR TTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTATYYCARAGYSYGYGYFDYWGQG TLVTVSS
2058.	IGF1R10-HCDR1	artificial	aa	NYHMA
2059.	IGF1R10-HCDR2	artificial	aa	VISPTGGRTTYADSVKG
2060.	IGF1R10-HCDR3	artificial	aa	AGYSYGYGYFDY
2061.	IGF1R10-H	artificial	nt	GAAGTGCAGCTCTTGGAGAGCGGAGGGGGACTTGTGCAGCCTGGCGGATCCTTGA GACTTTCTTGCGCTGCCTCCGGTTTCACCTTCTCAAATTACCACATGGCCTGGGTGA GACAGGCTCCTGGAAAAGGGCTCGAATGGGTTTCCGTGATTAGCCCAACCGGAGG GAGGACCACATATGCCGATAGCGTCAAGGGGAGGTTTACAATCAGCCGTGACAACT CCAAGAACACCCTGTACCTCCAGATGAACTCACTGCGAGCCGAGGATACTGCAACC TACTACTGCGCTCGAGCCGGATACTCATACGGCTATGGCTACTTCGACTACTGGGG ACAGGGAACACTGGTGACCGTTAGTAGC
2062.	IGF1R10-L	artificial	aa	DIQMTQFPATLSVSPGERATLSCRASQSVMRNLAWYQQKPGQPPRLLIYGASKRATGI PARFSGSGSGTAFTLTISNLEPEDFAVYYCHQRSTWPLGTFGPGTKLEAK
2063.	IGF1R10-LCDR1	artificial	aa	RASQSVMRNLA
2064.	IGF1R10-LCDR2	artificial	aa	GASKRAT
2065.	IGF1R10-LCDR3	artificial	aa	HQRSTWPLGT
2066.	IGF1R10-L	artificial	nt	GATATTCAGATGACCCAGTCCAGTTCCCTGCAACCTTGAGCGTGTCACCTGGCGAAAGAGC CACACTGTCTTGCCGAGCAAGCCAGAGCGTGATGCGGAACCTGGCATGGTACCAG CAGAAACCTGGCCAGCCTCCACGACTGCTGATCTATGGAGCTAGCAAAAGAGCCAC CGGAATCCCCGCTAGGTTTAGCGGAAGCGGGAAGCGGAACTGCCTTTACCCTGACC ATCTCCAATCTCGAGCCTGAGGACTTTGCCGTCTACTACTGTCACCAGCGTAGCAC TTGGCCTCTGGGGACATTTGGACCTGGCACAAAGCTGGAAGCTAAG
2067.	IGF1R10-HL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYHMAWVRQAPGKGLEWVSVISPTGGR TTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTATYYCARAGYSYGYGYFDYWGQG TLVTVSSGGGGSGGGGSGGGGSDIQMTQFPATLSVSPGERATLSCRASQSVMRNLA

				WYQQKPGQPPRLLIYGASKRATGIPARFSGSGSGTAFTLTISNLEPEDFAVYYCHQRST WPLGTFGPGTKLEAK
2068.	IGF1R10-HL	artificial	nt	GAAGTGCAGCTCTTGGAGAGCGGAGGGGGACTTGTGCAGCCTGGCGGATCCTTGA GACTTTCTTGCGCTGCCTCCGGTTTCACCTTCTCAAATTACCACATGGCCTGGGTGA GACAGGCTCCTGGAAAAGGGCTCGAATGGGTTTCCGTGATTAGCCCAACCGGAGG GAGGACCACATATGCCGATAGCGTCAAGGGGAGGTTTACAATCAGCCGTGACAACT CCAAGAACACCCTGTACCTCCAGATGAACTCACTGCGAGCCGAGGATACTGCAACC TACTACTGCGCTCGAGCCGGATACTCATACGGCTATGGCTACTTCGACTACTGGGG ACAGGGAACACTGGTGACCGTTAGTAGCGGAGGGGGAGGTTCTGGCGGAGGTGG AAGCGGGGGCGGGGGAAGCGATATTCAGATGACCCAGTTCCCTGCAACCTTGAGC GTGTCACCTGGCGAAAGAGCCACACTGTCTTGCCGAGCAAGCCAGAGCGTGATGC GGAACCTGGCATGGTACCAGCAGAAACCTGGCCAGCCTCCACGACTGCTGATCTAT GGAGCTAGCAAAAGAGCCACCGGAATCCCCGCTAGGTTTAGCGGAAGCGGAAGCG GAACTGCCTTTACCCTGACCATCTCCAATCTCGAGCCTGAGGACTTTGCCGTCTACT ACTGTCACCAGCGTAGCACTTGGCCTCTGGGGACATTTGGACCTGGCACAAAGCTG GAAGCTAAG
2069.	IGF1R10HLxl2CHL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYHMAWVRQAPGKGLEWVSVISPTGGR TTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAYYCARAGYSYGYGYFDYWGQG TLVTVSSGGGGSGGGGSGGGGSDIQMTQFPATLSVSPGERATLSCRASQSVMRNLA WYQQKPGQPPRLLIYGASKRATGIPARFSGSGSGTAFTLTISNLEPEDFAVYYCHQRST WPLGTFGPGTKLEAKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2070.	IGF1R10HLxl2CHL	artificial	nt	GAAGTGCAGCTCTTGGAGAGCGGAGGGGGACTTGTGCAGCCTGGCGGATCCTTGA GACTTTCTTGCGCTGCCTCCGGTTTCACCTTCTCAAATTACCACATGGCCTGGGTGA GACAGGCTCCTGGAAAAGGGCTCGAATGGGTTTCCGTGATTAGCCCAACCGGAGG GAGGACCACATATGCCGATAGCGTCAAGGGGAGGTTTACAATCAGCCGTGACAACT CCAAGAACACCCTGTACCTCCAGATGAACTCACTGCGAGCCGAGGATACTGCAACC TACTACTGCGCTCGAGCCGGATACTCATACGGCTATGGCTACTTCGACTACTGGGG ACAGGGAACACTGGTGACCGTTAGTAGCGGAGGGGGAGGTTCTGGCGGAGGTGG AAGCGGGGGCGGGGGAAGCGATATTCAGATGACCCAGTTCCCTGCAACCTTGAGC GTGTCACCTGGCGAAAGAGCCACACTGTCTTGCCGAGCAAGCCAGAGCGTGATGC GGAACCTGGCATGGTACCAGCAGAAACCTGGCCAGCCTCCACGACTGCTGATCTAT GGAGCTAGCAAAAGAGCCACCGGAATCCCCGCTAGGTTTAGCGGAAGCGGAAGCG

				GAACTGCCTTTACCCTGACCATCTCCAATCTCGAGCCTGAGGACTTTGCCGTCTACT ACTGTCACCAGCGTAGCACTTGGCCTCTGGGGACATTTGGACCTGGCACAAAGCTG GAAGCTAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAG GATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACC TTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATG GGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTG AAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATG AACAACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTT CGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCG TCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCA GACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACAC TCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTC CAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGC CCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTC ACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTA CAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2071.	IGF1R11-H	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYMMSWVRQAPGKGLEWVSYISPSGGL TWYADSVKGRFTISRDNSKNTLYLQMNSLREADTAVYYCARDGARGYGMDVWGQGT TVTVSS
2072.	IGF1R11-HCDR1	artificial	aa	KYMMS
2073.	IGF1R11-HCDR2	artificial	aa	YISPSGGLTWYADSVKG
2074.	IGF1R11-HCDR3	artificial	aa	DGARGYGMDV
2075.	IGF1R11-H	artificial	nt	GAGGTCCAGCTGTTGGAAAGCGGAGGCGGACTCGTGCAGCCTGGCGGATCTTTGC GACTTTCCTGTGCTGCCTCCGGTTTCACCTTCTCCAAGTACATGATGAGCTGGGTG AGACAGGCACCAGGCAAAGGACTGGAATGGGTGAGCTACATTAGCCCATCTGGCG GACTGACATGGTATGCCGATAGTGTTAAGGGGAGGTTCACCATCAGTAGGGACAAT AGCAAGAACACCCTGTACCTGCAGATGAACTCACTGCGAGAGGCTGATACTGCCGT GTATTACTGCGCAAGGGATGGAGCTAGAGGCTATGGAATGGACGTGTGGGGACAG GGAACAACCGTCACCGTGAGCAGT
2076.	IGF1R11-L	artificial	aa	DIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIP ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPEVTFGPGTKVDIK
2077.	IGF1R11-LCDR1	artificial	aa	RASQSVSSYLA
2078.	IGF1R11-LCDR2	artificial	aa	DASNRAT
2079.	IGF1R11-LCDR3	artificial	aa	QQRSNWPPEVT
2080.	IGF1R11-L	artificial	nt	GACATTCAGATGACACAGAGCCCTGCCACACTGAGCCTGTCACCTGGAGAGCGAG CTACATTGAGCTGTCGCGCTAGCCAGAGCGTGTCTTCCTATCTTGCCTGGTACCAG

				CAGAAACCTGGACAGGCACCAAGACTCCTGATCTACGACGCCTCCAACCGTGCAAC TGGCATCCCTGCTCGCTTTTCTGGCTCTGGCTCTGGGACCGACTTTACCTTGACCA TCTCCTCACTGGAACCCGAGGATTTTGCCGTGTACTATTGCCAGCAGCGGAGCAAT TGGCCTCCCGAAGTCACTTTTGGCCCTGGCACCAAAGTGGATATCAAG
2081.	IGF1R11-HL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYMMSWVRQAPGKGLEWVSYISPSGGL TWYADSVKGRFTISRDNSKNTLYLQMNSLREADTAVYYCARDGARGYGMDVWGQGT TVTVSSGGGGSGGGGSGGGGSDIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWY QQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP PEVTFGPGTKVDIK
2082.	IGF1R11-HL	artificial	nt	GAGGTCCAGCTGTTGGAAAGCGGAGGCGGACTCGTGCAGCCTGGCGGATCTTTGC GACTTTCCTGTGCTGCCTCCGGTTTCACCTTCTCCAAGTACATGATGAGCTGGGTG AGACAGGCACCAGGCAAAGGACTGGAATGGGTGAGCTACATTAGCCCATCTGGCG GACTGACATGGTATGCCGATAGTGTTAAGGGGAGGTTCACCATCAGTAGGGACAAT AGCAAGAACACCCTGTACCTGCAGATGAACTCACTGCGAGAGGCTGATACTGCCGT GTATTACTGCGCAAGGGATGGAGCTAGAGGCTATGGAATGGACGTGTGGGGACAG GGAACAACCGTCACCGTGAGCAGTGGGGGAGGCGGAAGCGGAGGGGGAGGTAGT GGAGGGGGAGGCTCAGACATTCAGATGACACAGAGCCCTGCCACACTGAGCCTGT CACCTGGAGAGCGAGCTACATTGAGCTGTCGCGCTAGCCAGAGCGGTGTCTTCCTAT CTTGCCTGGTACCAGCAGAAACCTGGACAGGCACCAAGACTCCTGATCTACGACGC CTCCAACCGTGCAACTGGCATCCCTGCTCGCTTTTCTGGCTCTGGCTCTGGGACCG ACTTTACCTTGACCATCTCCTCACTGGAACCCGAGGATTTTGCCGTGTACTATTGCC AGCAGCGGAGCAATTGGCCTCCCGAAGTCACTTTTGGCCCTGGCACCAAAGTGGAT ATCAAG
2083.	IGF1R11HLxl2CHL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYMMSWVRQAPGKGLEWVSYISPSGGL TWYADSVKGRFTISRDNSKNTLYLQMNSLREADTAVYYCARDGARGYGMDVWGQGT TVTVSSGGGGSGGGGSGGGGSDIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWY QQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP PEVTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2084.	IGF1R11HLxl2CHL	artificial	nt	GAGGTCCAGCTGTTGGAAAGCGGAGGCGGACTCGTGCAGCCTGGCGGATCTTTGC GACTTTCCTGTGCTGCCTCCGGTTTCACCTTCTCCAAGTACATGATGAGCTGGGTG AGACAGGCACCAGGCAAAGGACTGGAATGGGTGAGCTACATTAGCCCATCTGGCG

				GACTGACATGGTATGCCGATAGTGTTAAGGGGAGGTTCACCATCAGTAGGGACAAT AGCAAGAACACCCTGTACCTGCAGATGAACTCACTGCGAGAGGCTGATACTGCCGT GTATTACTGCGCAAGGGATGGAGCTAGAGGCTATGGAATGGACGTGTGGGGACAG GGAACAACCGTCACCGTGAGCAGTGGGGGAAGGCGGAAGCGGAGGGGGAGGTAGT GGAGGGGGAGGCTCAGACATTCAGATGACACAGAGCCCTGCCACACTGAGCCTGT CACCTGGAGAGCGAGCTACATTGAGCTGTCGCGCTAGCCAGAGCGGTGTCTTCCTAT CTTGCCTGGTACCAGCAGAAACCTGGACAGGCACCAAGACTCCTGATCTACGACGC CTCCAACCGTGCAACTGGCATCCCTGCTCGCTTTTCTGGCTCTGGCTCTGGGACCG ACTTTACCTTGACCATCTCCTCACTGGAACCCGAGGATTTTGCCGTGTACTATTGCC AGCAGCGGAGCAATTGGCCTCCCGAAGTCACTTTTGGCCCTGGCACCAAAGTGGAT ATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGAT TGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTC AATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGG TTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCGATTCAGTGAA AGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAA CAACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCG GTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTC TCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGA CTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTC ACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCA ACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCC CCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCAC CCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACA GCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2085.	IGF1R12-H	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYPMYWVRQAPGKGLEWVSRISSSGGR TVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRWSRSAAEYGLGGYW GQGTLVTVSS
2086.	IGF1R12-HCDR1	artificial	aa	NYPMY
2087.	IGF1R12-HCDR2	artificial	aa	RISSSGGRTVYADSVKG
2088.	IGF1R12-HCDR3	artificial	aa	DRWSRSAAEYGLGGY
2089.	IGF1R12-H	artificial	nt	GAAGTCCAGCTCCTTGAAAGCGGTGGCGGATTGGTCCAGCCTGGAGGCTCTTTGA GACTCTCCTGTGCCGCATCAGGCTTCACCTTTTCCAACTATCCTATGTACTGGGTTC GCCAGGCTCCTGGAAAAGGCTTGGAATGGGTGTCACGGATTAGCTCTAGCGGGGG AAGGACTGTCTATGCCGATTCCGTGAAAGGGAGATTCACCATCTCTCGGGACAATA GCAAGAACACCCTGTATCTCCAGATGAACTCTCTTCGTGCCGAAGACACTGCCGTG TATTACTGCGCACGAGACCGATGGAGCCGATCAGCAGCTGAATACGGCTTGGGAG

				GCTACTGGGGTCAGGGAACTCTTGTGACTGTCTCTAGC
2090.	IGF1R12-L	artificial	aa	DIQMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYLAST RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTWTFGQGTKVEIK
2091.	IGF1R12-LCDR1	artificial	aa	KSSQSVLYSSNNKNYLA
2092.	IGF1R12-LCDR2	artificial	aa	LASTRES
2093.	IGF1R12-LCDR3	artificial	aa	QQYYSTWT
2094.	IGF1R12-L	artificial	nt	GATATCCAGATGACTCAGAGCCCTGATTCACTGGCAGTGTCTCTCGGAGAACGTGC CACAATCAACTGCAAGAGTAGCCAGTCCGTCCTTTACTCCTCCAACAACAAAACTA CCTCGCATGGTACCAGCAGAAACCTGGGCAGCCACCCAAACTTCTCATCTATCTTG CTTCCACACGTGAGAGTGGCGTGCCTGACCGTTTTAGCGGATCCGGTAGCGGAAC AGATTTCACTCTCACAATCTCAAGCCTGCAGGCTGAAGATGTCGCAGTCTACTATTG CCAGCAGTATTACTCAACCTGGACATTCGGACAGGGGACAAAAGTGGAGATCAAA
2095.	IGF1R12-HL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYPMYWVRQAPGKGLEWVSRISSSGGR TVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRWSRSAAEYGLGGYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPDSLAVSLGERATINCKSSQSVLYS SNNKNYLAWYQQKPGQPPKLLIYLASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQQYYSTWTFGQGTKVEIK
2096.	IGF1R12-HL	artificial	nt	GAAGTCCAGCTCCTTGAAAGCGGTGGCGGATTGGTCCAGCCTGGAGGCTCTTTGA GACTCTCCTGTGCCGCATCAGGCTTCACCTTTCCAACTATCCTATGTACTGGGTTC GCCAGGCTCCTGGAAAGGCTTGGAATGGGTGTCACGGATTAGCTCTAGCGGGGG AAGGACTGTCTATGCCGATTCCGTGAAGGGAGATTCACCATCTCTCGGGACAATA GCAAGAACACCCTGTATCTCCAGATGAACTCTCTTCGTGCCGAAGACACTGCCGTG TATTACTGCGCACGAGACCGATGGAGCCGATCAGCAGCTGAATACGGCTTGGGAG GCTACTGGGGTCAGGGAACTCTTGTGACTGTCTCTAGCGGAGGCGGTGGAAGCGG GGGAGGCGGATCTGGTGGAGGCGGAAGCGATATCCAGATGACTCAGAGCCCTGAT TCACTGGCAGTGTCTCTCGGAGAACGTGCCACAATCAACTGCAAGAGTAGCCAGTC CGTCCTTTACTCCTCCAACAACAAAAACTACCTCGCATGGTACCAGCAGAAACCTGG GCAGCCACCCAAACTTCTCATCTATCTTGCTTCCACACGTGAGAGTGGCGTGCCTG ACCGTTTTAGCGGATCCGGTAGCGGAACAGATTTCACTCTCACAATCTCAAGCCTG CAGGCTGAAGATGTCGCAGTCTACTATTGCCAGCAGTATTACTCAACCTGGACATTC GGACAGGGGACAAAAGTGGAGATCAAA
2097.	IGF1R12HLxl2CHL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYPMYWVRQAPGKGLEWVSRISSSGGR TVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRWSRSAAEYGLGGYW GQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPDSLAVSLGERATINCKSSQSVLYS SNNKNYLAWYQQKPGQPPKLLIYLASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQQYYSTWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN

				KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2098.	IGF1R12HLxl2CHL	artificial	nt	GAAGTCCAGCTCCTTGAAAGCGGTGGCGGATTGGTCCAGCCTGGAGGCTCTTTGA GACTCTCCTGTGCCGCATCAGGCTTCACCTTTTCCAACTATCCTATGTACTGGGTTC GCCAGGCTCCTGGAAAAGGCTTGGAATGGGTGTCACGGATTAGCTCTAGCGGGGG AAGGACTGTCTATGCCGATTCCGTGAAAGGGAGATTCACCATCTCTCGGGACAATA GCAAGAACACCCTGTATCTCCAGATGAACTCTCTTCGTGCCGAAGACACTGCCGTG TATTACTGCGCACGAGACCGATGGAGCCGATCAGCAGCTGAATACGGCTTGGGAG GCTACTGGGGTCAGGGAACTCTTGTGACTGTCTCTAGCGGAGGCGGTGGAAGCGG GGGAGGCGGATCTGGTGGAGGCGGAAGCGATATCCAGATGACTCAGAGCCCTGAT TCACTGGCAGTGTCTCTCGGAGAACGTGCCACACAATCAACTGCAAGAGTAGCCAGTC CGTCCTTTACTCCTCCAACAACAAAAACTACCTCGCATGGTACCAGCAGAAACCTGG GCAGCCACCCAAACTTCTCATCTATCTTGCTTCCACACGGTGAGAGTGGCGTGCCTG ACCGTTTTAGCGGATCCGGTAGCGGAACAGATTTCACTCTCACAATCTCAAGCCTG CAGGCTGAAGATGTCGCAGTCTACTATTGCCAGCAGTATTACTCAACCTGGACATTC GGACAGGGGACAAAAGTGGAGATCAAATCCGGAGGTGGTGGATCCGAGGTGCAGC TGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGT GCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCC AGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAAC ATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAA CACTGCCTATCTACAAATGAACAACTTGAAGACTGAGGACACTGCCGTGTACTACTG TGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCC AAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCGGCTC CGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCAC CTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGC AACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGG TGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTG GAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATA TTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGA CTGTCCTA
2099.	IGF1R13-H	artificial	aa	EVQLVQSGAEVKKPGESLTISCKGPGYNFFNYWIGWVRQMPGKGLEWMGIIYPTDSDT RYSPSFQGQVTISVDKSISTAYLQWSSLKASDTAMYYCARSIRYCPGGRCYSGYYGMD VWGQGTMVTVSS
2100.	IGF1R13-HCDR1	artificial	aa	NYWIG

2101.	IGF1R13-HCDR2	artificial	aa	IIYPTDSDTRYSPSFQG
2102.	IGF1R13-HCDR3	artificial	aa	SIRYCPGGRCYSGYYGMDV
2103.	IGF1R13-H	artificial	nt	GAAGTCCAGTTGGTGCAGAGTGGTGCCGAAGTCAAAAAGCCTGGCGAGAGCCTGA CCATCTCATGTAAGGGTCCTGGCTACAACTTCTTCAACTACTGGATCGGATGGGTG CGACAGATGCCTGGAAAAGGGCTCGAATGGATGGGCATTATCTATCCCACCGACTC CGACACACGGTATTCCCCATCATTTCAGGGACAGGTCACCATCTCCGTTGACAAGA GCATCTCCACCGCTTATCTCCAGTGGAGTTCCCTGAAAGCCTCCGACACCGCAATG TATTACTGCGCACGTAGTATCCGTTACTGCCCAGGAGGCAGATGCTATAGCGGATA TTACGGCATGGACGTTTGGGGACAGGGAACAATGGTGACTGTGAGCTCA
2104.	IGF1R13-L	artificial	aa	SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIP DRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVL
2105.	IGF1R13-LCDR1	artificial	aa	QGDSLRSYYAS
2106.	IGF1R13-LCDR2	artificial	aa	GKNNRPS
2107.	IGF1R13-LCDR3	artificial	aa	NSRDSSGNHVV
2108.	IGF1R13-L	artificial	nt	TCAAGCGAACTGACTCAGGATCCAGCTGTTTCTGTCGCCTTGGGACAGACTGTGCG CATTACATGTCAGGGTGATAGCTTGCGTAGCTACTACGCTTCATGGTACCAGCAGA AGCCTGGACAGGCACCTGTCCTGGTGATCTACGGCAAGAACAATAGGCCAAGCGG TATTCCCGATCGGTTTTCTGGATCCTCATCCGGCAATACTGCCTCTCTGACAATCAC CGGTGCTCAGGCTGAAGATGAGGCTGACTACTACTGCAACTCCCGAGATTCTAGCG GAAATCACGTGGTCTTCGGAGGTGGGACAAAACTTACCGTGCTC
2109.	IGF1R13-HL	artificial	aa	EVQLVQSGAEVKKPGESLTISCKGPGYNFFNYWIGWVRQMPGKGLEWMGIIYPTDSDT RYSPSFQGQVTISVDKSISTAYLQWSSLKASDTAMYYCARSIRYCPGGRCYSGYYGMD VWGQGTMVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRS YYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC NSRDSSGNHVVFGGGTKLTVL
2110.	IGF1R13-HL	artificial	nt	GAAGTCCAGTTGGTGCAGAGTGGTGCCGAAGTCAAAAAGCCTGGCGAGAGCCTGA CCATCTCATGTAAGGGTCCTGGCTACAACTTCTTCAACTACTGGATCGGATGGGTG CGACAGATGCCTGGAAAAGGGCTCGAATGGATGGGCATTATCTATCCCACCGACTC CGACACACGGTATTCCCCATCATTTCAGGGACAGGTCACCATCTCCGTTGACAAGA GCATCTCCACCGCTTATCTCCAGTGGAGTTCCCTGAAAGCCTCCGACACCGCAATG TATTACTGCGCACGTAGTATCCGTTACTGCCCAGGAGGCAGATGCTATAGCGGATA TTACGGCATGGACGTTTGGGGACAGGGAACAATGGTGACTGTGAGCTCAGGAGGG GGAGGCTCTGGTGGGGGAGGTTCTGGAGGTGGAGGCTCTTCAAGCGAACTGACTC AGGATCCAGCTGTTTCTGTCGCCTTGGGACAGACTGTGCGCATTACATGTCAGGGT GATAGCTTGCGTAGCTACTACGCTTCATGGTACCAGCAGAAGCCTGGACAGGCACC TGTCCTGGTGATCTACGGCAAGAACAATAGGCCAAGCGGTATTCCCGATCGGTTTT

				CTGGATCCTCATCCGGCAATACTGCCTCTCTGACAATCACCGGTGCTCAGGCTGAA GATGAGGCTGACTACTACTGCAACTCCCGAGATTCTAGCGGAAATCACGTGGTCTT CGGAGGTGGGACAAAACTTACCGTGCTC
2111.	IGF1R13HLxl2CHL	artificial	aa	EVQLVQSGAEVKKPGESLTISCKGPGYNFFNYWIGWVRQMPGKGLEWMGIIYPTDSDT RYSPSFQGQVTISVDKSISTAYLQWSSLKASDTAMYYCARSIRYCPGGRCYSGYYGMD VWGQGTMVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRS YYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC NSRDSSGNHVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2112.	IGF1R13HLxl2CHL	artificial	nt	GAAGTCCAGTTGGTGCAGAGTGGTGCCGAAGTCAAAAAGCCTGGCGAGAGCCTGA CCATCTCATGTAAGGGTCCTGGCTACAACTTCTTCAACTACTGGATCGGATGGGTG CGACAGATGCCTGGAAAAGGGCTCGAATGGATGGGCATTATCTATCCCACCGACTC CGACACACGGTATTCCCCATCATTTCAGGGACAGGTCACCATCTCCGTTGACAAGA GCATCTCCACCGCTTATCTCCAGTGGAGTTCCCTGAAAGCCTCCGACACCGCAATG TATTACTGCGCACGTAGTATCCGTTACTGCCCAGGAGGCAGATGCTATAGCGGATA TTACGGCATGGACGTTTGGGGACAGGGAACAATGGTGACTGTGAGCTCAGGAGGG GGAGGCTCTGGTGGGGGAGGTTCTGGAGGTGGAGGCTCTTCAAGCGAACTGACTC AGGATCCAGCTGTTTCTGTCGCCTTGGGACAGACTGTGCGCATTACATGTCAGGGT GATAGCTTGCGTAGCTACTACGCTTCATGGTACCAGCAGAAGCCTGGACAGGCACC TGTCCTGGTGATCTACGGCAAGAACAATAGGCCAAGCGGTATTCCCGATCGGTTTT CTGGATCCTCATCCGGCAATACTGCCTCTCTGACAATCACCGGTGCTCAGGCTGAA GATGAGGCTGACTACTACTGCAACTCCCGAGATTCTAGCGGAAATCACGTGGTCTT CGGAGGTGGGACAAAACTTACCGTGCTCTCCGGAGGGTGGTGGATCCGAGGTGCAG CTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCAT GTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCT CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATATAATTATGCA ACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAA AACACTGCCTATCTACAAATGAACAACTTGAAGACTGAGGACACTGCCGTGTACTAC TGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGG CCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGC TCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATC ACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTG GCAACTACCCAAACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATA

				GGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCT TGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAA TATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACT GACTGTCCTA
2113.	IGF1R15-H	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASSPYSSRWYSFDPWGQG TMVTVSS
2114.	IGF1R15-HCDR1	artificial	aa	SYAMS
2115.	IGF1R15-HCDR2	artificial	aa	AISGSGGSTYYADSVKG
2116.	IGF1R15-HCDR3	artificial	aa	SPYSSRWYSFDP
2117.	IGF1R15-H	artificial	nt	GAGGTTCAGCTGCTCGAAAGCGGAGGCGGTTTGGTGCAGCCTGGGGGAAGCCTGA GACTTAGCTGTGCTGCAAGCGGATTCACCTTCTCCAGCTATGCCATGAGCTGGGTG AGGCAGGCCCCTGGCAAAGGACTGGAGTGGGTGAGCGCTATCTCAGGAAGCGGC GGTTCTACCTACTACGCCGATAGCGTCAAGGGGAGGTTCACCATCAGCCGTGACAA CAGCAAGAACACCCTGTACCTCCAGATGAATAGCCTGCGTGCTGAGGACACTGCCG TTTACTACTGCGCAAGCTCCCCATACTCCTCACGGTGGTATAGCTTCGATCCATGG GGACAGGGGACTATGGTGACCGTGAGTAGT
2118.	IGF1R15-L	artificial	aa	SYELTQPPSVSVSPGQTATITCSGDDLGNKYVSWYQQKPGQSPVLVIYQDTKRPSGIPE RFSGSNSGNIATLTISGTQAVDEADYYCQVWDTGTVVFGGGTKLTVL
2119.	IGF1R15-LCDR1	artificial	aa	SGDDLGNKYVS
2120.	IGF1R15-LCDR2	artificial	aa	QDTKRPS
2121.	IGF1R15-LCDR3	artificial	aa	QVWDTGTVV
2122.	IGF1R15-L	artificial	nt	AGCTATGAACTGACACAGCCACCTAGCGTGAGCGTTAGCCCTGGACAGACTGCCAC AATCACCTGTAGTGGGGATGACCTTGGCAACACAAGTACGTGAGCTGGTATCAGCAGA AGCCTGGCCAGTCTCCCGTGCTGGTGATCTACCAGGACACCAAACGACCTAGCGG AATCCCAGAGCGATTCAGCGGAAGCAACAGCGGGAACATCGCAACTCTCACCATTT CCGGCACTCAGGCCGTGGATGAAGCCGACTACTATTGCCAGGTGTGGGACACTGG AACCGTCGTGTTTGGGGGAGGCACAAAACTGACCGTCCTG
2123.	IGF1R15-HL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASSPYSSRWYSFDPWGQG TMVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTATITCSGDDLGNKYVSW YQQKPGQSPVLVIYQDTKRPSGIPERFSGSNSGNIATLTISGTQAVDEADYYCQVWDTG TVVFGGGTKLTVL
2124.	IGF1R15-HL	artificial	nt	GAGGTTCAGCTGCTCGAAAGCGGAGGCGGTTTGGTGCAGCCTGGGGGAAGCCTGA GACTTAGCTGTGCTGCAAGCGGATTCACCTTCTCCAGCTATGCCATGAGCTGGGTG AGGCAGGCCCCTGGCAAAGGACTGGAGTGGGTGAGCGCTATCTCAGGAAGCGGC

				GGTTCTACCTACTACGCCGATAGCGTCAAGGGGAGGTTCACCATCAGCCGTGACAA CAGCAAGAACACCCTGTACCTCCAGATGAATAGCCTGCGTGCTGAGGACACTGCCG TTTACTACTGCGCAAGCTCCCCATACTCCTCACGGTGGTATAGCTTCGATCCATGG GGACAGGGGACTATGGTGACCGTGAGTAGTGGCGGAGGGGGAAGCGGAGGAGGC GGGAGCGGCGGAGGCGGAAGCAGCTATGAACTGACACAGCCACCTAGCGTGAGC GTTAGCCCTGGACAGACTGCCACAATCACCTGTAGTGGGGATGACCTTGGCAACAA GTACGTGAGCTGGTATCAGCAGAAGCCTGGCCAGTCTCCCGTGCTGGTGATCTACC AGGACACCCAAACGACCTAGCGGAATCCCAGAGCGATTCAGCGGAAGCAACAGCGG GAACATCGCAACTCTCACCATTTCCGGCACTCAGGCCGTGGATGAAGCCGACTACT ATTGCCAGGTGTGGGACACTGGAACCGTCGTGTTTGGGGGAGGCACAAAACTGAC CGTCCTG
2125.	IGF1R15HLxl2CHL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASSPYSSRWYSFDPWGQG TMVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTATITCSGDDLGNKYVSW YQQKPGQSPVLVIYQDTKRPSGIPERFSGSNSGNIATLTISGTQAVDEADYYCQVWDTG TVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2126.	IGF1R15HLxl2CHL	artificial	nt	GAGGTTCAGCTGCTCGAAAGCGGAGGCGGTTTGGTGCAGCCTGGGGGGAAGCCTGA GACTTAGCTGTGCTGCAAGCGGATTCACCTTCTCCAGCTATGCCATGAGCTGGGTG AGGCAGGCCCCTGGCAAAGGACTGGAGTGGGTGAGCGCTATCTCAGGAAGCGGC GGTTCTACCTACTACGCCGATAGCGTCAAGGGGAGGTTCACCATCAGCCGTGACAA CAGCAAGAACACCCTGTACCTCCAGATGAATAGCCTGCGTGCTGAGGACACTGCCG TTTACTACTGCGCAAGCTCCCCATACTCCTCACGGTGGTATAGCTTCGATCCATGG GGACAGGGGACTATGGTGACCGTGAGTAGTGGCGGAGGGGGAAGCGGAGGAGGC GGGAGCGGCGGAGGCGGAAGCAGCTATGAACTGACACAGCCACCTAGCGTGAGC GTTAGCCCTGGACAGACTGCCACAATCACCTGTAGTGGGGATGACCTTGGCAACAA GTACGTGAGCTGGTATCAGCAGAAGCCTGGCCAGTCTCCCGTGCTGGTGATCTACC AGGACACCCAAACGACCTAGCGGAATCCCAGAGCGATTCAGCGGAAGCAACAGCGG GAACATCGCAACTCTCACCATTTCCGGCACTCAGGCCGTGGATGAAGCCGACTACT ATTGCCAGGTGTGGGACACTGGAACCGTCGTGTTTGGGGGAGGCACAAAACTGAC CGTCCTGTCCGGAGGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGG ATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCT TCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGG

				GTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGA AAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGA ACAACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTC GGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGT CTCCTCAGGTGGTGGTTCTGGCGGCGGCGCTCCGGTGGTGGTTCTCAG ACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACT CACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCC AACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCC CCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCA CCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTAC AGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2127.	IGF1R16-H	artificial	aa	QVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINPSNGR TNYNEKFKRKATLTVDKSSSTAYMQLSSLTSEDSAVYYFARGRPDYYGSSKWYFDVW GAGTTVTVSS
2128.	IGF1R16-HCDR1	artificial	aa	SYWMH
2129.	IGF1R16-HCDR2	artificial	aa	EINPSNGRTNYNEKFKR
2130.	IGF1R16-HCDR3	artificial	aa	GRPDYYGSSKWYFDV
2131.	IGF1R16-H	artificial	nt	CAGGTTCAGCTGCAGCAGAGCGGAGCTGAGCTCGTTAAACCTGGTGCTTCCGTGA AACTGAGCTGCAAAGCCTCCGGCTATACCTTCACAAGCTACTGGATGCACTGGGTC AAACAGCGTCCTGGTCAGGGTCTCGAATGGATTGGGGAGATCAACCCCTCCAACG GCCGCACCAATTACAATGAGAAGTTCAAGCGGAAGGCCACCCTTACCGTGGATAAG AGCTCATCTACCGCCTACATGCAGCTGTCTTCACTGACATCTGAGGACTCTGCCGT GTATTACTTTGCAAGAGGGAGGCCTGACTACTACGGGTCATCCAAGTGGTACTTTG ACGTCTGGGGAGCTGGGACTACCGTGACTGTCTAGC
2132.	IGF1R16-L	artificial	aa	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNVNTYLEWYLQKPGQSPKLLIYKVSNR FSGVPDRFSGSGSGTDFTLRISRVEAEDLGIYYCFQGSHVPPTFGGGTKLEIK
2133.	IGF1R16-LCDR1	artificial	aa	RSSQSIVHSNVNTYLE
2134.	IGF1R16-LCDR2	artificial	aa	KVSNRFS
2135.	IGF1R16-LCDR3	artificial	aa	FQGSHVPPT
2136.	IGF1R16-L	artificial	nt	GATGTCTTGATGACTCAGACTCCACTGTCACTTCCTGTGTCACTGGGAGATCAGGC ATCCATTAGCTGCAGGAGTAGCCAGAGCATCGTGCACTCCAACGTCAACACATACC TGGAGTGGTACCTGCAGAAACCTGGCCAGAGCCCAAAGCTGCTCATCTACAAGGTG AGCAATCGGTTTTCCGGCGTTCCCGATAGATTCAGCGGCGGAAGCGGGAAGCGGTACAG ACTTTACCCTGCGCATTTCTCGAGTGGAAGCCGAAGACCTGGGCATCTACTATTGC TTCCAGGGTTCTCATGTTCCCCCAACCTTCGGTGGCGGAACAAAACTCGAAATCAA G

2137.	IGF1R16-HL	artificial	aa	QVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINPSNGR TNYNEKFKRKATLTVDKSSSTAYMQLSSLTSEDSAVYYFARGRPDYYGSSKWYFDVW GAGTTVTVSSGGGGSGGGGSGGGGSDVLMTQTPLSLPVSLGDQASISCRSSQSIVHS NVNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLRISRVEAEDLGIY YCFQGSHVPPTFGGGTKLEIK
2138.	IGF1R16-HL	artificial	nt	CAGGTTCAGCTGCAGCAGAGCGGAGCTGAGCTCGTTAAACCTGGTGCTTCCGTGA AACTGAGCTGCAAAGCCTCCGGCTATACCTTCACAAGCTACTGGATGCACTGGGTC AAACAGCGTCCTGGTCAGGGTCTCGAATGGATTGGGGAGATCAACCCCTCCAACG GCCGCACCAATTACAATGAGAAGTTCAAGCGGAAGGCCACCCTTACCGTGGATAAG AGCTCATCTACCGCCTACATGCAGCTGTCTTCACTGACATCTGAGGACTCTGCCGT GTATTACTTTGCAAGAGGGAGGCCTGACTACTACGGGTCATCCAAGTGGTACTTTG ACGTCTGGGGAGCTGGGACTACCGTGACTGTGTCTAGCGGAGGCGGAGGGAGCG GAGGGGGAGGCTCCGGTGGCGGGGGATCTGATGTCTTGATGACTCAGACTCCACT GTCACTTCCTGTGTCACTGGGAGATCAGGCATCCATTAGCTGCAGGAGTAGCCAGA GCATCGTGCACTCCAACGTCAACACATACCTGGAGTGGTACCTGCAGAAACCTGGC CAGAGCCCAAAGCTGCTCATCTACAAGGTGAGCAATCGGTTTTCCGGCGTTCCCGA TAGATTCAGCGGAAGCGGAAGCGGTACAGACTTTACCCTGCGCATTTCTCGAGTGG AAGCCGAAGACCTGGGCATCTACTATTGCTTCCAGGGTTCTCATGTTCCCCCAACC TTCGGTGGCGGAACACAAAACTCGAAATCAAG
2139.	IGF1R16HLxl2CHL	artificial	aa	QVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINPSNGR TNYNEKFKRKATLTVDKSSSTAYMQLSSLTSEDSAVYYFARGRPDYYGSSKWYFDVW GAGTTVTVSSGGGGSGGGGSGGGGSDVLMTQTPLSLPVSLGDQASISCRSSQSIVHS NVNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLRISRVEAEDLGIY YCFQGSHVPPTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2140.	IGF1R16HLxl2CHL	artificial	nt	CAGGTTCAGCTGCAGCAGAGCGGAGCTGAGCTCGTTAAACCTGGTGCTTCCGTGA AACTGAGCTGCAAAGCCTCCGGCTATACCTTCACAAGCTACTGGATGCACTGGGTC AAACAGCGTCCTGGTCAGGGTCTCGAATGGATTGGGGAGATCAACCCCTCCAACG GCCGCACCAATTACAATGAGAAGTTCAAGCGGAAGGCCACCCTTACCGTGGATAAG AGCTCATCTACCGCCTACATGCAGCTGTCTTCACTGACATCTGAGGACTCTGCCGT GTATTACTTTGCAAGAGGGAGGCCTGACTACTACGGGTCATCCAAGTGGTACTTTG ACGTCTGGGGAGCTGGGACTACCGTGACTGTGTCTAGCGGAGGCGGAGGGAGCG GAGGGGGAGGCTCCGGTGGCGGGGGATCTGATGTCTTGATGACTCAGACTCCACT

				GTCACTTCCTGTGTCACTGGGAGATCAGGCATCCATTAGCTGCAGGAGTAGCCAGA GCATCGTGCACTCCAACGTCAACACATACCTGGAGTGGTACCTGCAGAAACCTGGC CAGAGCCCAAAGCTGCTCATCTACAAGGTGAGCAATCGGTTTTCCGGCGTTCCCGA TAGATTCAGCGGAAGCGGAAGCGGTACAGACTTTACCCTGCGCATTTCTCGAGTGG AAGCCGAAGACCTGGGCATCTACTATTGCTTCCAGGGTTCTCATGTTCCCCCAACC TTCGGTGGCGGAACAAAACTCGAAATCAAGTCCGGAGGTGGTGGATCCGAGGTGC AGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTC ATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGG CTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATG CAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAA AAAACACTGCCTATCTACAAATGAACAACTTGAAGACTGAGGACACTGCCGTGTACT ACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGG GGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTTCTGGCGGCGGCG GCTCCGGTGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTA TCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATC TGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAA TAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTG CTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAG AATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAA CTGACTGTCCTA
2141.	IGF1R17-H	artificial	aa	QAQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGST RDYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRDGVETTFYYYYYGMDV WGQGTTVTVSS
2142.	IGF1R17-HCDR1	artificial	aa	DYYMS
2143.	IGF1R17-HCDR2	artificial	aa	YISSSGSTRDYADSVKG
2144.	IGF1R17-HCDR3	artificial	aa	DGVETTFYYYYYGMDV
2145.	IGF1R17-H	artificial	nt	CAGGCACAGCTGGTGGAAAGTGGCGGGTGGCTTAGTTAAGCCTGGTGGATCCCTGC GACTTTCTTGTGCTGCCTCCGGCTTTACGTTTTCCGACTACTACATGTCCTGGATTA GACAAGCCCCTGGCAAGGGCTTGGAATGGGTGAGCTACATAAGCTCCTCGGGAAG CACTAGGGACTATGCCGATAGCGTTAAGGGGAGATTCACGATAAGCAGGGATAACG CCAAGAACTCCCTGTATCTGCAGATGAATAGTCTCCGTGCTGAGGACACTGCCGTG TACTATTGCGTGAGGGATGGCGTCGAAACAACCTTCTACTACTACTATGGCATG GACGTTTGGGGACAGGGAACAACTGTAACCGTGAGCTCA
2146.	IGF1R17-L	artificial	aa	DIQMTQSPSSLSASVGDRVTFTCRASQDIRRDLGWYQQKPGKAPKRLIYAASRLQSGV PSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPRTFGQGTEVEII
2147.	IGF1R17-LCDR1	artificial	aa	RASQDIRRDLG

2148.	IGF1R17-LCDR2	artificial	aa	AASRLQS
2149.	IGF1R17-LCDR3	artificial	aa	LQHNNYPRT
2150.	IGF1R17-L	artificial	nt	GATATCCAGATGACACAAAGCCCAAGCTCGCTGAGCGCTAGGCGATCGAG TGACATTCACCTGTAGGGCTAGCCAGGATATTAGACGGGACCTAGGGTGGTACCAG CAGAAACCTGGCAAAGCTCCCCAAACGCCTTATCTATCGCGGCTTCACGGCTGCAATC GGGAGTCCCCCTCTCGCTTTTCTGGAAGTGGGAGCGGAACCGAGTTTACATTGACGA TTAGCTCCCTCCAACCTGAGGACTTTGCAACCTATTACTGCCTCCAGCACAATAACT ATCCACGGACCTTCGGACAAGGGACCGAGGTCGAGATCATC
2151.	IGF1R17-HL	artificial	aa	QAQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGST RDYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRDGVETTFYYYYYGMDV WGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTFTCRASQDIR RDLGWYQQKPGKAPKRLIYAASRLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCL QHNNYPRTFGQGTEVEII
2152.	IGF1R17-HL	artificial	nt	CAGGCACAGCTGGTGGAAAGTGGCGGTGGCTTAGTTAAGCCTGGTGGATCCCTGC GACTTTCTTGTGCTGCCTCCGGCTTTACGTTTTCCGACTACTACATGTCCTGGATTA GACAAGCCCCCTGGCAAGGGCTTGGAATGGGTGAGCTACATAAGCTCCTCGGGAAG CACTAGGGACTATGCCGATAGCGTTAAGGGGAGATTCACGATAAGCAGGGATAACG CCAAGAACTCCCTGTATCTGCAGATGAATAGTCTCCGTGCTGAGGACACTGCCGTG TACTATTGCGTGAGGGATGGCGTCGAAACAACCTTCTACTACTACTATGGCATG GACGTTTGGGGACAGGGAACAACTGTAACCGTGAGCTCAGGAGGTGGAGGTAGCG GAGGTGGAGGTAGTGGTGGAGGTGGCTCGGATATCCAGATGACACAAAGCCCAAG CTCGCTGAGCGCTAGCGTAGGCGATCGAGTGACATTCACCTGTAGGGCTAGCCAG GATATTAGACGGGACCTAGGGTGGTACCAGCAGAAACCTGGCAAAGCTCCCAAAC GCCTTATCTATGCGGCTTCACGGCTGCAATCGGGAGTCCCCCTCTCGCTTTTCTGGA AGTGGGAGCGGAACCGAGTTTACATTGACGATTAGCTCCCTCCAACCTGAGGACTT TGCAACCTATTACTGCCTCCAGCACAATAACTATCCACGGACCTTCGGACAAGGGA CCGAGGTCGAGATCATC
2153.	IGF1R17HLxI2CHL	artificial	aa	QAQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGST RDYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRDGVETTFYYYYYGMDV WGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTFTCRASQDIR RDLGWYQQKPGKAPKRLIYAASRLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCL QHNNYPRTFGQGTEVEIISGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

2154.	IGF1R17HLxl2CHL	artificial	nt	CAGGCACAGCTGGTGGAAAGTGGCGGTGGCTTAGTTAAGCCTGGTGGATCCCTGC GACTTTCTTGTGCTGCCTCCGGCTTTACGTTTTCCGACTACTACATGTCCTGGATTA GACAAGCCCCTGGCAAGGGCTTGGAATGGGTGAGCTACATAAGCTCCTCGGGAAG CACTAGGGACTATGCCGATAGCGTTAAGGGGAGATTCACGATAAGCAGGGATAACG CCAAGAACTCCCTGTATCTGCAGATGAATAGTCTCCGTGCTGAGGACACTGCCGTG TACTATTGCGTGAGGGATGGCGTCGAAACAACCTTCTACTACTACTATGGCATG GACGTTTGGGGACAGGGAACAACTGTAACCGTGAGCTCAGGAGGTGGAGGTAGCG GAGGTGGAGGTAGTGGTGGAGGTGGCTCGGATATCCAGATGACACAAAGCCCAAG CTCGCTGAGCGCTAGCGTAGGCGATCGAGTGACATTCACCTGTAGGGCTAGCCAG GATATTAGACGGGACCTAGGGTGGTACCAGCAGAAACCTGGCAAAGCTCCCAAAC GCCTTATCTATGCGGCTTCACGGCTGCAATCGGGAGTCCCCTCTCGCTTTTCTGGA AGTGGGAGCGGAACCGAGTTTACATTGACGATTAGCTCCCTCCAACCTGAGGACTT TGCAACCTATTACTGCCTCCAGCACACAATAACTATCCACGGACCTTCGGACAAGGGA CCGAGGTCGAGATCATCTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTC TGGAGGAGGATTGGTGCAGCCTGGAGGGGTCATTGAAACTCTCATGTGCAGCCTCTG GATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGT TTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACAT GGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCT GGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGG TGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAA CAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCA AACTGGGTCCAACAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAA GTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAG GCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGT TCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2155.	IGF1R19-H	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGI TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGYGDFYYYYYGMDVW GQGTTVTVSS
2156.	IGF1R19-HCDR1	artificial	aa	SYAMS
2157.	IGF1R19-HCDR2	artificial	aa	AISGSGGITYYADSVKG
2158.	IGF1R19-HCDR3	artificial	aa	DLGYGDFYYYYYGMDV
2159.	IGF1R19-H	artificial	nt	GAGGTTCAGCTGCTTGAATCTGGCGGAGGTTTGGTTCAGCCTGGGGGTTCACTTCG TCTGAGCTGTGCTGCCAGCGGGTTTACATTCTCCTCATATGCCATGTCTCCTGGGTGC GACAGGCACCAGGCAAAGGCTTGGAATGGGTGTCCGCTATTAGCGGAAGCGGAGG

				CATCACATACTACGCTGATAGCGTCAAGGGGAGATTCACCATCTCACGGGACAATT CCAAGAACACCCTGTATCTCCAGATGAACTCCCTGCGTGCCGAAGATACTGCCGTG TACTATTGCGCCAAGGATCTTGGCTACGGGGACTTCTACTACTACTATGGGATG GACGTGTGGGGACAGGGAACAACCGTGACTGTGAGCTCT
2160.	IGF1R19-L	artificial	aa	DIQMTQSPSSLSASVGDRVTITCRASQGIRSDLGWFQQKPGKAPKRLIYAASKLHRGVP SRFSGSGSGTEFTLTISRLQPEDFATYYCLQHNSYPLTFGGGTKVEIK
2161.	IGF1R19-LCDR1	artificial	aa	RASQGIRSDLG
2162.	IGF1R19-LCDR2	artificial	aa	AASKLHR
2163.	IGF1R19-LCDR3	artificial	aa	LQHNSYPLT
2164.	IGF1R19-L	artificial	nt	GACATTCAGATGACTCAGAGCCCAAGCTCTCTGTCTGCTTCTGTGGGAGACCGCGT TACCATCACCTGTAGAGCAAGCCAGGGCATTCGATCCGATCTCGGATGGTTTCAGC AGAAACCTGGCAAGGCACCCAAACGGCTGATCTATGCTGCCAGCAAACTGCATAGG GGAGTGCCCTCACGCTTTAGCGGATCTGGTAGTGGTACCGAGTTCACACTGACAAT CTCACGGCTGCAGCCTGAGGATTTCGCCACCTATTACTGCCTCCAGCACAATTCCT ACCCACTGACCTTTGGCGGTGGGACTAAGGTCGAGATCAAG
2165.	IGF1R19-HL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGI TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGYGDFYYYYYGMDVW GQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGIRSD LGWFQQKPGKAPKRLIYAASKLHRGVPSRFSGSGSGTEFTLTISRLQPEDFATYYCLQH NSYPLTFGGGTKVEIK
2166.	IGF1R19-HL	artificial	nt	GAGGTTCAGCTGCTTGAATCTGGCGGAGGTTTGGTTCAGCCTGGGGGTTCACTTCG TCTGAGCTGTGCTGCCAGCGGGTTTACATTCTCCTCATATGCCATGTCCTGGGTGC GACAGGCACCAGGCAAAGGCTTGGAATGGGTGTCCGCTATTAGCGGAAGCGGAGG CATCACATACTACGCTGATAGCGTCAAGGGGAGATTCACCATCTCACGGGACAATT CCAAGAACACCCTGTATCTCCAGATGAACTCCCTGCGTGCCGAAGATACTGCCGTG TACTATTGCGCCAAGGATCTTGGCTACGGGGACTTCTACTACTACTATGGGATG GACGTGTGGGGACAGGGAACAACCGTGACTGTGAGCTCTGGTGGCGGAGGATCTG GCGGAGGTGGAAGCGGAGGGGGAGGGAGCGACATTCAGATGACTCAGAGCCCAA GCTCTCTGTCTGCTTCTGTGGGAGACCGCGTTACCATCACCTGTAGAGCAAGCCAG GGCATTCGATCCGATCTCGGATGGTTTCAGCAGAAACCTGGCAAGGCACCCAAACG GCTGATCTATGCTGCCAGCAAACTGCATAGGGGAGTGCCCTCACGCTTTAGCGGAT CTGGTAGTGGTACCGAGTTCACACTGACAATCTCACGGCTGCAGCCTGAGGATTTC GCCACCTATTACTGCCTCCAGCACAATTCCTACCCACTGACCTTTGGCGGTGGGAC TAAGGTCGAGATCAAG
2167.	IGF1R19HLxl2CHL	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGI TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGYGDFYYYYYGMDVW

				GQGTTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGIRSD LGWFQQKPGKAPKRLIYAASKLHRGVPSRFSGSGSGTEFTLTISRLQPEDFATYYCLQH NSYPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2168.	IGF1R19HLxl2CHL	artificial	nt	GAGGTTCAGCTGCTTGAATCTGGCGGAGGTTTGGTTCAGCCTGGGGGTTCACTTCG TCTGAGCTGTGCTGCCAGCGGGTTTACATTCTCCTCATATGCCATGTCCTGGGTGC GACAGGCACCAGGCAAAGGCTTGGAATGGGTGTCCGCTATTAGCGGAAGCGGAGG CATCACATACTACGCTGATAGCGTCAAGGGGAGATTCACCATCTCACGGGACAATT CCAAGAACACCCTGTATCTCCAGATGAACTCCCTGCGTGCCGAAGATACTGCCGTG TACTATTGCGCCAAGGATCTTGGCTACGGGGACTTCTACTACTACTATGGGATG GACGTGTGGGGACAGGGAACAACCGTGACTGTGAGCTCTGGTGGCGGAGGATCTG GCGGAGGTGGAAGCGGAGGGGGAGGGAGCGACATTCAGATGACTCAGAGCCCAA GCTCTCTGTCTGCTTCTGTGGGAGACCGCGTTACCATCACCTGTAGAGCCAAGCCAG GGCATTCGATCCGATCTCGGATGGTTTCAGCAGAAACCTGGCAAGGCACCCAAACG GCTGATCTATGCTGCCAGCAAACTGCATAGGGGAGTGCCCTCACGCTTTAGCGGAT CTGGTAGTGGTACCGAGTTCACACTGACAATCTCTCACGGCTGCAGCCTGAGGATTTC GCCACCTATTACTGCCTCCAGCACACAATTCCTACCCACTGACCTTTGGCGGTGGGAC TAAGGTCGAGATCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCT GGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTG GATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGT TTGGAATGGGTTGCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCG ATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATC TACAAATGAACAACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACAT GGGAACTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAGGGACTCT GGTCACCGTCTCCTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGG TGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAA CAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCA AACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAA GTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAG GCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATTACTGTGT TCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2169.	IGF1R20-H	artificial	aa	QIQLVQSGPELKKPGETVKISCKASGYNLANYGLNWVKQAPGEGLKWMGWINTNTGA PTYAEEFKGRFVFFLETSASTAYLQINNLSDEDTATYFCARSIYYYASRYFNVWGAGTS

				VTVSS
2170.	IGF1R20-HCDR1	artificial	aa	KASGYNLANYGLN
2171.	IGF1R20-HCDR2	artificial	aa	WINTNTGAPTYAEEFKG
2172.	IGF1R20-HCDR3	artificial	aa	SIYYYASRYFNV
2173.	IGF1R20-H	artificial	nt	CAGATCCAGCTGGTGCAGAGCGGACCTGAGCTTAAGAAGCCTGGCGAGACCGTCA AGATCTCATGCAAAGCTAGCGGATACAACCTGGCCAACTATGGCCTCAACTGGGTG AAACAGGCCCCCTGGAGAGGGCCTGAAGTGGATGGGATGGATCAACACCAATACTG GCGCCCCAACATACGCAGAGGAATTTAAGGGGAGGTTCGTGTTCTTCCTGGAAACC TCCGCTAGTACTGCCTACCTGCAGATCAACAACCTCTCCGATGAAGATACCGCCAC CTACTTTTGTGCCCGCTCTATCTACTACTACGCATCCAGGTACTTCAATGTCTGGGG AGCCGGAACCTCCGTGACTGTTAGCTCT
2174.	IGF1R20-L	artificial	aa	DIQMTQTTSSLSASLGDKVTISCRASQDISNYLNWYQQKPDGTIKLLIYYTSRLHSGIPSR FSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKVEIK
2175.	IGF1R20-LCDR1	artificial	aa	RASQDISNYLN
2176.	IGF1R20-LCDR2	artificial	aa	YTSRLHS
2177.	IGF1R20-LCDR3	artificial	aa	QQGNTLPWT
2178.	IGF1R20-L	artificial	nt	GATATCCAGATGACACAGACTACATCTTCCCTCTCCGCTTCACTTGGCGACAAAGTC ACCATTTCATGCCGTGCAAGCCAGGACATCAGCAACTACCTCAATTGGTACCAGCA GAAACCCGACGGGACAATCAAGCTGCTGATCTACTACACAAGCCGACTGCACAGCG GGATTCCATCAAGATTCAGCGGAAGCGGAAGTGGGACCGATTACAGCTTGACAATC AGCAATCTGGAGCAGGAGACATCGCTACTTACTTTTGCCAGCAGGGGAATACCTT GCCATGGACATTTGGGGGCGGTACCAAAGTGGAAATCAAG
2179.	IGF1R20-HL	artificial	aa	QIQLVQSGPELKKPGETVKISCKASGYNLANYGLNWVKQAPGEGLKWMGWINTNTGA PTYAEEFKGRFVFFLETSASTAYLQINNLSDEDTATYFCARSIYYYASRYFNVWGAGTS VTVSSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDKVTISCRASQDISNYLNWYQ QKPDGTIKLLIYYTSRLHSGIPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTF GGGTKVEIK
2180.	IGF1R20-HL	artificial	nt	CAGATCCAGCTGGTGCAGAGCGGACCTGAGCTTAAGAAGCCTGGCGAGACCGTCA AGATCTCATGCAAAGCTAGCGGATACAACCTGGCCAACTATGGCCTCAACTGGGTG AAACAGGCCCCCTGGAGAGGGCCTGAAGTGGATGGGATGGATCAACACCAATACTG GCGCCCCAACATACGCAGAGGAATTTAAGGGGAGGTTCGTGTTCTTCCTGGAAACC TCCGCTAGTACTGCCTACCTGCAGATCAACAACCTCTCCGATGAAGATACCGCCAC CTACTTTTGTGCCCGCTCTATCTACTACTACGCATCCAGGTACTTCAATGTCTGGGG AGCCGGAACCTCCGTGACTGTTAGCTCTGGAGGAGGCGGTAGCGGTGGCGGTGG AAGTGGCGGAGGTGGCTCTGATATCCAGATGACACAGACTACATCTTCCCTCTCCG CTTCACTTGGCGACAAAGTCACCATTTCATGCCGTGCAAGCCAGGACATCAGCAAC

				TACCTCAATTGGTACCAGCAGAAACCCGACGGGACAATCAAGCTGCTGATCTACTA CACAAGCCGACTGCACAGCGGGATTCCATCAAGATTCAGCGGAAGCGGAAGTGGG ACCGATTACAGCTTGACAATCAGCAATCTGGAGCAGGAGGACATCGCTACTTACTTT TGCCAGCAGGGGAATACCTTGCCATGGACATTTGGGGGCGGTACCAAAGTGGAAA TCAAG
2181.	IGF1R20HLxl2CHL	artificial	aa	QIQLVQSGPELKKPGETVKISCKASGYNLANYGLNWVKQAPGEGLKWMGWINTNTGA PTYAEEFKGRFVFFLETSASTAYLQINNLSDEDTATYFCARSIYYYASRYFNVWGAGTS VTVSSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDKVTISCRASQDISNYLNWYQ QKPDGTIKLLIYYTSRLHSGIPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTF GGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2182.	IGF1R20HLxl2CHL	artificial	nt	CAGATCCAGCTGGTGCAGAGCGGACCTGAAGCTTAAGAAGCCTGGCGAGACCGTCA AGATCTCATGCAAAGCTAGCGGATACAACCTGGCCCAACTATGGCCTCAACTGGGTG AAACAGGCCCCCTGGAGAGGGCCTGAAGTGGGATGGATCAACACCAATACTG GCGCCCCAACATACGCAGAGGAATTTAAGGGGAGGTTCGTGTTCTTCCTGGAAACC TCCGCTAGTACTGCCTACCTGCAGATCAACAACCTCTCCGATGAAGATACCGCCAC CTACTTTTGTGCCCGCTCTATCTACTACGCATCCAGGTACTTCAATGTCTGGGG AGCCGGAACCTCCGTGACTGTTAGCTCTGGAGGAGGCGGTAGCGGTGGCGGTGG AAGTGGCGGAGGTGGCTCTGATATCCAGATGACACAGACTACATCTTCCCTCTCCG CTTCACTTGGCGACAAAGTCACCATTTCATGCCGTGCAAGCCAGGACATCAGCAAC TACCTCAATTGGTACCAGCAGAAACCCGACGGGACAATCAAGCTGCTGATCTACTA CACAAGCCGACTGCACAGCGGGATTCCATCAAGATTCAGCGGAAGCGGAAGTGGG ACCGATTACAGCTTGACAATCAGCAATCTGGAGCAGGAGGACATCGCTACTTACTTT TGCCAGCAGGGGAATACCTTGCCATGGACATTTGGGGGCGGTACCAAAGTGGAAA TCAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATT GGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCA ATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTT GCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAG ACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACA ACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGT AATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTC CTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACT GTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC

				TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAAC AAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCC GGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCA ACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2183.	IGF1R21-H	artificial	aa	QIQLVQSGPELKKPGETVKISCKASGYTLANYGMNWVKQAPGKGFKWMGWINTNTGK PTYSDEFKGRFVFSLETSASTAYLLINNLSNEDTATYFCARSIYYYGSRYFNVWGAGTTV TVSS
2184.	IGF1R21-HCDR1	artificial	aa	KASGYTLANYGMN
2185.	IGF1R21-HCDR2	artificial	aa	WINTNTGKPTYSDEFKG
2186.	IGF1R21-HCDR3	artificial	aa	SIYYYGSRYFNV
2187.	IGF1R21-H	artificial	nt	CAGATCCAGCTTGTCCAGAGTGGTCCCGAGCTGAAGAAACCTGGCGAAACCGTGA AAATCAGCTGCAAGGCAAGCGGCTATACACTGGCCAACTATGGCATGAATTGGGTG AAGCAGGCCCACCTGGGAAGGGTTTCAAGTGGATGGGCTGGATCAACACCAACACTG GCAAACCAACCTATTCCGACGAGTTCAAGGGGCGTTTCGTGTTTCACTGGAAACC TCCGCATCAACCGCTTACCTCTTGATCAACAACCTGAGCAACGAGGACACCGCCAC ATACTTCTGCGCTAGGAGCATCTACTACTATGGGAGCCGCTACTTCAATGTGTGGG GAGCTGGGACAACTGTTACTGTGAGCTCA
2188.	IGF1R21-L	artificial	aa	DIQMTQSTSSLSASLGDRVTISCRASQDINNYLTWYQQKPDGTVKLLIYYTSRLHSGVPS RFSGSGSGTDYSLTITNLEQEDFATYFCQQGNTLPWTFGEGTKVEIK
2189.	IGF1R21-LCDR1	artificial	aa	RASQDINNYLT
2190.	IGF1R21-LCDR2	artificial	aa	YTSRLHS
2191.	IGF1R21-LCDR3	artificial	aa	QQGNTLPWT
2192.	IGF1R21-L	artificial	nt	GATATCCAGATGACACAGAGCACAAGTTCATTGTCCGCCTCTCTTGGCGATCGAGT GACCATTAGCTGCCGAGCAAGCCAGGACATTAACAACTACCTGACCTGGTATCAGC AGAAACCCGACGGGACTGTGAAGCTGCTGATCTATTACACCTCTAGACTGCACAGT GGCGTTCCTAGCCGGTTTAGCGGATCCGGTAGCGGAACAGATTACTCCCTGACCAT CACCAATCTCGAGCAGGAAGACTTTGCCACCTACTTTTGCCAGCAGGGCAATACTC TCCCATGGACATTTGGTGAGGGGACCAAAGTCGAGATTAAG
2193.	IGF1R21-HL	artificial	aa	QIQLVQSGPELKKPGETVKISCKASGYTLANYGMNWVKQAPGKGFKWMGWINTNTGK PTYSDEFKGRFVFSLETSASTAYLLINNLSNEDTATYFCARSIYYYGSRYFNVWGAGTTV TVSSGGGGSGGGGSGGGGSDIQMTQSTSSLSASLGDRVTISCRASQDINNYLTWYQQ KPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTITNLEQEDFATYFCQQGNTLPWT FGEGTKVEIK
2194.	IGF1R21-HL	artificial	nt	CAGATCCAGCTTGTCCAGAGTGGTCCCGAGCTGAAGAAACCTGGCGAAACCGTGA AAATCAGCTGCAAGGCAAGCGGCTATACACTGGCCAACTATGGCATGAATTGGGTG

				AAGCAGGCACCTGGGAAGGGTTTCAAGTGGATGGCTGGATCAACACCAACACTG GCAAACCAACCTATTCCGACGAGTTCAAGGGGCGTTTCGTGTTTTCACTGGAAACC TCCGCATCAACCGCTTACCTCTTGATCAACACAACCTGAGCAACGAGGACACCGCCAC ATACTTCTGCGCTAGGAGCATCTACTACTATGGGAGCCGCTACTTCAATGTGTGGG GAGCTGGGACAACTGTTACTGTGAGCTCAGGAGGGGGAGGTAGCGGAGGAGGCG GTAGCGGAGGCGGTGGATCCGATATCCAGATGACACACAGAGCACAAGTTCATTGTCC GCCTCTCTTGGCGATCGAGTGACCATTAGCTGCCGAGCAAGCCAGGACATTAACAA CTACCTGACCTGGTATCAGCAGAAACCCGACGGGACTGTGAAGCTGCTGATCTATT ACACCTCTAGACTGCACAGTGGCGTTCCTAGCCGGTTTAGCGGATCCGGTAGCGG AACAGATTACTCCCTGACCATCACCAATCTCGAGCAGGAAGACTTTGCCACCTACTT TTGCCAGCAGGGCAATACTCTCCCATGGACATTTGGTGAGGGGACCAAAGTCGAGA TTAAG
2195.	IGF1R21HLxl2CHL	artificial	aa	QIQLVQSGPELKKPGETVKISCKASGYTLANYGMNWVKQAPGKGFKWMGWINTNTGK PTYSDEFKGRFVFSLETSASTAYLLINNLSNEDTATYFCARSIYYYGSRYFNVWGAGTTV TVSSGGGGSGGGGSGGGGSDIQMTQSTSSLSASLGDRVTISCRASQDINNYLTWYQQ KPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTITNLEQEDFATYFCQQGNTLPWT FGEGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2196.	IGF1R21HLxl2CHL	artificial	nt	CAGATCCAGCTTGTCCAGAGTGGTCCCGAGCTGAAGAAACCTGGCGAAACCGTGA AAATCAGCTGCAAGGCAAGCGGCTATACACTGGCCAACTATGGCATGAATTGGGTG AAGCAGGCACCTGGGAAGGGTTTCAAGTGGATGGGCTGGATCAACACCAACACTG GCAAACCAACCTATTCCGACGAGTTCAAGGGGCGTTTCGTGTTTTCACTGGAAACC TCCGCATCAACCGCTTACCTCTTGATCAACACAACCTGAGCAACGAGGACACCGCCAC ATACTTCTGCGCTAGGAGCATCTACTACTATGGGAGCCGCTACTTCAATGTGTGGG GAGCTGGGACAACTGTTACTGTGAGCTCAGGAGGGGGAGGTAGCGGAGGAGGCG GTAGCGGAGGCGGTGGATCCGATATCCAGATGACACACAGAGCACAAGTTCATTGTCC GCCTCTCTTGGCGATCGAGTGACCATTAGCTGCCGAGCAAGCCAGGACATTAACAA CTACCTGACCTGGTATCAGCAGAAACCCGACGGGACTGTGAAGCTGCTGATCTATT ACACCTCTAGACTGCACAGTGGCGTTCCTAGCCGGTTTAGCGGATCCGGTAGCGG AACAGATTACTCCCTGACCATCACCAATCTCGAGCAGGAAGACTTTGCCACCTACTT TTGCCAGCAGGGCAATACTCTCCCATGGACATTTGGTGAGGGGACCAAAGTCGAGA TTAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATT GGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCA

				ATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTT GCTCGCATAAGAAGTAAATATATAATTATGCAACATATTATGCCGATTCAGTGAAAG ACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACA ACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGT AATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTC CTCAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACT GTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAAC AAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCC GGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCA ACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2197.	IGF1R23-H	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGYTFTRFWIHWVRQAPGKGLEWVGEINPSNGR TNYNENFKNRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGRLDQWGQGTLVTVSS
2198.	IGF1R23-HCDR1	artificial	aa	RFWIH
2199.	IGF1R23-HCDR2	artificial	aa	EINPSNGRTNYNENFKN
2200.	IGF1R23-HCDR3	artificial	aa	GGRLDQ
2201.	IGF1R23-H	artificial	nt	GAAGTCCAGCTTGTTGAAAGCGGAGGCGGTCTGGTTCAGCCTGGTGGATCTCTGA GACTGAGCTGCGCTGCAAGCGGCTACACATTCACACGCTTTTGGATTCATTGGGTG AGGCAGGCCCCTGGAAAAGGACTCGAATGGGTGGGCGAGATCAATCCTAGCAACG GTCGGACCAACTACAACGAGAACTTCAAGAACCGGTTCACCATCTCTGCCGACACC TCCAAGAATACCGCATACCTGCAGATGAATAGCCTCCGAGCCGAGGACACTGCCGT CTATTACTGTGCTAGGGGAGGACGCCTTGATCAGTGGGGACAGGGGACACTTGTG ACTGTGTCATCC
2202.	IGF1R23-L	artificial	aa	DIQMTQSPSSLSASVGDRVTITCKASQNLRSKVAWYQQKPGKAPKLLIYSASYRYSGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNYPYTFGQGTKVEIK
2203.	IGF1R23-LCDR1	artificial	aa	KASQNLRSKVA
2204.	IGF1R23-LCDR2	artificial	aa	SASYRYS
2205.	IGF1R23-LCDR3	artificial	aa	QQYSNYPYT
2206.	IGF1R23-L	artificial	nt	GATATTCAGATGACCCAGAGCCCAAGCTCCTTGAGCGCTAGCGTTGGCGATCGTGT GACTATCACCTGTAAGGCTAGCCAGAACCTGCGAAGCAAGGTCGCATGGTATCAGC AGAAACCCGGCAAAGCCCCAAAGCTGCTGATCTACTCCGCATCCTATCGGTATTCC GGCGTGCCAAGCAGATTCAGTGGGAGTGGGAGCGGAACTGACTTTACCCTCACCA TCTCATCCCTGCAGCCTGAGGACTTTGCCACCTACTATTGCCAGCAGTATTCCAACT ACCCCTACACCTTTGGCCAGGGCACAAAAGTGGAGATCAAG
2207.	IGF1R23-HL	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGYTFTRFWIHWVRQAPGKGLEWVGEINPSNGR

				TNYNENFKNRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGRLDQWGQGTLVTVSS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQNLRSKVAWYQQKPG KAPKLLIYSASYRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNYPYTFGQ GTKVEIK
2208.	IGF1R23-HL	artificial	nt	GAAGTCCAGCTTGTTGAAAGCGGAGGCGGTCTGGTTCAGCCTGGTGGATCTCTGA GACTGAGCTGCGCTGCAAGCGGCTACACATTCACACGCTTTTGGATTCATTGGGTG AGGCAGGCCCCTGGAAAAGGACTCGAATGGGTGGGCGAGATCAATCCTAGCAACG GTCGGACCAACTACAACGAGAAGTTCAAGAACCGGTTCACCATCTCTGCCGACACC TCCAAGAATACCGCATACCTGCAGATGAATAGCCTCCGAGCCGAGGACACTGCCGT CTATTACTGTGCTAGGGGAGGACGCCTTGATCAGTGGGGACAGGGGACACTTGTG ACTGTGTCATCCGGTGGGGGAGGTAGTGGGGGAGGTGGAAGCGGCGGAGGAGGC AGCGATATTCAGATGACCCAGAGCCCAAGCTCCTTGAGCGCTAGCGTTGGCGATCG TGTGACTATCACCTGTAAGGCTAGCCAGAACCTGCGAAGCAAGGTCGCATGGTATC AGCAGAAACCCGGCAAAGCCCCAAAGCTGCTGATCTACTCCGCATCCTATCGGTAT TCCGGCGTGCCAAGCAGATTCAGTGGGAGTGGGAGCGGAACTGACTTTACCCTCA CCATCTCATCCCTGCAGCCTGAGGACTTTGCCACCTACTATTGCCAGCAGTATTCCA ACTACCCCTACACCTTTGGCCAGGGCACAAAAGTGGAGATCAAG
2209.	IGF1R23HLxl2CHL	artificial	aa	EVQLVESGGGLVQPGGSLRLSCAASGYTFTRFWIHWVRQAPGKGLEWVGEINPSNGR TNYNENFKNRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGRLDQWGQGTLVTVSS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQNLRSKVAWYQQKPG KAPKLLIYSASYRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNYPYTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKG LEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTV TLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2210.	IGF1R23HLxl2CHL	artificial	nt	GAAGTCCAGCTTGTTGAAAGCGGAGGCGGTCTGGTTCAGCCTGGTGGATCTCTGA GACTGAGCTGCGCTGCAAGCGGCTACACATTCACACGCTTTTGGATTCATTGGGTG AGGCAGGCCCCTGGAAAAGGACTCGAATGGGTGGGCGAGATCAATCCTAGCAACG GTCGGACCAACTACAACGAGAAGTTCAAGAACCGGTTCACCATCTCTGCCGACACC TCCAAGAATACCGCATACCTGCAGATGAATAGCCTCCGAGCCGAGGACACTGCCGT CTATTACTGTGCTAGGGGAGGACGCCTTGATCAGTGGGGACAGGGGACACTTGTG ACTGTGTCATCCGGTGGGGGAGGTAGTGGGGGAGGTGGAAGCGGCGGAGGAGGC AGCGATATTCAGATGACCCAGAGCCCAAGCTCCTTGAGCGCTAGCGTTGGCGATCG TGTGACTATCACCTGTAAGGCTAGCCAGAACCTGCGAAGCAAGGTCGCATGGTATC AGCAGAAACCCGGCAAAGCCCCAAAGCTGCTGATCTACTCCGCATCCTATCGGTAT

				TCCGGCGTGCCAAGCAGATTCAGTGGGAGTGGGAGCGGAACTGACTTTACCCTCA CCATCTCATCCCTGCAGCCTGAGGACTTTGCCACCTACTATTGCCAGCAGTATTCCA ACTACCCCTACACCTTTGGCCAGGGCACAAAAGTGGAGATCAAGTCCGGAGGTGGT GGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGG TCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAATAAGTACGCCATGAAC TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTA AATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTC CAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACAACTTGAAGACTGAGGA CACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGTAATAGCTACATATCCTA CTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTGGT TCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAAC CTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGACT GGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGC ACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGAT TCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGGTACAGCC AGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCG GTGGAGGAACCAAACTGACTGTCCTA
2211.	IGF1R24-H	artificial	aa	EVQLVESGGELVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSRISPSGGS TYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAREEYYYWGAMDVWGQGT LVTVSS
2212.	IGF1R24-HCDR1	artificial	aa	SYAMS
2213.	IGF1R24-HCDR2	artificial	aa	RISPSGGSTYYADSVKG
2214.	IGF1R24-HCDR3	artificial	aa	EEYYYWGAMDV
2215.	IGF1R24-H	artificial	nt	GAAGTTCAGCTGGTGGAATCCGGGGGAGAGCTTGTTCAGCCTGGCGGATCACTTA GGCTGTCCTGTGCTGCAAGCGGCTTCACCTTCTCTAGCTATGCCATGTCATGGGTG CGACAGGCCCCCTGGAAAAGGACTGGAGTGGGTCTCACGTATCTCTCCAAGTGGCG GATCCACATACTACGCCGATAGCGTGAAAGGGAGGTTTACCATTTCCGCTGACACC TCCAAGAACACCGCCTACCTGCAGATGAACTCACTGAGAGCCGAAGACACTGCCGT GTACTATTGCGCACGGGAGGAGTACTACTATTGGGGAGCTATGGACGTGTGGGGA CAGGGAACATTGGTGACTGTGTCTTCC
2216.	IGF1R24-L	artificial	aa	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLAWYQQKPGKAPKLLIYGASSRASGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSSPLTFGQGTKVEIK
2217.	IGF1R24-LCDR1	artificial	aa	RASQSISSYLA
2218.	IGF1R24-LCDR2	artificial	aa	GASSRAS
2219.	IGF1R24-LCDR3	artificial	aa	QQYYSSPLT
2220.	IGF1R24-L	artificial	nt	GATATCCAGATGACACAGAGCCCCAAGCTCACTGAGCGCTAGCGTCGGAGATAGAGT

				CACCATCACCTGTAGGGCAAGCCAGAGCATCTCTAGCTACCTGGCATGGTACCAGC AGAAACCTGGCAAGGCTCCCAAGCTCCTGATCTACGGCGCTTCATCTAGAGCTAGC GGCGTTCCCTCACGATTTAGCGGAAGCGGAACTGACTTCACCCTGACCAT TTCAAGCCTCCAGCCTGAGGATTTCGCCACCTACTACTGCCAGCAGTACTACTCTA GCCCACTCACATTTGGCAGGGACAAAGGTGGAGATCAAG
2221.	IGF1R24-HL	artificial	aa	EVQLVESGGELVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSRISPSGGS TYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAREEYYYWGAMDVWGQGT LVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLAWY QQKPGKAPKLLIYGASSRASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSSP LTFGQGTKVEIK
2222.	IGF1R24-HL	artificial	nt	GAAGTTCAGCTGGTGGAATCCGGGGGAGAGCTTGTTCAGCCTGGCGGATCACTTA GGCTGTCCTGTGCTGCAAGCGGCTTCACCTTCTCTAGCTATGCCATGTCATGGGTG CGACAGGCCCCTGGAAAAGGACTGGAGTGGGTCTCACGTATCTCTCCAAGTGGCG GATCCACATACTACGCCGATAGCGTGAAAGGGAGGTTTACCATTTCCGCTGACACC TCCAAGAACACCGCCTACCTGCAGATGAACTCACTGAGAGCCGAAGACACTGCCGT GTACTATTGCGCACGGGAGGAGTACTACTATTGGGGAGCTATGGACGTGTGGGGA CAGGGAACATTGGTGACTGTGTCTTCCGGTGGCGGAGGAAGCGGAGGTGGCGGAA GCGGAGGCGGTGGAAGCGATATCCAGATGACACAGAGCCCAAGCTCACTGAGCGC TAGCGTCGGAGATAGAGTCACCATCACCTGTAGGGCAAGCCAGAGCATCTCTAGCT ACCTGGCATGGTACCAGCAGAAACCTGGCAAGGCTCCCAAGCTCCTGATCTACGG CGCTTCATCTAGAGCTAGCGGCGTTCCCTCACGATTTAGCGGAAGCGGAAGCGGA ACTGACTTCACCCTGACCATTTCAAGCCTCCAGCCTGAGGATTTCGCCACCTACTAC TGCCAGCAGTACTACTCTAGCCCACTCACATTTGGGCAGGGGACAAAGGTGGAGAT CAAG
2223.	IGF1R24HLxl2CHL	artificial	aa	EVQLVESGGELVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSRISPSGGS TYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAREEYYYWGAMDVWGQGT LVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLAWY QQKPGKAPKLLIYGASSRASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSSP LTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2224.	IGF1R24HLxl2CHL	artificial	nt	GAAGTTCAGCTGGTGGAATCCGGGGGAGAGCTTGTTCAGCCTGGCGGATCACTTA GGCTGTCCTGTGCTGCAAGCGGCTTCACCTTCTCTAGCTATGCCATGTCATGGGTG CGACAGGCCCCTGGAAAAGGACTGGAGTGGGTCTCACGTATCTCTCCAAGTGGCG

				GATCCACATACTACGCCGATAGCGTGAAAGGGAGGTTTACCATTTCCGCTGACACC TCCAAGAACACCGCCTACCTGCAGATGAACTCACTGAGAGCCGAAGACACTGCCGT GTACTATTGCGCACGGGAGGAGTACTACTATTGGGGAGCTATGGACGTGTGGGGA CAGGGAACATTGGTGACTGTGTCTTCCGGTGGCGGAGGAAGCGGAGGTGGCGGAA GCGGAGGCGGTGGAAGCGATATCCAGATGACACAGAGCCCAAGCTCACTGAGCGC TAGCGTCGGAGATAGAGTCACCATCACCTGTAGGGCAAGCCAGAGCATCTCTAGCT ACCTGGCATGGTACCAGCAGAAACCTGGCAAGGCTCCCAAGCTCCTGATCTACGG CGCTTCATCTAGAGCTAGCGGCGTTCCCTCACGATTTAGCGGAAGCGGAAGCGGA ACTGACTTCACCCTGACCATTTCAAGCCTCCAGCCTGAGGATTTCGCCACCTACTAC TGCCAGCAGTACTACTCTAGCCCACTCACATTTGGGCAGGGGACAAAGGTGGAGAT CAAGTCCGGAGGTGGTGGATCCGAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTG GTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCACCTTCAA TAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTT GCTCGCATAAGAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAG ACAGGTTCACCATCTCCAGAGATGATTCAAAAAACACTGCCTATCTACAAATGAACA ACTTGAAGACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAACTTCGGT AATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTC CTCAGGTGGTGGTGGTTCTGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGACT GTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCAC TTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAAC AAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCC GGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCT CTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCA ACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
2225.	Macaca fascicularis CD3□ 1-27	Macaca fascicularis	aa	QDGNEEMGSITQTPYQVSISGTTILTC
2226.	Macaca fascicularis CD3Γ 1-27	Macaca fascicularis	aa	QDGNEEMGSITQTPYQVSISGTTVILT
2227.	Macaca mulatta CD3□ 1-27	Macaca mulatta	aa	QDGNEEMGSITQTPYHVSISGTTVILT

Claims

1. A bispecific single chain antibody molecule comprising a first binding domain which specifically binds to an epitope of human and Callithrix jacchus, Saguinus oedipus or Saimiri sciureus CD3ε (epsilon) chain, wherein said epitope is part of an amino acid sequence comprised in the group consisting of SEQ ID NOs. 2, 4, 6, or 8 and comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu, and a second binding domain binding to an antigen selected from the group consisting of Prostate Stem Cell Antigen (PSCA), B-Lymphocyte antigen CD19 (CD19), hepatocyte growth factor receptor (C-MET), Endosialin, the EGF-like domain 1 of EpCAM, encoded by exon 2, Fibroblast activation protein alpha (FAP alpha) and Insulin-like growth factor I receptor (IGF-IR or IGF-1R).

2. The bispecific single chain antibody molecule according to claim 1, wherein the first binding domain comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:
   (a) CDR-L1 as depicted in SEQ ID NO. 27, CDR-L2 as depicted in SEQ ID NO. 28 and CDR-L3 as depicted in SEQ ID NO. 29;
   (b) CDR-L1 as depicted in SEQ ID NO. 117, CDR-L2 as depicted in SEQ ID NO. 118 and CDR-L3 as depicted in SEQ ID NO. 119; and
   (c) CDR-L1 as depicted in SEQ ID NO. 153, CDR-L2 as depicted in SEQ ID NO. 154 and CDR-L3 as depicted in SEQ ID NO. 155.

3. The bispecific single chain antibody molecule according to claim 1 or 2, wherein the first binding domain comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:
   (a) CDR-H1 as depicted in SEQ ID NO. 12, CDR-H2 as depicted in SEQ ID NO. 13 and CDR-H3 as depicted in SEQ ID NO. 14;
   (b) CDR-H1 as depicted in SEQ ID NO. 30, CDR-H2 as depicted in SEQ ID NO. 31 and CDR-H3 as depicted in SEQ ID NO. 32;
   (c) CDR-H1 as depicted in SEQ ID NO. 48, CDR-H2 as depicted in SEQ ID NO. 49 and CDR-H3 as depicted in SEQ ID NO. 50;
   (d) CDR-H1 as depicted in SEQ ID NO. 66, CDR-H2 as depicted in SEQ ID NO. 67 and CDR-H3 as depicted in SEQ ID NO. 68;
   (e) CDR-H1 as depicted in SEQ ID NO. 84, CDR-H2 as depicted in SEQ ID NO. 85 and CDR-H3 as depicted in SEQ ID NO. 86;
   (f) CDR-H1 as depicted in SEQ ID NO. 102, CDR-H2 as depicted in SEQ ID NO. 103 and CDR-H3 as depicted in SEQ ID NO. 104;

(g) CDR-H1 as depicted in SEQ ID NO. 120, CDR-H2 as depicted in SEQ ID NO. 121 and CDR-H3 as depicted in SEQ ID NO. 122;

(h) CDR-H1 as depicted in SEQ ID NO. 138, CDR-H2 as depicted in SEQ ID NO. 139 and CDR-H3 as depicted in SEQ ID NO. 140;

(i) CDR-H1 as depicted in SEQ ID NO. 156, CDR-H2 as depicted in SEQ ID NO. 157 and CDR-H3 as depicted in SEQ ID NO. 158; and

(j) CDR-H1 as depicted in SEQ ID NO. 174, CDR-H2 as depicted in SEQ ID NO. 175 and CDR-H3 as depicted in SEQ ID NO. 176.

4. The bispecific single chain antibody molecule according to any one of claims 1 to 3, wherein the second binding domain is selected from the group consisting of binding domains binding to human Prostate Stem Cell Antigen (PSCA) and/or a non-human primate PSCA, binding to human B-Lymphocyte antigen CD19 (CD19), and/or a non-human primate CD19, binding to human hepatocyte growth factor receptor (C-MET), and/or a non-human primate C-MET, binding to human Endosialin, and/or a non-human primate Endosialin, binding to human EGF-like domain 1 of EpCAM, encoded by exon 2, and/or a non-human primate EGF-like domain 1 of EpCAM, encoded by exon 2, binding to human Fibroblast activation protein alpha (FAP alpha), and/or a non-human primate FAP alpha, and binding to human Insulin-like growth factor I receptor (IGF-IR or IGF-1R), and/or a non-human primate IGF-1R.

5. The bispecific single chain antibody molecule according to claim 4 binding to human Prostate Stem Cell Antigen (PSCA) and/or a non-human primate PSCA, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 382 – 384 and CDR-L1-3 of SEQ ID NO: 377 – 379;

b) CDR-H1-3 of SEQ ID NO: 400 – 402 and CDR-L1-3 of SEQ ID NO: 395 – 397;

c) CDR-H1-3 of SEQ ID NO: 414 – 416 and CDR-L1-3 of SEQ ID NO: 409 – 411;

d) CDR-H1-3 of SEQ ID NO: 432 – 434 and CDR-L1-3 of SEQ ID NO: 427 – 429;

e) CDR-H1-3 of SEQ ID NO: 1215 – 1217 and CDR-L1-3 of SEQ ID NO: 1220 – 1222;

f) CDR-H1-3 of SEQ ID NO: 1187 – 1189 and CDR-L1-3 of SEQ ID NO: 1192 – 1194;

g) CDR-H1-3 of SEQ ID NO: 1173 – 1175 and CDR-L1-3 of SEQ ID NO: 1178 – 1180;

h) CDR-H1-3 of SEQ ID NO: 1229 – 1231 and CDR-L1-3 of SEQ ID NO: 1234 – 1236;

i) CDR-H1-3 of SEQ ID NO: 1201 – 1203 and CDR-L1-3 of SEQ ID NO: 1206 – 1208;

k) CDR-H1-3 of SEQ ID NO: 1257 – 1259 and CDR-L1-3 of SEQ ID NO: 1262 – 1264; and

l) CDR-H1-3 of SEQ ID NO: 1243 – 1245 and CDR-L1-3 of SEQ ID NO: 1248 – 1250.

6. The bispecific single chain antibody molecule according to claim 4 binding to human B-Lymphocyte antigen CD19 (CD19), and/or a non-human primate CD19, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR H1, CDR H2, CDR H3, CDR L1, CDR L2 and CDR L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 478 - 480 and CDR-L1-3 of SEQ ID NO: 473 - 475;

b) CDR-H1-3 of SEQ ID NO: 530 - 532 and CDR-L1-3 of SEQ ID NO: 525 - 527;

c) CDR-H1-3 of SEQ ID NO: 518 - 520 and CDR-L1-3 of SEQ ID NO: 513 - 515;

d) CDR-H1-3 of SEQ ID NO: 506 - 508 and CDR-L1-3 of SEQ ID NO: 501 – 503;

e) CDR-H1-3 of SEQ ID NO: 494 – 496 and CDR-L1-3 of SEQ ID NO: 489 – 491;

f) CDR-H1-3 of SEQ ID NO: 542 – 544 and CDR-L1-3 of SEQ ID NO: 537 – 539;

g) CDR-H1-3 of SEQ ID NO: 554 – 556 and CDR-L1-3 of SEQ ID NO: 549 – 551;

h) CDR-H1-3 of SEQ ID NO: 566 – 568 and CDR-L1-3 of SEQ ID NO: 561 – 563;

i) CDR-H1-3 of SEQ ID NO: 578 – 580 and CDR-L1-3 of SEQ ID NO: 573 – 575;

j) CDR-H1-3 of SEQ ID NO: 590 – 592 and CDR-L1-3 of SEQ ID NO: 585 – 587;

k) CDR-H1-3 of SEQ ID NO: 602 – 604 and CDR-L1-3 of SEQ ID NO: 597 – 599;

l) CDR-H1-3 of SEQ ID NO: 614 – 616 and CDR-L1-3 of SEQ ID NO: 609 – 611;

m) CDR-H1-3 of SEQ ID NO: 626 – 628 and CDR-L1-3 of SEQ ID NO: 621 – 623;

n) CDR-H1-3 of SEQ ID NO: 638 – 640 and CDR-L1-3 of SEQ ID NO: 633 – 635;

o) CDR-H1-3 of SEQ ID NO: 650 – 652 and CDR-L1-3 of SEQ ID NO: 645 – 647;

p) CDR-H1-3 of SEQ ID NO: 662 – 664 and CDR-L1-3 of SEQ ID NO: 657 – 659;

q) CDR-H1-3 of SEQ ID NO: 674 – 676 and CDR-L1-3 of SEQ ID NO: 669 – 671;

r) CDR-H1-3 of SEQ ID NO: 686 – 688 and CDR-L1-3 of SEQ ID NO: 681 – 683;

s) CDR-H1-3 of SEQ ID NO: 698 – 700 and CDR-L1-3 of SEQ ID NO: 693 – 695;

t) CDR-H1-3 of SEQ ID NO: 710 – 712 and CDR-L1-3 of SEQ ID NO: 705 – 707;

u) CDR-H1-3 of SEQ ID NO: 722 – 724 and CDR-L1-3 of SEQ ID NO: 717 – 719;

v) CDR-H1-3 of SEQ ID NO: 734 – 736 and CDR-L1-3 of SEQ ID NO: 729 – 731;

w) CDR-H1-3 of SEQ ID NO: 746 – 748 and CDR-L1-3 of SEQ ID NO: 741 – 743;

x) CDR-H1-3 of SEQ ID NO: 758 – 760 and CDR-L1-3 of SEQ ID NO: 753 – 755;

y) CDR-H1-3 of SEQ ID NO: 1271 - 1273 and CDR-L1-3 of SEQ ID NO: 1276 – 1278;

z) CDR-H1-3 of SEQ ID NO: 1285 – 1287 and CDR-L1-3 of SEQ ID NO: 1290 – 1292;

aa) CDR-H1-3 of SEQ ID NO: 1299 – 1301 and CDR-L1-3 of SEQ ID NO: 1304 – 1306;

ab) CDR-H1-3 of SEQ ID NO: 1313 – 1315 and CDR-L1-3 of SEQ ID NO: 1318 – 1320;

ac) CDR-H1-3 of SEQ ID NO: 1327 – 1329 and CDR-L1-3 of SEQ ID NO: 1332 – 1334;

ad) CDR-H1-3 of SEQ ID NO: 1341 – 1343 and CDR-L1-3 of SEQ ID NO: 1346 – 1348;

ae) CDR-H1-3 of SEQ ID NO: 1355 – 1357 and CDR-L1-3 of SEQ ID NO: 1360 – 1362;

af) CDR-H1-3 of SEQ ID NO: 1369 – 1371 and CDR-L1-3 of SEQ ID NO: 1374 – 1376; and

ag) CDR-H1-3 of SEQ ID NO: 1383 – 1385 and CDR-L1-3 of SEQ ID NO: 1388 – 1390.

7. The bispecific single chain antibody molecule according to claim 4 binding to human hepatocyte growth factor receptor (C-MET), and/or a non-human primate C-MET, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 821 - 823 and CDR-L1-3 of SEQ ID NO: 816 - 818;

b) CDR-H1-3 of SEQ ID NO: 836 - 838 and CDR-L1-3 of SEQ ID NO: 833 - 835;

c) CDR-H1-3 of SEQ ID NO: 845 – 847 and CDR-L1-3 of SEQ ID NO: 840 - 842;

d) CDR-H1-3 of SEQ ID NO: 863 - 865 and CDR-L1-3 of SEQ ID NO: 858 – 860;

e) CDR-H1-3 of SEQ ID NO: 881 – 883 and CDR-L1-3 of SEQ ID NO: 876 – 878;

f) CDR-H1-3 of SEQ ID NO: 899 – 901 and CDR-L1-3 of SEQ ID NO: 894 – 896;

g) CDR-H1-3 of SEQ ID NO: 1401 – 1403 and CDR-L1-3 of SEQ ID NO: 1406 – 1408;

h) CDR-H1-3 of SEQ ID NO: 1415 – 1417 and CDR-L1-3 of SEQ ID NO: 1420 – 1422;

i) CDR-H1-3 of SEQ ID NO: 1429 – 1431 and CDR-L1-3 of SEQ ID NO: 1434 – 1436;

j) CDR-H1-3 of SEQ ID NO: 1443 – 1445 and CDR-L1-3 of SEQ ID NO: 1448 – 1450;

k) CDR-H1-3 of SEQ ID NO: 1457 – 1459 and CDR-L1-3 of SEQ ID NO: 1462 – 1464;

l) CDR-H1-3 of SEQ ID NO: 1471 – 1473 and CDR-L1-3 of SEQ ID NO: 1476 – 1478;

m) CDR-H1-3 of SEQ ID NO: 1639 – 1641 and CDR-L1-3 of SEQ ID NO: 1644 – 1646;

n) CDR-H1-3 of SEQ ID NO: 1625 – 1627 and CDR-L1-3 of SEQ ID NO: 1630 – 1632;

o) CDR-H1-3 of SEQ ID NO: 1611 – 1613 and CDR-L1-3 of SEQ ID NO: 1616 – 1618;

p) CDR-H1-3 of SEQ ID NO: 1597 – 1599 and CDR-L1-3 of SEQ ID NO: 1602 – 1604;

q) CDR-H1-3 of SEQ ID NO: 1569 – 1571 and CDR-L1-3 of SEQ ID NO: 1574 – 1576;

r) CDR-H1-3 of SEQ ID NO: 1555 – 1557 and CDR-L1-3 of SEQ ID NO: 1560 – 1562;

s) CDR-H1-3 of SEQ ID NO: 1583 – 1585 and CDR-L1-3 of SEQ ID NO: 1588 – 1590;

t) CDR-H1-3 of SEQ ID NO: 1541 – 1543 and CDR-L1-3 of SEQ ID NO: 1546 – 1548;

u) CDR-H1-3 of SEQ ID NO: 1513 – 1515 and CDR-L1-3 of SEQ ID NO: 1518 – 1520;

v) CDR-H1-3 of SEQ ID NO: 1527 – 1529 and CDR-L1-3 of SEQ ID NO: 1532 – 1534;

w) CDR-H1-3 of SEQ ID NO: 1499 – 1501 and CDR-L1-3 of SEQ ID NO: 1504 – 1506; and

x) CDR-H1-3 of SEQ ID NO: 1485 – 1487 and CDR-L1-3 of SEQ ID NO: 1490 – 1492.

8. The bispecific single chain antibody molecule according to claim 4 binding to human Endosialin, and/or a non-human primate Endosialin, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 1653 – 1655 and CDR-L1-3 of SEQ ID NO: 1658 - 1660;

b) CDR-H1-3 of SEQ ID NO: 1667 - 1669 and CDR-L1-3 of SEQ ID NO: 1672 - 1674;

c) CDR-H1-3 of SEQ ID NO: 1681 – 1683 and CDR-L1-3 of SEQ ID NO: 1686 – 1688;

d) CDR-H1-3 of SEQ ID NO: 1695 – 1697 and CDR-L1-3 of SEQ ID NO: 1700 – 1702;

e) CDR-H1-3 of SEQ ID NO: 1709 – 1711 and CDR-L1-3 of SEQ ID NO: 1714 – 1716; and

f) CDR-H1-3 of SEQ ID NO: 1723 – 1725 and CDR-L1-3 of SEQ ID NO: 1728 – 1730.

9. The bispecific single chain antibody molecule according to claim 4 binding to human EGF-like domain 1 of EpCAM, encoded by exon 2, and/or a non-human primate EGF-like domain 1 of EpCAM, encoded by exon 2, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR-H1, CDR-

H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 940 - 942 and CDR-L1-3 of SEQ ID NO: 935 - 937;

b) CDR-H1-3 of SEQ ID NO: 956 - 958 and CDR-L1-3 of SEQ ID NO: 951 - 953;

c) CDR-H1-3 of SEQ ID NO: 968 - 970 and CDR-L1-3 of SEQ ID NO: 963 - 965;

d) CDR-H1-3 of SEQ ID NO: 980 - 982 and CDR-L1-3 of SEQ ID NO: 975-977;

e) CDR-H1-3 of SEQ ID NO: 992 – 994 and CDR-L1-3 of SEQ ID NO: 987 – 989;

f) CDR-H1-3 of SEQ ID NO: 1004 – 1006 and CDR-L1-3 of SEQ ID NO: 999 – 1001;

g) CDR-H1-3 of SEQ ID NO: 1028 – 1030 and CDR-L1-3 of SEQ ID NO: 1023 – 1025;

h) CDR-H1-3 of SEQ ID NO: 1040 – 1042 and CDR-L1-3 of SEQ ID NO: 1035 – 1037;

i) CDR-H1-3 of SEQ ID NO: 1052 – 1054 and CDR-L1-3 of SEQ ID NO: 1047 – 1049;

j) CDR-H1-3 of SEQ ID NO: 1074 – 1076 and CDR-L1-3 of SEQ ID NO: 1069 – 1071;

k) CDR-H1-3 of SEQ ID NO: 1086 – 1088 and CDR-L1-3 of SEQ ID NO: 1081 – 1083;

l) CDR-H1-3 of SEQ ID NO: 1098 – 1100 and CDR-L1-3 of SEQ ID NO: 1093 – 1095;

m) CDR-H1-3 of SEQ ID NO: 1110 – 1112 and CDR-L1-3 of SEQ ID NO: 1105 – 1107;

n) CDR-H1-3 of SEQ ID NO: 1122 – 1124 and CDR-L1-3 of SEQ ID NO: 1117 – 1119;

o) CDR-H1-3 of SEQ ID NO: 1016 – 1018 and CDR-L1-3 of SEQ ID NO: 1011 – 1013; and

p) CDR-H1-3 of SEQ ID NO: 1765 – 1767 and CDR-L1-3 of SEQ ID NO: 1770 – 1772.

10. The bispecific single chain antibody molecule according to claim 4 binding to human Fibroblast activation protein alpha (FAP alpha), and/or a non-human primate FAP alpha, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 1137 - 1139 and CDR-L1-3 of SEQ ID NO: 1132 - 1134;

b) CDR-H1-3 of SEQ ID NO: 1849 - 1851 and CDR-L1-3 of SEQ ID NO: 1854 - 1856;

c) CDR-H1-3 of SEQ ID NO: 1835 - 1837 and CDR-L1-3 of SEQ ID NO: 1840 - 1842;

d) CDR-H1-3 of SEQ ID NO: 1779 - 1781 and CDR-L1-3 of SEQ ID NO: 1784 - 1786;

e) CDR-H1-3 of SEQ ID NO: 1793 – 1795 and CDR-L1-3 of SEQ ID NO: 1798 – 1800;

f) CDR-H1-3 of SEQ ID NO: 1863 – 1865 and CDR-L1-3 of SEQ ID NO: 1868 – 1870;

g) CDR-H1-3 of SEQ ID NO: 1807 – 1809 and CDR-L1-3 of SEQ ID NO: 1812 – 1814;

h) CDR-H1-3 of SEQ ID NO: 1821 – 1823 and CDR-L1-3 of SEQ ID NO: 1826 – 1828;

i) CDR-H1-3 of SEQ ID NO: 1891 – 1893 and CDR-L1-3 of SEQ ID NO: 1896 – 1898;

j) CDR-H1-3 of SEQ ID NO: 1877 – 1879 and CDR-L1-3 of SEQ ID NO: 1882 – 1884;

k) CDR-H1-3 of SEQ ID NO: 1961 – 1963 and CDR-L1-3 of SEQ ID NO: 1966 – 1968;

l) CDR-H1-3 of SEQ ID NO: 1947 – 1949 and CDR-L1-3 of SEQ ID NO: 1952-1954;

m) CDR-H1-3 of SEQ ID NO: 1975 – 1977 and CDR-L1-3 of SEQ ID NO: 1980 – 1982;

n) CDR-H1-3 of SEQ ID NO: 1933 – 1935 and CDR-L1-3 of SEQ ID NO: 1938 – 1940;

o) CDR-H1-3 of SEQ ID NO: 1919 – 1921 and CDR-L1-3 of SEQ ID NO: 1924 – 1926; and

p) CDR-H1-3 of SEQ ID NO: 1905 – 1907 and CDR-L1-3 of SEQ ID NO: 1910 – 1912.

11. The bispecific single chain antibody molecule according to claim 4 binding to human Insulin-like growth factor I receptor (IGF-IR or IGF-1R), and/or a non-human primate IGF-1R, wherein the bispecific single chain antibody molecule comprises a group of the following sequences as CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 in the second binding domain selected from:

a) CDR-H1-3 of SEQ ID NO: 2016 - 2018 and CDR-L1-3 of SEQ ID NO: 2021 - 2023;

b) CDR-H1-3 of SEQ ID NO: 2030 - 2032 and CDR-L1-3 of SEQ ID NO: 2035 - 2037;

c) CDR-H1-3 of SEQ ID NO: 2044 - 2046 and CDR-L1-3 of SEQ ID NO: 2049 - 2051;

d) CDR-H1-3 of SEQ ID NO: 2058 - 2060 and CDR-L1-3 of SEQ ID NO: 2063 – 2065;

e) CDR-H1-3 of SEQ ID NO: 2072 – 2074 and CDR-L1-3 of SEQ ID NO: 2077 – 2079;

f) CDR-H1-3 of SEQ ID NO: 2086 – 2088 and CDR-L1-3 of SEQ ID NO: 2091 – 2093;

g) CDR-H1-3 of SEQ ID NO: 2100 – 2102 and CDR-L1-3 of SEQ ID NO: 2105 – 2107;

h) CDR-H1-3 of SEQ ID NO: 2114 – 2116 and CDR-L1-3 of SEQ ID NO: 2119 – 2121;

i) CDR-H1-3 of SEQ ID NO: 2128 – 2130 and CDR-L1-3 of SEQ ID NO: 2133 – 2135;

j) CDR-H1-3 of SEQ ID NO: 2142 – 2144 and CDR-L1-3 of SEQ ID NO: 2147 – 2149:

k) CDR-H1-3 of SEQ ID NO: 2156 – 2158 and CDR-L1-3 of SEQ ID NO: 2161 – 2163;

l) CDR-H1-3 of SEQ ID NO: 2170 – 2172 and CDR-L1-3 of SEQ ID NO: 2175 – 2177;
m) CDR-H1-3 of SEQ ID NO: 2184 – 2186 and CDR-L1-3 of SEQ ID NO: 2189 – 2191;
n) CDR-H1-3 of SEQ ID NO: 2198 – 2200 and CDR-L1-3 of SEQ ID NO: 2203 – 2205; and
o) CDR-H1-3 of SEQ ID NO: 2212 – 2214 and CDR-L1-3 of SEQ ID NO: 2217 – 2219.

12. A nucleic acid sequence encoding a bispecific single chain antibody molecule as defined in any of claims 1 to 11.

13. A vector, which comprises a nucleic acid sequence as defined in claim 12.

14. A host cell transformed or transfected with a vector defined in claim 13.

15. A process for the production of a bispecific single chain antibody molecule according to any of claims 1 to 11, said process comprising culturing a host cell defined in claim 14 under conditions allowing the expression of the polypeptide as defined in any of claims 1 to 11 and recovering the produced polypeptide from the culture.

16. A pharmaceutical composition comprising a bispecific single chain antibody molecule according to any one of claims 1 to 11, or produced according to the process of claim 15.

17. The bispecific single chain antibody molecule of claim 1, wherein said first binding domain binds to the N-terminal CD3 epsilon polypeptide fragment in vitro and to the native CD3 epsilon subunit of the CD3 complex on T cells in vivo with the same binding affinity.

18. The bispecific single chain antibody molecule of claim 1, wherein the homogeneity of the bispecific single chain antibody molecule is at least 90%, 95% or 98%.