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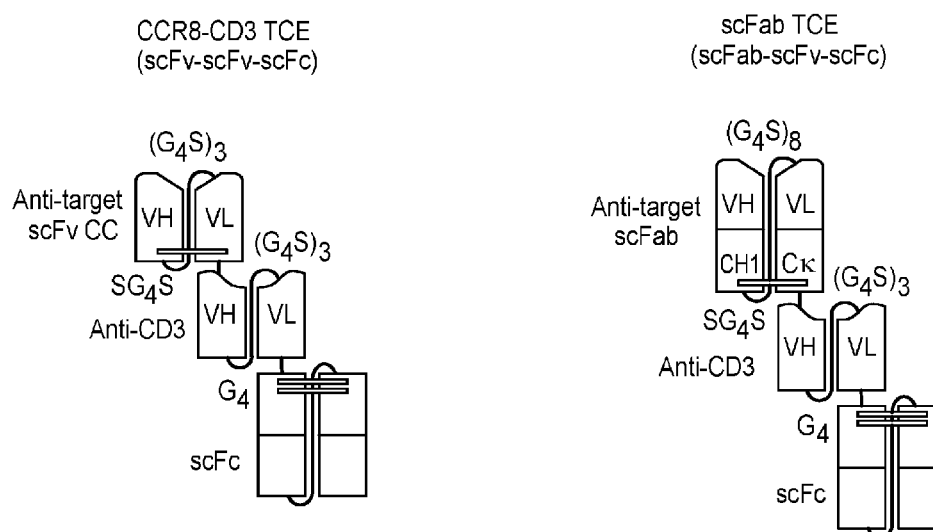
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(54) Title: T CELL ENGAGER MOLECULES AND USES THEREOF

FIG. 1



(57) Abstract: The present invention provides single chain T cell engager (TCE) molecules having an scFab that binds a target antigen and an scFv that binds CD3, and TCE molecules that bind CCR8 and CD3. Methods of treating cancer are also provided.

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T CELL ENGAGER MOLECULES AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 63/197,265, filed June 4, 2021, and U.S. Provisional Application No. 63/236,547, filed August 24, 2021, each of which is incorporated by reference herein in its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to the field of oncology, in particular, to bispecific T cell engager (TCE) molecules and treatment of cancer patients with said molecules.

BACKGROUND OF THE INVENTION

[0003] The redirection of T cell activity against tumor cells by means of bispecific molecules independent of T cell receptor specificity is an evolving approach in immuno-oncology (Frankel SR, Baeuerle PA. Targeting T cells to tumor cells using bispecific antibodies. *Curr Opin Chem Biol* 2013;17:385–92). Such new protein-based pharmaceuticals typically can simultaneously bind to two different types of antigen. They are known in several structural formats, and current applications have been explored for cancer immunotherapy and drug delivery (Fan, Gaowei; Wang, Zujian; Hao, Mingju; Li, Jinming (2015). "Bispecific antibodies and their applications". *Journal of Hematology & Oncology*. 8: 130).

[0004] Bispecific molecules useful in immuno-oncology can be antigen-binding polypeptides such as antibodies, e.g. IgG-like, i.e. full-length bispecific antibodies, or non-IgG-like bispecific antibodies, which are not full-length antibody constructs. Full length bispecific antibodies typically retain the traditional monoclonal antibody (mAb) structure of two Fab arms and one Fc region, except the two Fab sites bind different antigens. Non-full-length bispecific antibodies can lack an Fc region entirely. These include chemically linked Fabs, consisting of only the Fab regions, and various types of bivalent and trivalent single-chain variable fragments (scFvs). There are also fusion proteins mimicking the variable domains of two antibodies. An example of such a format is the bispecific T-cell engager (BiTE®) (Yang, Fa; Wen, Weihong; Qin, Weijun (2016). "Bispecific Antibodies as a Development Platform for New Concepts and Treatment Strategies". *International Journal of Molecular Sciences*. 18 (1): 48).

[0005] BiTE molecules are recombinant protein constructs made from two flexibly linked antibody derived binding domains. One binding domain of BiTE is specific for a selected tumor-

associated surface antigen on target cells; the second binding domain is specific for CD3, a subunit of the T cell receptor complex on T cells. By their particular design, BiTE molecules are uniquely suited to transiently connect T cells with target cells and, at the same time, potentially activate the inherent cytolytic potential of T cells against target cells.

[0006] There exists a need for bispecific molecules, specifically T cell engager (“TCE”) molecules, that bind a target antigen and CD3, and that demonstrate increased lysis of target cells and have desirable manufacturing properties such as increased aggregation temperatures and steeper HIC elution peak slopes. The present invention provides single-chain TCE molecules having an scFab that binds a target antigen (e.g. tumor antigen) and an scFv that binds CD3. Some TCE molecules further have an scFc, connected by a linker to the scFv, to extend the molecule half-life. The TCE molecules of the present invention demonstrate improved lysis of target cells and improved properties related to manufacturing.

[0007] The present invention also provides CCR8 TCE molecules that bind CCR8 and CD3. The C-C chemokine receptor type 8 (CCR8) is a member of the beta chemokine receptor family and is a seven transmembrane G-protein-coupled receptor with a 35 amino acid extracellular N-terminus. The ligand for CCR8 is CCL1, and CCL1-induced CCR8 signaling occurs via G-coupled proteins. CCR8 is expressed with much higher prevalence and at higher levels on the surface of cancer-resident Tregs compared to circulating or normal tissue Tregs and conventional T effector (Teff) cells. Treg cell infiltration in solid tumors is associated with poor clinical outcome, and Tregs suppress the anti-cancer immune response through inhibition of Teff cell cytotoxicity.

[0008] CCR8 TCE molecules of the present invention are thought to induce redirected T cell lysis of tumor-resident CCR8+ Tregs while sparing normal tissue Tregs that have little to no CCR8 expression. CCR8 TCE molecules of the present invention are thought to have an improved safety profile compared to other Treg-depleting therapeutic candidates targeting other markers that do not specifically deplete cancer-resident Tregs.

[0009] CCR8 TCE molecules of the present invention are single chain molecules and have either an (i) scFv that binds CCR8 and an scFv that binds CD3, wherein the two scFvs are connected by a linker; or (ii) an scFab that binds CCR8 and an scFv that binds CD3, wherein the scFab and scFv are connected by a linker. Some TCE molecules further have a scFc, connected by a linker to the scFv that binds CD3, to extend the half-life of the molecule. The CCR8 TCE molecules of the present invention demonstrate pM range cytotoxicity and bind both cynomolgus monkey and human CCR8. Interestingly, CCR8 TCE molecules were discovered that bind a unique epitope on CCR8 and do not block ligand binding to CCR8. Binding to this unique

epitope is thought to contribute to high affinity and bioactivity of the TCE molecule. Binding to this unique epitope may also contribute to an acceptable pharmacokinetic profile.

SUMMARY OF THE INVENTION

[0010] The present invention provides a T cell engager (TCE) molecule, which may be referred to as an scFab-containing TCE molecule, comprising (i) an scFab that binds a tumor antigen, wherein the scFab comprises a first heavy chain variable region (scFab VH), a CH1 domain, a first light chain variable region (scFab VL), and a C κ or C λ domain, and (ii) an scFv that binds CD3, comprising a second VL and a second VH, wherein the TCE molecule is a single chain. In some embodiments, the scFab comprises a C-terminus portion that is connected by a linker to an N-terminal portion of the scFv. In some embodiment the TCE molecule further comprises an scFc. In some embodiments, the scFc comprises an N-terminus portion that is connected by a linker to the C-terminal portion of the scFv. In a particular embodiment, the scFv binds human CD3. In some embodiments, the tumor antigen is CCR8.

[0011] In some embodiments, the scFab of a TCE molecule of the present invention has an orientation in the following order, from N-terminus to C-terminus, VH, CH1, VL, and either C κ or C λ . In other embodiments, the scFab has an orientation in the following order, from N-terminus to C-terminus, VL, either C κ or C λ , VH, and CH1. In some embodiments, the scFab comprises a linker that connects the CH1 and VL, wherein the linker is (G4S)₆, (G4S)₇, (G4S)₈, (G4Q)₆, (G4Q)₇, or (G4Q)₈. In some embodiments, the scFab comprises a linker that connects C κ or C λ and VH, wherein the linker is (G4S)₆, (G4S)₇, (G4S)₈, (G4Q)₆, (G4Q)₇, or (G4Q)₈. In some embodiments, the scFab contains a natural cysteine clamp between the heavy and light chain constant domains. In some embodiments, the TCE molecule comprises an engineered cysteine clamp in the scFab between residue 44 in the VH domain and residue 100 in the VL domain (Kabat numbering). In some embodiments, the scFab contains a natural cysteine clamp between the heavy and light chain constant domains and an engineered cysteine clamp between residue 44 in the VH domain and residue 100 in the VL domain. In some embodiments, the TCE molecule CH1, C κ and/or C λ domains are IgG, IgM, IgA, IgD, or IgE. In a particular embodiment, the domains are IgG. In a more particular embodiment, the domains are IgG1. In some embodiments, the domains are human. In a particular embodiment, the domains are human IgG1.

[0012] The present invention provides a single-chain TCE molecule having the following orientation, from N-terminus to C-terminus: scFab (VH, CH1, linker, VL, either C κ or C λ), linker, scFv (VH, linker, VL). In an embodiment, the TCE molecule further comprises a scFc, and has the following orientation: scFab (VH, CH1, linker, VL, either C κ or C λ), linker, scFv (VH, linker, VL), linker, Fc1 (hinge, CH2, CH3), linker, Fc2 (hinge, CH2, CH3).

[0013] The present invention provides a single-chain TCE molecule having the following orientation, from N-terminus to C-terminus: scFab (VL, either C κ or C λ , linker, VH, CH1), linker, scFv (VH, linker, VL). In an embodiment, the TCE molecule further comprises a scFc, and has the following orientation: scFab (VL, either C κ or C λ , linker, VH, CH1), linker, scFv (VH, linker, VL), linker, Fc1 (hinge, CH2, CH3), linker, Fc2 (hinge, CH2, CH3).

[0014] The present invention provides a single-chain TCE molecule having the following orientation: scFv that binds CCR8 (VH, linker, VL), linker, scFv that binds CD3 (VH, linker, VL). In an embodiment, the TCE molecule further comprises a scFc, and has the following orientation: scFv that binds CCR8 (VH, linker, VL), linker, scFv that binds CD3 (VH, linker, VL)-Linker- Fc1 (hinge, CH2, CH3), linker, Fc2 (hinge, CH2, CH3).

[0015] The present invention also provides a TCE molecule having the following orientation from N-terminus to C-terminus: scFv that binds CCR8 (VH, linker, VL)-Linker- scFv that binds CD3 (VH, linker, VL)-Linker-Fc1 (CH2-CH3) -Linker-Fc2 (CH2-CH3). In an embodiment, the TCE molecule binds CCR8 and CD3. The present invention provides a TCE molecule having the following orientation from N-terminus to C-terminus: scFv that binds CCR8 (VL-Linker-VH)-Linker-scFv that binds CD3 (VH-Linker-VL)-Linker-Fc1 (CH2-CH3) -Linker-Fc2 (CH2-CH3). In an embodiment, the TCE molecule binds CCR8 and CD3.

[0016] The present invention provides a single-chain TCE molecule having a scFab-scFv-scFc format. In some embodiments, the TCE molecule comprises the following orientation: VH-CH1-Linker-VL-C κ /C λ -Linker-VH-Linker-VL-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VL-C κ /C λ -Linker-VH-CH1-Linker-VH-Linker-VL-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VL-C κ /C λ -Linker-VH-CH1-Linker- VL-Linker-VH-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VH-CH1-Linker-VL-C κ /C λ -Linker-VL-Linker-VH-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises C κ . In some embodiments, the TCE molecule comprises C λ .

[0017] The present invention also provides a single-chain TCE molecule having an scFab-scFab-scFv-scFc format. In some embodiments, the TCE molecule comprises the following orientation: VH-CH1-Linker-VL- C κ /C λ -Linker- VH-CH1-Linker-VL- C κ /C λ -Linker-VH -Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VL-C κ /C λ -Linker-VH-CH1-Linker- VH-CH1-Linker-VL- C κ /C λ -Linker-VH -Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VH-CH1-Linker-VL- C κ /C λ -Linker- VL-C κ /C λ -Linker-VH-CH1-Linker-VH -Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VL-C κ /C λ -Linker-VH-CH1-Linker- VL- C κ /C λ -Linker-VH-CH1-Linker-VH -Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises C κ . In some embodiments, the TCE molecule comprises C λ . In some embodiments, the TCE molecule comprises C κ and C λ .

[0018] In an embodiment, the scFab VH and CH1 of an scFab-containing TCE molecule of the present invention comprise an amino acid sequence given by SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 44, SEQ ID NO: 60, SEQ ID NO: 76, SEQ ID NO: 92, SEQ ID NO: 108, or SEQ ID NO: 124. In an embodiment, the TCE molecule of the present invention comprises a C κ . In a particular embodiment, the scFab VL and C κ of an scFab-containing TCE molecule of the present invention comprise an amino acid sequence given by SEQ ID NO: 13, SEQ ID NO: 29, SEQ ID NO: 45, SEQ ID NO: 61, SEQ ID NO: 77, SEQ ID NO: 93, SEQ ID NO: 109, or SEQ ID NO: 125. In another particular embodiment, the TCE molecule comprises an amino acid sequence given by SEQ ID NO: 14, SEQ ID NO: 30, SEQ ID NO: 46, SEQ ID NO: 62, SEQ ID NO: 78, SEQ ID NO: 94, SEQ ID NO: 110, or SEQ ID NO: 126. In another particular embodiment, the TCE molecule comprises an amino acid sequence given by SEQ ID NO: 15, SEQ ID NO: 31, SEQ ID NO: 47, SEQ ID NO: 63, SEQ ID NO: 79, SEQ ID NO: 95, SEQ ID NO: 111, or SEQ ID NO: 127. In another particular embodiment, the TCE molecule comprises an amino acid sequence given by SEQ ID NO: 16, SEQ ID NO: 32, SEQ ID NO: 48, SEQ ID NO: 64, SEQ ID NO: 80, SEQ ID NO: 96, SEQ ID NO: 112, or SEQ ID NO: 128.

[0019] In another embodiment, the scFab VH and CH1 or scFab VL and C κ comprise a sequence of amino acids that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of a scFab VH and CH1 or scFab VL and C κ sequence listed herein. In another embodiment, the TCE molecule comprises a sequence of amino acids that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of a TCE molecule sequence listed herein.

[0020] The present invention also provides a TCE molecule comprising (i) a first scFv that binds CCR8, wherein the first scFv comprises a first VH region (CCR8 scFv VH) and a first VL region (CCR8 scFv VL), and (ii) a second scFv that binds CD3, wherein the second scFv comprises a second VH region and a second VL region. A molecule having this structure and that binds CCR8 and CD3 may be referred to as a CCR8 TCE molecule. In a preferred embodiment, the CCR8 TCE molecule is a single chain.

[0021] In an embodiment, the CCR8 TCE molecule scFv VH comprises an amino acid sequence given by SEQ ID NO: 7, SEQ ID NO: 23, SEQ ID NO: 39, SEQ ID NO: 55, SEQ ID NO: 71, SEQ ID NO: 87, SEQ ID NO: 103, or SEQ ID NO: 119, and wherein the CCR8 scFv VL comprises an amino acid sequence given by SEQ ID NO: 8, SEQ ID NO: 24, SEQ ID NO: 40, SEQ ID NO: 56, SEQ ID NO: 72, SEQ ID NO: 88, SEQ ID NO: 104, or SEQ ID NO: 120. In another embodiment, the first scFv comprises an amino acid sequence given by SEQ ID NO: 9, 25, 41, 57, 73, 89, 105, or 121. In another embodiment, the TCE molecule comprises an amino acid sequence given by SEQ ID NO: 10, SEQ ID NO: 26, SEQ ID NO: 42, SEQ ID NO: 58, SEQ ID NO: 74, SEQ ID NO: 90, SEQ ID NO: 106, or SEQ ID NO: 122. In another embodiment, the TCE molecule further comprises an scFc, wherein the TCE molecule comprises an amino acid sequence given by SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 59, SEQ ID NO: 75, SEQ ID NO: 91, SEQ ID NO: 107, or SEQ ID NO: 123. In another embodiment, the CCR8 scFv VH comprises a sequence of amino acids that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to CCR8 scFv VH sequences listed herein. In another embodiment, the CCR8 scFv VL comprises a sequence of amino acids that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the CCR8 scFv VL sequences listed herein.

[0022] In another embodiment, the first scFv (that binds CCR8) comprises a sequence of amino acids that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the first scFv sequences listed herein.

[0023] In another embodiment, a CCR8 TCE molecule of the present invention comprises a sequence of amino acids that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to CCR8 TCE molecule sequences listed herein.

[0024] In some embodiments, the first VH (scFab VH and/or CCR8 scFv VH) of a TCE molecule of the present invention comprises HCDR1, HCDR2, HCDR3, and the first VL (scFab VL and/or CCR8 scFv VL) comprises LCDR1, LCDR2, and LCDR3, and wherein:

- a) HCDR1 comprises an amino acid sequence given by SEQ ID NO: 1, SEQ ID NO: 17, SEQ ID NO: 33, SEQ ID NO: 49, SEQ ID NO: 65, SEQ ID NO: 81, SEQ ID NO: 97, or SEQ ID NO: 113;
- b) HCDR2 comprises an amino acid sequence given by SEQ ID NO: 2, SEQ ID NO: 18, SEQ ID NO: 34, SEQ ID NO: 50, SEQ ID NO: 66, or SEQ ID NO: 82;
- c) HCDR3 comprises an amino acid sequence given by SEQ ID NO: 3, SEQ ID NO: 19, SEQ ID NO: 35, SEQ ID NO: 51, SEQ ID NO: 67, or SEQ ID NO: 83;
- d) LCDR1 comprises an amino acid sequence given by SEQ ID NO: 4, SEQ ID NO: 20, SEQ ID NO: 36, SEQ ID NO: 52, SEQ ID NO: 68, or SEQ ID NO: 84;
- e) LCDR2 comprises an amino acid sequence given by SEQ ID NO: 5, SEQ ID NO: 21, SEQ ID NO: 37, SEQ ID NO: 53, SEQ ID NO: 69, or SEQ ID NO: 85; and
- f) LCDR3 comprises an amino acid sequence given by SEQ ID NO: 6, SEQ ID NO: 22, SEQ ID NO: 38, SEQ ID NO: 54, SEQ ID NO: 70, or SEQ ID NO: 86.

[0025] In a particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 1, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 2, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 3, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 4, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 5, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 6.

[0026] In another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 17, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 18, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 19, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 20, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 21, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 22.

[0027] In another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 33, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 34, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 35, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 36, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 37, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 38.

[0028] In yet another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 49, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 50, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 51, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 52, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 53, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 54.

[0029] In another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 65, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 66, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 67, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 68, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 69, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 70.

[0030] In another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 81, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 82, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 83, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 84, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 85, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 86.

[0031] In yet another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 97, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 98, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 99, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 100, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 101, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 102.

[0032] In another particular embodiment, HCDR1 comprises an amino acid sequence given by SEQ ID NO: 113, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 114, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 115, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 116 or SEQ ID NO: 336 (KSSQSVLYSSNNX1NYLA, wherein X1 is K or R), LCDR2 comprises an amino acid sequence given by SEQ ID NO: 117, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 118.

[0033] The present invention provides a TCE molecule comprising an orientation, from N-terminus to C-terminus, of an scFv that binds CCR8 (VH, linker, VL), linker, scFv that binds CD3 (VH, linker, VL), wherein the scFv that binds CCR8 comprises CDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprising amino acid residues given by SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, and SEQ ID NO: 222, respectively. In an embodiment, the scFv that binds CCR8 comprises a VH and VL given by SEQ ID NO: 223 and SEQ ID NO: 224, respectively. In a particular embodiment, the scFv that binds CCR8 comprises amino acid residues given by SEQ ID NO: 225. In an embodiment, the TCE molecule comprises G4S linkers. In an embodiment, the TCE molecule comprises G4Q linkers. In an embodiment, the CD3-binding scFv is I2E. In another embodiment, the CD3-binding scFv is I2C. In another embodiment, the TCE molecule comprises the amino sequence

given by SEQ ID NO: 226. In a further embodiment, the TCE molecule comprises the amino acid sequence given by SEQ ID NO: 227. In some such embodiments, the TCE molecule is TCE 1.1. In a preferred embodiment, the TCE molecule is a single chain. In some embodiments, the TCE molecule may have an orientation such that the VL is N-terminal to the VH.

[0034] The present invention provides a TCE molecule comprising an orientation, from N-terminus to C-terminus, of an scFv that binds CCR8 (VH, linker, VL), linker, scFv that binds CD3 (VH, linker, VL)-Linker- Fc1 (hinge, CH2, CH3), linker, Fc2 (hinge, CH2, CH3), wherein the scFv that binds CCR8 comprises CDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprising amino acid residues given by SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, and SEQ ID NO: 233, respectively. In an embodiment, the scFv that binds CCR8 comprises a VH and VL given by SEQ ID NO: 234 and SEQ ID NO: 235, respectively. In a particular embodiment, the an scFv that binds CCR8 comprises amino acid residues given by SEQ ID NO: 236. In an embodiment, the TCE molecule comprises G4S linkers. In an embodiment, the TCE molecule comprises G4Q linkers. In an embodiment, the CD3-binding scFv is I2E. In another embodiment, the CD3-binding scFv is I2C. In another embodiment, the TCE molecule comprises the amino sequence given by SEQ ID NO: 237. In a further embodiment, the TCE molecule comprises the amino acid sequence given by SEQ ID NO: 238. In some such embodiments, the TCE molecule is TCE 1.2. In a preferred embodiment, the TCE molecule is a single chain. In some embodiments, the TCE molecule may have an orientation such that the VL is N-terminal to the VH.

[0035] The present invention provides a TCE molecule comprising an orientation, from N-terminus to C-terminus, of a scFab that binds CCR8 (VH, CH1, linker, VL, either C κ or C λ), linker, an scFv that binds CD3 (VH, linker, VL), wherein the scFab that binds CCR8 comprises CDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprising amino acid residues given by SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, and SEQ ID NO: 244, respectively. In an embodiment, the scFab comprises a VH and VL given by SEQ ID NO: 245 and SEQ ID NO: 246, respectively. In a particular embodiment, the scFab comprises amino acid residues given by SEQ ID NO: 247. In an embodiment, the TCE molecule comprises G4S linkers. In an embodiment, the TCE molecule comprises G4Q linkers. In an embodiment, the CD3-binding scFv is I2E. In another embodiment, the CD3-binding scFv is I2C. In another embodiment, the TCE molecule comprises the amino sequence given by SEQ ID NO: 248. In a further embodiment, the TCE molecule comprises the amino acid sequence given by SEQ ID NO: 249. In some such embodiments, the TCE molecule is TCE 1.3. In a preferred

embodiment, the TCE molecule is a single chain. In some embodiments, the TCE molecule may have an orientation such that the VL is N-terminal to the VH.

[0036] The present invention provides a TCE molecule comprising an orientation, from N-terminus to C-terminus, of scFab that binds CCR8 (VH, CH1, linker, VL, either C κ or C λ), linker, scFv that binds CD3 (VH, linker, VL), linker, Fc1 (hinge, CH2, CH3), linker, Fc2 (hinge, CH2, CH3), wherein the scFab that binds CCR8 comprises CDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprising amino acid residues given by SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, and SEQ ID NO: 255, respectively. In an embodiment, the scFab comprises a VH and VL given by SEQ ID NO: 256 and SEQ ID NO: 257, respectively. In a particular embodiment, the scFab comprises amino acid residues given by SEQ ID NO: 258. In an embodiment, the TCE molecule comprises G4S linkers. In an embodiment, the TCE molecule comprises G4Q linkers. In an embodiment, the CD3-binding scFv is I2E. In another embodiment, the CD3-binding scFv is I2C. In another embodiment, the TCE molecule comprises the amino sequence given by SEQ ID NO: 259. In a further embodiment, the TCE molecule comprises the amino acid sequence given by SEQ ID NO: 260. In some such embodiments, the TCE molecule is TCE 1.4. In a preferred embodiment, the TCE molecule is a single chain. In some embodiments, the TCE molecule may have an orientation such that the VL is N-terminal to the VH.

[0037] The present invention further provides a TCE molecule that binds to human CCR8, which comprises an HCDR1 amino acid sequence of SEQ ID NO: 787; an HCDR2 amino acid sequence of SEQ ID NO: 788; an HCDR3 amino acid sequence of SEQ ID NO: 789; an LCDR1 amino acid sequence of SEQ ID NO: 790; an LCDR2 amino acid sequence of SEQ ID NO: 791; and an LCDR3 amino acid sequence of SEQ ID NO: 792. In some embodiments, the TCE molecule comprises a VH amino acid sequence of SEQ ID NO: 965 and a VL amino acid sequence of SEQ ID NO: 966.

[0038] The present invention further provides a TCE molecule that binds to human CCR8, which comprises an HCDR1 amino acid sequence of SEQ ID NO: 787; an HCDR2 amino acid sequence of SEQ ID NO: 788; an HCDR3 amino acid sequence of SEQ ID NO: 789; an LCDR1 amino acid sequence of SEQ ID NO: 336, wherein X₁ is K or R; an LCDR2 amino acid sequence of SEQ ID NO: 791; and an LCDR3 amino acid sequence of SEQ ID NO: 792. In some embodiments, the TCE molecule comprises a VH amino acid sequence of SEQ ID NO: 965 and a VL amino acid sequence of SEQ ID NO: 342, wherein X₁ is K or R, X₂ is H or Q, and/or X₃ is S or P.

[0039] The present invention further provides a TCE molecule that binds to human CCR8, which comprises an HCDR1 amino acid sequence of SEQ ID NO: 805, an HCDR2 amino acid sequence of SEQ ID NO: 806, an HCDR3 amino acid sequence of SEQ ID NO: 807, an LCDR1 amino acid sequence of SEQ ID NO: 808, an LCDR2 amino acid sequence of SEQ ID NO: 809, and an LCDR3 amino acid sequence of SEQ ID NO: 810.

[0040] The present invention further provides a TCE molecule that binds to human CCR8, which comprises: (a) an HCDR1 amino acid sequence of $X_1X_2GX_4H$, (SEQ ID NO: 1181), wherein (i) X_1 is N, S, D, G, T, or R, (ii) X_2 is C, N, Y, S, or F, and (iii) X_4 is M or F; (b) an HCDR2 amino acid sequence of SEQ ID NOs: 596, 602, 608, 614, 620, 626, 632, 638, 644, 650, 656, 662, 668, 674, 680, 686, 692, 698, 704, 710, 716, 722, 728, 734, 740, 746, 752, 758, 764, 770, 776, 782, 788, 794, 800, 806, 815, 821, 827, 833, 839, 845, 851, 857, 863, 869, 875, 881, 887, or 893, or a variant thereof that comprises 1-4 amino acid substitutions or is at least 90% identical to any one of the foregoing HCDR2 amino acid sequences; (c) an HCDR3 amino acid sequence of SEQ ID NOs: 597, 603, 609, 615, 621, 627, 633, 639, 645, 651, 657, 663, 669, 675, 681, 687, 693, 699, 705, 711, 717, 723, 729, 735, 741, 747, 753, 759, 765, 771, 777, 783, 795, 801, 807, 816, 822, 828, 834, 840, 846, 852, 858, 864, 870, 876, 882, 888, or 894 or a variant thereof that comprises 1-4 amino acid substitutions or is at least 90% identical to any one of the foregoing HCDR3 amino acid sequences; (d) an LCDR1 amino acid sequence of SEQ ID NOs: 598, 604, 610, 616, 622, 628, 634, 640, 646, 652, 658, 664, 670, 676, 682, 688, 694, 700, 706, 712, 718, 724, 730, 736, 742, 748, 754, 760, 766, 772, 778, 784, 796, 802, 808, 811, 817, 823, 829, 835, 841, 847, 853, 859, 865, 871, 877, 883, or 889 or a variant thereof that comprises 1-4 amino acid substitutions or is at least 90% identical to any one of the foregoing LCDR1 amino acid sequences; (e) an LCDR2 amino acid sequence of $RX_2X_3X_4RPS$ (SEQ ID NO: 1182), wherein (i) X_2 is A, N, D, S, or Q, (ii) X_3 is S, T, N, I, F, or A, and (iii) X_4 is N or V; and (f) an LCDR3 amino acid sequence of SEQ ID NOs: 600, 606, 612, 618, 624, 630, 636, 642, 648, 654, 660, 666, 672, 678, 684, 690, 696, 702, 708, 714, 720, 726, 732, 738, 744, 750, 756, 762, 768, 774, 780, 786, 798, 804, 810, 813, 819, 825, 831, 837, 843, 849, 855, 861, 867, 873, 879, 885, or 891 or a variant thereof that comprises 1-4 amino acid substitutions or is at least 90% identical to any one of the foregoing LCDR3 amino acid sequences. In some embodiments, the HCDR1 comprises an amino acid sequence of SEQ ID NOs: 595, 601, 607, 613, 619, 625, 631, 637, 643, 649, 655, 661, 667, 673, 679, 685, 691, 697, 703, 709, 715, 721, 727, 733, 739, 745, 751, 757, 763, 769, 775, 781, 793, 799, 805, 814, 820, 826, 832, 838, 844, 850, 856, 862, 868, 874, 880, 886, or 892. In some embodiments, the LCDR2 comprises an amino acid sequence of SEQ ID NOs: 599, 605, 611, 617, 623, 629, 635, 641, 647, 653, 659, 665, 671, 677, 683, 689, 695, 701,

707, 713, 719, 725, 731, 737, 743, 749, 755, 761, 767, 773, 779, 785, 797, 803, 809, 812, 818, 824, 830, 836, 842, 848, 854, 860, 866, 872, 878, 884, or 890. In some embodiments, the VH comprises an amino acid sequence of SEQ ID NOs: 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 967, 969, 971, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, or 1000. In some embodiments, the VL comprises an amino acid sequence of SEQ ID NOs: 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, or 999.

[0041] In some embodiments, the TCE molecule comprises: (a) a VH comprising an amino acid sequence of SEQ ID NO: 967 and a VL comprising an amino acid sequence of SEQ ID NO: 968; (b) a VH comprising an amino acid sequence of SEQ ID NO: 969 and a VL comprising an amino acid sequence of SEQ ID NO: 970; (c) a VH comprising an amino acid sequence of SEQ ID NO: 971 and a VL comprising an amino acid sequence of SEQ ID NO: 972; (d) a VH comprising an amino acid sequence of SEQ ID NO: 974 and a VL comprising an amino acid sequence of SEQ ID NO: 973; (e) a VH comprising an amino acid sequence of SEQ ID NO: 976 and a VL comprising an amino acid sequence of SEQ ID NO: 975; (f) a VH comprising an amino acid sequence of SEQ ID NO: 978 and a VL comprising an amino acid sequence of SEQ ID NO: 977; (g) a VH comprising an amino acid sequence of SEQ ID NO: 980 and a VL comprising an amino acid sequence of SEQ ID NO: 979; (h) a VH comprising an amino acid sequence of SEQ ID NO: 982 and a VL comprising an amino acid sequence of SEQ ID NO: 981; (i) a VH comprising an amino acid sequence of SEQ ID NO: 984 and a VL comprising an amino acid sequence of SEQ ID NO: 983; (j) a VH comprising an amino acid sequence of SEQ ID NO: 986 and a VL comprising an amino acid sequence of SEQ ID NO: 985; (k) a VH comprising an amino acid sequence of SEQ ID NO: 988 and a VL comprising an amino acid sequence of SEQ ID NO: 987; (l) a VH comprising an amino acid sequence of SEQ ID NO: 990 and a VL comprising an amino acid sequence of SEQ ID NO: 989; (m) a VH comprising an amino acid sequence of SEQ ID NO: 992 and a VL comprising an amino acid sequence of SEQ ID NO: 991; (n) a VH comprising an amino acid sequence of SEQ ID NO: 994 and a VL comprising an amino acid sequence of SEQ ID NO: 993; (o) a VH comprising an amino acid sequence of SEQ ID NO: 996 and a VL comprising an amino acid sequence of SEQ ID NO: 995; (p) a VH comprising an amino acid sequence of SEQ ID NO: 998 and a VL comprising an amino acid sequence of SEQ ID NO: 997; or (q) a VH comprising an amino acid sequence of SEQ ID NO: 1000 and a VL comprising an amino acid sequence of SEQ ID NO: 999.

[0042] In some embodiments, the TCE molecule comprises a heavy chain variable region (VH) amino acid sequence of SEQ ID NO: 965, and a light chain variable region (VL) comprising the amino acid sequence:

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNX1NYLAWYX2QKPGQX3PKLLISWA
STRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSSIPITFGGGTKVEIKR (SEQ
ID NO: 342), wherein X1 is K or R, X2 is H or Q, and/or X3 is S or P. In some embodiments, a TCE molecule of the present invention comprises a YTE motif in the Fc region, corresponding to M252Y/S254T/T256E in the constant heavy chain region of IgG1 or IgG4. The YTE extends the half-life of the molecule (see e.g. Booth et al., MAbs 2018 Oct; 10(7): 1098-1110). In some embodiments, the TCE molecule of the present invention comprising YTE is a TCE molecule that binds CCR8 and CD3.

[0043] In some embodiments, a TCE molecule of the present invention comprises an I2E scFv. In some embodiments, a TCE molecule of the present invention comprises an I2C scFv. The amino acid sequences of I2E are given by SEQ ID NOs. 199 to 206. The amino acid sequences of I2C are given by SEQ ID NOs. 191 to 198.

[0044] The present invention provides additional TCE molecules described in Table 25. The amino acid sequences of these TCE molecules are given by SEQ ID NOs 261 to 589 in Table 25.

[0045] The present invention also provides a method of treating cancer in a patient comprising administering an effective amount of a TCE molecule of the present invention to the patient. In an embodiment, the cancer is a solid tumor. In a particular embodiment, the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer. In some embodiments, the method further comprises administering to the patient a PD-1 antagonist antibody or a PD-L1 antagonist antibody. In some such embodiments, the PD-1 antagonist antibody or PD-L1 antagonist antibody is administered prior to, concurrently with, and/or after administration of the TCE molecule. In particular embodiments, the PD-1 antagonist antibody is pembrolizumab, nivolumab, cemiplimab, or antibody 20C1.009. In other particular embodiments, the PD-L1 antagonist antibody is atezolizumab, avelumab, or durvalumab. In some embodiments, the method further comprises administering to the patient a chemotherapeutic agent. In some such embodiments, the chemotherapeutic agent may be administered prior to, concurrently with, or after administration of the TCE molecule. In some embodiments, the method comprises administering to the patient a TCE molecule of the present invention and a chemotherapeutic

agent. In some embodiments, the method comprises administering to the patient a TCE molecule of the present invention, a PD-1 or PD-L1 antagonist antibody, and a chemotherapeutic agent.

[0046] The present invention provides a TCE molecule of the present invention for use in therapy.

[0047] The present invention also provides a TCE molecule for use in treating cancer. In an embodiment, the cancer is a solid tumor. In a particular embodiment, the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer. In a more particular embodiment, the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, or triple-negative breast cancer. In some embodiments, the use further comprises administering to the patient a PD-1 antagonist antibody or PD-L1 antagonist antibody. In some such embodiments, the PD-1 antagonist antibody or PD-L1 antagonist antibody is administered prior to, concurrently with, and/or after administration of the TCE molecule. In particular embodiments, the PD-1 antagonist antibody is pembrolizumab, nivolumab, cemiplimab, or antibody 20C1.009. In other particular embodiments, the PD-L1 antagonist antibody is atezolizumab, avelumab, or durvalumab. In some embodiments, the use further comprises administering to the patient a chemotherapeutic agent. In some such embodiments, the chemotherapeutic agent may be administered prior to, concurrently with, or after administration of the TCE molecule. In some embodiments, the use comprises administering to the patient a TCE molecule of the present invention and a chemotherapeutic agent. In some embodiments, the use comprises administering to the patient a TCE molecule of the present invention, a PD-1 or PD-L1 antagonist antibody, and a chemotherapeutic agent.

[0048] The present invention provides the use of a TCE molecule of the present invention for the manufacture of a medicament for the treatment of cancer. In an embodiment, the cancer is a solid tumor. In a particular embodiment, the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer. In a more particular embodiment, the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, or triple-negative breast cancer.

[0049] The present invention also provides a pharmaceutical composition comprising a TCE molecule of the present invention and one or more pharmaceutically acceptable carriers, diluents, or excipients.

[0050] The present invention also provides a polynucleotide that encodes an amino acid sequence of a TCE molecule of the present invention. The term “encoding” or “encodes” refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon. The present invention encompasses nucleic acid molecules encoding anti-CCR8 TCE polypeptide sequences.

[0051] In an embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 590. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 590 comprises the amino acid sequence given by SEQ ID NO: 227.

[0052] In an embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 592. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 592 comprises the amino acid sequence given by SEQ ID NO: 249.

[0053] In an embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 593. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 593 comprises the amino acid sequence given by SEQ ID NO: 260.

[0054] In an embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 591. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 591 comprises the amino acid sequence given by SEQ ID NO: 238.

[0055] The present invention also provides a DNA molecule comprising a polynucleotide that encodes an amino acid sequence of a TCE molecule of the present invention. In an embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 590. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 590 comprises the amino acid sequence given by SEQ ID NO: 227. In another embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 592. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 592 comprises the amino acid sequence given by SEQ ID NO: 249. In another embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence given by SEQ ID NO: 593. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 593 comprises the amino acid sequence given by SEQ ID NO: 260. In another embodiment, the TCE molecule of the present invention is encoded by a polynucleotide sequence

given by SEQ ID NO: 591. In a particular embodiment, the TCE molecule encoded by the polynucleotide sequence given by SEQ ID NO: 591 comprises the amino acid sequence given by SEQ ID NO: 238.

[0056] The present invention further provides a mammalian cell transformed with a DNA molecule of the present invention, wherein the transformed mammalian cell is capable of expressing a TCE molecule of the present invention.

[0057] The present invention also provides a process for producing a TCE molecule of the present invention, wherein the process comprises cultivating a mammalian cell under conditions such that the TCE molecule is expressed and recovering the expressed TCE molecule. The present invention also provides a mammalian cell transformed with a DNA molecule of the present invention, wherein the transformed mammalian cell is capable of expressing a TCE molecule of the present invention. The present invention also provides a TCE molecule obtainable by the process.

[0058] In another embodiment, the present invention provides a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope comprises at least one residue of SEQ ID NO: 134. In an embodiment, the epitope comprises at least two residues of SEQ ID NO: 134. In an embodiment, the epitope comprises at least three residues of SEQ ID NO: 134. In an embodiment, the epitope comprises at least four residues of SEQ ID NO: 134. In an embodiment, the epitope comprises at least five residues of SEQ ID NO: 134. In an embodiment, the epitope comprises six or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises seven or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises eight or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises nine or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises ten or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises eleven or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises twelve residues of SEQ ID NO: 134. In a particular embodiment, the epitope comprises the threonine residue at position 4 of SEQ ID NO: 134. The term “epitope” as used herein refers to sites of an antigen that are in contact with (e.g. binds) the molecule. The epitope may be determined by a method known to a person of ordinary skill, including flow cytometry of bound TCE molecule to peptides, hydrogen-deuterium exchange, alanine scanning, and/or x-ray crystallography. In an embodiment, the epitope is determined by epitope binning. In an embodiment, the epitope is determined by TCE molecule binding to CCR8 peptide-nanobody complexes. In an embodiment, the epitope is determined by screening TCE molecule binding to CCR8 by phage display. In an embodiment, the epitope is determined by determining binding to a CCR8 peptide expressed in

human cells, wherein the peptide comprises an amino acid sequence given by SEQ ID NO: 134 or amino acid residues 1-12 of SEQ ID NO: 133. In some embodiments, the epitope is determined by anti-CCR8 TCE molecule binding to the T4R mutation in cynomolgus monkey CCR8. In an embodiment, binding to the T4R mutation is determined in a cell based affinity assay, wherein TCE molecule binding to cells expressing cynomolgus monkey cells CCR8 containing a T4R mutation is compared to TCE molecule binding to cells expressing wild-type cynomolgus monkey CCR8 (comprising a threonine at position four). In some embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows reduced binding to CCR8 comprising a T4R mutation. In particular embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows no detectable binding to CCR8 comprising a T4R mutation. In some embodiments, wild-type cynomolgus monkey CCR8 comprises an amino acid sequence given by SEQ ID NO: 129. In some embodiments, cynomolgus monkey CCR8 comprising a T4R mutation comprises an amino acid sequence given by SEQ ID NO: 130.

[0059] The present invention provides a method of treating cancer in a patient comprising administering to the patient an effective amount of a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope comprises at least one residue of SEQ ID NO: 134. In an embodiment, the epitope comprises at least two residues of SEQ ID NO: 134. In an embodiment, the epitope comprises at least three residues of SEQ ID NO: 134. In an embodiment, the epitope comprises at least four residues of SEQ ID NO: 134. In an embodiment, the epitope comprises at least five residues of SEQ ID NO: 134. In an embodiment, the epitope comprises six or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises seven or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises eight or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises nine or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises ten or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises eleven or more residues of SEQ ID NO: 134. In an embodiment, the epitope comprises twelve residues of SEQ ID NO: 134. In an embodiment, the epitope comprises a threonine residue at position 4 of SEQ ID NO: 134. In an embodiment, the epitope is determined by epitope binning. In an embodiment, the epitope is determined by TCE molecule binding to CCR8 peptide-nanobody complexes. In an embodiment, the epitope is determined by screening TCE molecule binding to CCR8 by phage display. In an embodiment, the epitope is determined by determining binding to a CCR8 peptide expressed in human cells, wherein the peptide comprises an amino acid sequence given by SEQ ID NO: 134 or amino acid residues 1-12 of SEQ ID NO: 133. In some embodiments, the epitope is determined by anti-CCR8 TCE molecule binding to the T4R

mutation in cynomolgus monkey CCR8. In an embodiment, binding to the T4R mutation is determined in a cell based affinity assay, wherein TCE molecule binding to cells expressing cynomolgus monkey cells CCR8 containing a T4R mutation is compared to TCE molecule binding to cells expressing wild-type cynomolgus monkey CCR8 (comprising a threonine at position four). In some embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows reduced binding to CCR8 comprising a T4R mutation. In particular embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows no detectable binding to CCR8 comprising a T4R mutation. In some embodiments, wild-type cynomolgus monkey CCR8 comprises an amino acid sequence given by SEQ ID NO: 129. In some embodiments, cynomolgus monkey CCR8 comprising a T4R mutation comprises an amino acid sequence given by SEQ ID NO: 130.

[0060] In another embodiment, the present invention provides a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope consists of one residue of SEQ ID NO: 134. In an embodiment, the epitope consists of two residues of SEQ ID NO: 134. In an embodiment, the epitope consists of three residues of SEQ ID NO: 134. In an embodiment, the epitope consists of four residues of SEQ ID NO: 134. In an embodiment, the epitope consists of five residues of SEQ ID NO: 134. In an embodiment, the epitope consists of six residues of SEQ ID NO: 134. In an embodiment, the epitope consists of seven residues of SEQ ID NO: 134. In an embodiment, the epitope consists of eight residues of SEQ ID NO: 134. In an embodiment, the epitope consists of nine residues of SEQ ID NO: 134. In an embodiment, the epitope consists of ten residues of SEQ ID NO: 134. In an embodiment, the epitope consists of eleven residues of SEQ ID NO: 134. In an embodiment, the epitope consists of twelve residues of SEQ ID NO: 134. In an embodiment, the epitope consists of a threonine residue at position 4 of SEQ ID NO: 134.

[0061] The present invention provides a method of treating cancer in a patient comprising administering to the patient an effective amount of a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope consists of one residue of SEQ ID NO: 134. In an embodiment, the epitope consists of two residues of SEQ ID NO: 134. In an embodiment, the epitope consists of three residues of SEQ ID NO: 134. In an embodiment, the epitope consists of four residues of SEQ ID NO: 134. In an embodiment, the epitope consists of five residues of SEQ ID NO: 134. In an embodiment, the epitope consists of six residues of SEQ ID NO: 134. In an embodiment, the epitope consists of seven residues of SEQ ID NO: 134. In an embodiment, the epitope consists of eight residues of SEQ ID NO: 134. In an embodiment, the epitope consists of nine residues of SEQ ID NO: 134. In an embodiment, the epitope consists of

ten residues of SEQ ID NO: 134. In an embodiment, the epitope consists of eleven residues of SEQ ID NO: 134. In an embodiment, the epitope consists of twelve residues of SEQ ID NO: 134. In an embodiment, the epitope consists of a threonine residue at position 4 of SEQ ID NO: 134.

[0062] In another embodiment, the present invention provides a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope comprises at least one residue of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least two residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least three residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least four residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least five residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises six or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises seven or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises eight or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises nine or more residues of amino acid residues 1-12 of SEQ ID NO: 133. In an embodiment, the epitope comprises ten or more residues amino acid residues 1-12 of SEQ ID NO: 133. In an embodiment, the epitope comprises eleven or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises twelve residues of amino acid residues 1-12 OF SEQ ID NO: 133. In a particular embodiment, the epitope comprises the threonine residue at position 4 of amino acid residues 1-12 OF SEQ ID NO: 133. The term “epitope” as used herein refers to sites of an antigen that are in contact with (e.g. binds) the molecule. The epitope may be determined by a method known to a person of ordinary skill, including flow cytometry of bound TCE molecule to peptides, hydrogen-deuterium exchange, alanine scanning, and/or x-ray crystallography. In an embodiment, the epitope is determined by epitope binning. In an embodiment, the epitope is determined by TCE molecule binding to CCR8 peptide-nanobody complexes. In an embodiment, the epitope is determined by screening TCE molecule binding to CCR8 by phage display. In an embodiment, the epitope is determined by determining binding to a CCR8 peptide expressed in human cells, wherein the peptide comprises an amino acid sequence given by SEQ ID NO: 134 or amino acid residues 1-12 of SEQ ID NO: 133. In some embodiments, the epitope is determined by anti-CCR8 TCE molecule binding to the T4R mutation in cynomolgus monkey CCR8. In an embodiment, binding to the T4R mutation is determined in a cell based affinity assay, wherein TCE molecule binding to cells expressing cynomolgus monkey cells CCR8 containing a T4R

mutation is compared to TCE molecule binding to cells expressing wild-type cynomolgus monkey CCR8 (comprising a threonine at position four). In some embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows reduced binding to CCR8 comprising a T4R mutation. In particular embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows no detectable binding to CCR8 comprising a T4R mutation. In some embodiments, wild-type cynomolgus monkey CCR8 comprises an amino acid sequence given by SEQ ID NO: 129. In some embodiments, cynomolgus monkey CCR8 comprising a T4R mutation comprises an amino acid sequence given by SEQ ID NO: 130.

[0063] The present invention provides a method of treating cancer in a patient comprising administering to the patient an effective amount of a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope comprises at least one residue of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least two residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least three residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least four residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises at least five residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises six or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises seven or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises eight or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises nine or more residues of amino acid residues 1-12 of SEQ ID NO: 133. In an embodiment, the epitope comprises ten or more residues amino acid residues 1-12 of SEQ ID NO: 133. In an embodiment, the epitope comprises eleven or more residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises twelve residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope comprises a threonine residue at position 4 of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope is determined by epitope binning. In an embodiment, the epitope is determined by TCE molecule binding to CCR8 peptide-nanobody complexes. In an embodiment, the epitope is determined by screening TCE molecule binding to CCR8 by phage display. In an embodiment, the epitope is determined by determining binding to a CCR8 peptide expressed in human cells, wherein the peptide comprises an amino acid sequence given by SEQ ID NO: 134 or amino acid residues 1-12 of SEQ ID NO: 133. In some embodiments, the epitope is determined by anti-CCR8 TCE molecule binding to the T4R mutation in cynomolgus monkey CCR8. In an embodiment, binding to the T4R mutation is determined in a cell based affinity

assay, wherein TCE molecule binding to cells expressing cynomolgus monkey cells CCR8 containing a T4R mutation is compared to TCE molecule binding to cells expressing wild-type cynomolgus monkey CCR8 (comprising a threonine at position four). In some embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows reduced binding to CCR8 comprising a T4R mutation. In particular embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows no detectable binding to CCR8 comprising a T4R mutation. In some embodiments, wild-type cynomolgus monkey CCR8 comprises an amino acid sequence given by SEQ ID NO: 129. In some embodiments, cynomolgus monkey CCR8 comprising a T4R mutation comprises an amino acid sequence given by SEQ ID NO: 130.

[0064] In another embodiment, the present invention provides a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope consists of at least one residue of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of two residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of three residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of four residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of five residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of six residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of seven residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of eight residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of nine residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of ten residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of eleven residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of twelve residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of a threonine residue at position 4 of amino acid residues 1-12 OF SEQ ID NO: 133.

[0065] The present invention provides a method of treating cancer in a patient comprising administering to the patient an effective amount of a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope consists of one residue of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of two residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of three residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of four residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of five residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope

consists of six residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of seven residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of eight residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of nine residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of ten residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of eleven residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of twelve residues of amino acid residues 1-12 OF SEQ ID NO: 133. In an embodiment, the epitope consists of a threonine residue at position 4 of amino acid residues 1-12 OF SEQ ID NO: 133.

[0066] In an embodiment, the epitope is determined by epitope binning. In an embodiment, the epitope is determined by TCE molecule binding to CCR8 peptide-nanobody complexes. In an embodiment, the epitope is determined by screening TCE molecule binding to CCR8 by phage display. In an embodiment, the epitope is determined by determining binding to a CCR8 peptide expressed in human cells, wherein the peptide comprises an amino acid sequence given by SEQ ID NO: 134 or amino acid residues 1-12 of SEQ ID NO: 133. In some embodiments, the epitope is determined by anti-CCR8 TCE molecule binding to the T4R mutation in cynomolgus monkey CCR8. In an embodiment, binding to the T4R mutation is determined in a cell based affinity assay, wherein TCE molecule binding to cells expressing cynomolgus monkey cells CCR8 containing a T4R mutation is compared to TCE molecule binding to cells expressing wild-type cynomolgus monkey CCR8 (comprising a threonine at position four). In some embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows reduced binding to CCR8 comprising a T4R mutation. In particular embodiments, an anti-CCR8 TCE molecule binds threonine at position four if it shows no detectable binding to CCR8 comprising a T4R mutation. In some embodiments, wild-type cynomolgus monkey CCR8 comprises an amino acid sequence given by SEQ ID NO: 129. In some embodiments, cynomolgus monkey CCR8 comprising a T4R mutation comprises an amino acid sequence given by SEQ ID NO: 130.

[0067] In some embodiments, the present invention provides a molecule that competes for binding CCR8 with a CCR8 TCE molecule of the present invention. Such molecule that competes for binding may be, for example, a TCE molecule, an antibody, antibody fragment, or polypeptide. In some embodiments, the present invention provides a molecule that binds the same epitope as a CCR8 TCE molecule of the present invention.

[0068] In some embodiments, a TCE molecule of the present invention can be administered concurrently with, before, or after a variety of drugs and treatments widely

employed in cancer treatment such as, for example, chemotherapeutic agents, non-chemotherapeutic agents (e.g. anti-PD-1 or anti-PD-L1 inhibitors, such as antagonist antibodies), anti-neoplastic agents, and/or radiation. For example, administration can occur before, during, and/or after any of the treatments described herein. Examples of chemotherapeutic agents are discussed herein and include, but are not limited to, cisplatin, taxol, etoposide, mitoxantrone (Novantrone®), actinomycin D, cycloheximide, camptothecin (or water soluble derivatives thereof), methotrexate, mitomycin (e.g., mitomycin C), dacarbazine (DTIC), anti-neoplastic antibiotics such as adriamycin (doxorubicin) and daunomycin, and all the chemotherapeutic agents mentioned herein.

[0069] In some embodiments, a TCE molecule of the present invention may be administered concurrently with, before, or after a PD-1 antagonist antibody or a PD-L1 antagonist antibody. The term “PD-1 antagonist antibody” refers to an antibody that specifically binds to PD-1 and decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of PD-1 and one or more of its ligands, such as PD-L1 and PD-L2. In some embodiments, a PD-1 antagonist antibody inhibits the binding of PD-1 to PD-L1 and/or PD-L2. The term “PD-L1 antagonist antibody” refers to an antibody that specifically binds to PD-L1 and decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of PD-L1 with the PD-1 receptor. In some embodiments, a PD-L1 antagonist antibody inhibits the binding of PD-L1 to PD-1. In some embodiments, the PD-1 antagonist is any one of Antibody 20C1.006 (SEQ ID NOs: 179-188), Antibody 20C1.009 (SEQ ID NOs: 139-148, or 139-147 and 212), Antibody 20A2.3 (SEQ ID NOs: 149-158), Antibody 20D4.6 (SEQ ID NOs: 159-168), or Antibody 20D4.17 (SEQ ID NOs: 169-178). In one embodiment, the PD-1 antagonist antibody is pembrolizumab. In another embodiment, the PD-1 antagonist antibody is nivolumab. In yet another embodiment, the PD-1 antagonist antibody is cemiplimab. In a particular embodiment, the PD-1 antagonist antibody is antibody 20C1.009, for which the amino acid sequences of the CDRs, variable regions, and full light and heavy chains are provided in SEQ ID NOs: 139-148 and 212. 20C1.009 is also known as AMG 404 and is also known as zeluvalimab. In exemplary aspects, an anti-PD-1 antibody such as 20C1.009 comprises a HC comprising a C-terminal lysine, as in SEQ ID NO: 148. In alternative aspects, the antibody comprises a HC without the C-terminal lysine, as in SEQ ID NO: 212.

[0070] In some embodiments, the 1185-1200

BRIEF DESCRIPTION OF THE DRAWINGS

[0071] **Figure 1.** Depicted are the domains and domain order of TCE molecules of the present invention. Exemplary TCE molecules comprise the following domain order from N-terminus to C-terminus: VH-Linker-VL-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2 (left; “CCR8-CD3 TCE”). Other exemplary TCE molecules of the present invention comprise the following domain order from N-terminus to C-terminus: VH-CH1-Linker-VL-Ck/Cλ-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2 (right; “scFab TCE”). Abbreviations: scFab=single chain Fab (VH-CH1-Linker-VL-Ck/Cλ); scFv=single chain Fv (VH-Linker-VL); scFc=single chain Fc. Depicted formats may comprise scFab or scFv in either orientation, from N-terminus to C-terminus: VH-VL, VL-VH, VH-CH1-VL- Ck/Cλ, or VL- Ck/Cλ-VH-CH1, including linker. For simplicity, VH-VL and VH-CH1-VL- Ck/Cλ orientations are depicted. Depicted formats may comprise G4S linkers or G4Q linkers. For simplicity, G4S linkers are depicted.

[0072] **Figure 2.** Depicted are the domains and domain order of multitargeting BiTE HLE formats of the present invention. Multitargeting BiTE HLE molecules of the scFv-scFv-scFv-scFc format comprises the following domain order from N- to C-terminus: VH-Linker-VL-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2, whereas the scFab-scFv-scFv-scFc format comprises VH-CH1-Linker-VL-Ck/Cλ-Linker-VH-Linker-VL-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. The scFab-scFab-scFv-scFc format comprises VH-CH1-Linker-VL- Ck/Cλ -Linker- VH-CH1-Linker-VL- Ck/Cλ -Linker-VH -Linker-VL-Linker-Fc1-Linker-Fc2. Depicted BiTE formats can comprise scFab or scFv in either orientation, HL or LH; for simplicity only HL orientations are depicted. Ck/Cλ=either Ck or Cλ. Depicted BiTE formats may comprise G4S linkers or G4Q linkers. For simplicity, G4S linkers are depicted.

DETAILED DESCRIPTION OF THE INVENTION

[0073] The present disclosure provides single chain TCE molecules comprising an scFab that binds a target antigen and an scFv that binds CD3. The present disclosure also provides TCE molecules comprising an scFv that binds CCR8 and an scFv that binds CD3. Methods of treating cancer are also provided, as well as methods of making said TCE molecules.

[0074] A “single-chain variable fragment” (“scFv”) is a fusion protein in which a VL and a VH region are joined via a linker (e.g., a synthetic sequence of amino acid residues) to form a

continuous protein chain wherein the linker is long enough to allow the protein chain to fold back on itself and form a monovalent antigen binding site (see, e.g., Bird et al., Science 242:423-26 (1988) and Huston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-83 (1988)). When in the context of other additional moieties (e.g., an Fc region), the scFv can be arranged VH-linker-VL (anti-CD3 scFv), or VL-linker-VH, for example. An anti-target scFv is an scFv that binds an antigen, such as a tumor antigen. An anti-target scFv may bind CCR8. An anti-CD3 scFv binds CD3. Examples of anti-CD3 scFvs include I2E and I2C, given by amino acid sequences 199-206 and 191-198, respectively.

[0075] A “single-chain antigen-binding fragment” (“scFab”) is a fusion protein in which a VH and CH1 are joined via a linker to a VL and Cκ or Cλ to form a continuous protein chain wherein the linker is long enough to allow the protein chain to fold back on itself and form a monovalent antigen binding site independent of the orientation. The linker may be, for example, a (G4S)6, (G4S)7, or (G4S)8 linker. A G4S linker is a linker made of amino acids GGGGS (SEQ ID NO: 189), from N-terminus to C-terminus, and may be repeated multiple times. A (G4S)4 linker, for example, means a linker comprising the following amino acids, from N-terminus to C-terminus: GGGSGGGSGGGSGGGGS (SEQ ID NO: 190). Alternatively, the linker may be, for example, a (G4Q)6, (G4Q)7, or (G4Q)8 linker. A G4Q linker is a linker made of amino acids GGGGQ (SEQ ID NO: 207), from N-terminus to C-terminus, and may be repeated multiple times. A (G4Q)4 linker, for example, means a linker comprising the following amino acids, from N-terminus to C-terminus: GGGGQGGGGQGGGGQGGGGQ (SEQ ID NO: 208). The CCR8 TCEs of the present invention comprise G4Q linkers.

[0076] The scFab, scFv, and/or scFc may also have a cysteine clamp. A “cysteine clamp” involves the introduction of a cysteine into a polypeptide domain at a specific location, typically through replacing an existing amino acid at the specific location, so that when in proximity with another polypeptide domain, also having a cysteine introduced at a specific location, a disulfide bond (a “cysteine clamp”) may be formed between the two domains. In certain embodiments, an scFc comprises at least one cysteine clamp that results in a disulfide bond across both CH2 domains. In a further specific embodiment, an scFc comprises at least two cysteine clamps that results in a disulfide bond across both CH2 domains. In other embodiments, a binding construct’s VH and VL domains may comprise the cysteine clamp(s) to result in disulfide bond formation between the VH and VL domains. These cysteine clamps will stabilize the VH and VL domains in an antigen-binding configuration.

[0077] A cysteine clamp may be naturally occurring, or it may be a result of a molecule engineered to contain cysteines. For example, a scFab may have a natural cysteine clamp between the heavy and light chain constant domains. An scFab may also have a natural cysteine clamp between the heavy and light chain constant domains and an engineered cysteine clamp between cysteines at residue 44 of the heavy chain variable region and residue 100 of the light chain variable region. In addition, an anti-target scFv may also contain a cysteine clamp between cysteines at residue 44 of the heavy chain variable region and residue 100 of the light chain variable region, whereas an anti-CD3 scFv does not contain an engineered cysteine clamp. An scFc may contain hinge cysteine clamps, natural CH2/CH3 cysteine clamps, and/or an engineered CH2 cysteine clamp (intrachain).

[0078] The VH and VL contain CDRs, which are interspersed with regions that are more conserved, termed framework regions ("FR"). Each variable region is composed of 3 CDRs and 4 FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The 3 CDRs of the VL are referred to as "LCDR1, LCDR2, and LCDR3," and the 3 CDRs of the VH are referred to as "HCDR1, HCDR2, and HCDR3." The CDRs contain most of the residues which form specific interactions with the antigen. That is, the CDRs contain most of the residues that are in contact with the antigen's residues. Assignment of amino acids to CDR domains within the VL and HL regions of the TCE molecules of the present invention is based on the well-known Kabat numbering convention (Kabat, et al., Ann. NY Acad. Sci. 190:382-93 (1971); Kabat et al., Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242 (1991)). It is understood that other numbering conventions may also be used, such as Chothia (Chothia et al., "Canonical structures for the hypervariable regions of immunoglobulins", Journal of Molecular Biology, 196, 901-917 (1987); Al-Lazikani et al., "Standard conformations for the canonical structures of immunoglobulins", Journal of Molecular Biology, 273, 927-948 (1997)), and/or North (North et al., "A New Clustering of Antibody CDR Loop Conformations", Journal of Molecular Biology, 406, 228-256 (2011)).

[0079] In the most general sense, a T cell engager ("TCE") molecule as described herein comprises a single chain polypeptide that can bind to two different antigens. A "TCE molecule" may be used interchangeably with a "BiTE molecule". A BiTE molecule can comprise an scFv or scFab, as long as it is bispecific, meaning that it binds two targets (target antigen and CD3) at the same time. A TCE molecule is an antigen-binding molecule. A TCE molecule of the present invention may comprise an scFab that binds a target (e.g. tumor or target antigen) and an scFv that binds CD3. Such molecule may have the orientation, from N-terminus to C-terminus: scFab

(VH, CH1, linker, VL, either C κ or C λ), linker, scFv (VH, linker, VL). Such molecules may alternatively have the orientation, from N-terminus to C-terminus: scFab (VL, either C κ or C λ , linker, VH, CH1), linker, scFv (VH, linker, VL). In some embodiments, the scFab binds CCR8. In particular embodiments, the TCE molecule comprises a C κ .

[0080] A TCE molecule of the present invention may also be comprised of an scFv that binds CCR8 and an scFv that binds CD3. Such TCE molecule may have the following orientation, from N-terminus to C-terminus: scFv that binds CCR8 (VH, linker, VL), linker, scFv that binds CD3 (VH, linker, VL).

[0081] A TCE molecule of the present invention may also have a half-life extending (HLE) moiety. An HLE moiety may extend the in vivo half-life of the TCE molecules of the present invention. Nonlimiting examples of half-life extending moieties include an Fc polypeptide, a single-chain Fc polypeptide (scFc), albumin, an albumin fragment, a moiety that binds to albumin or to the neonatal Fc receptor (FcRn), a derivative of fibronectin that has been engineered to bind albumin or a fragment thereof, a peptide, a single domain protein fragment, or other polypeptide that can increase serum half-life. In other embodiments, a half-life-extending moiety can be a non-polypeptide molecule such as, for example, polyethylene glycol (PEG). In some embodiments, the HLE is a single-chain Fc ("scFc").

[0082] A scFc is a fusion protein in which a CH2 and CH3 (Fc1) are joined via a linker to another CH2 and CH3 (Fc2) to form a continuous protein chain wherein the linker is long enough to allow the protein chain to fold back on itself. In some embodiments, the scFc comprises cysteine clamps. An scFc may also comprise an Ig-Fc hinge region, or part of an Ig-Fc hinge region. The hinge is amino terminal to the CH2 domain, and the scFc may have the following orientation: (Fc1: hinge, CH2, CH3), linker, (Fc2: hinge, CH2, CH3). It is envisaged that the hinge region promotes dimerization. Such Fc polypeptide molecules can be obtained by papain digestion of an immunoglobulin region (resulting in a dimer of two Fc polypeptide), for example and not limitation. In an embodiment, the polypeptide sequence of an Fc monomer is substantially similar to an Fc polypeptide sequence of: an IgG₁ Fc region, an IgG₂ Fc region, an IgG₃ Fc region, an IgG₄ Fc region, an IgM Fc region, an IgA Fc region, an IgD Fc region and an IgE Fc region. (*See, e.g., Padlan, Molecular Immunology, 31(3), 169-217 (1993)*).

[0083] A TCE molecule of the present invention having an HLE moiety (e.g. scFc) may have the following orientation: scFab (VH, CH1, linker, VL, C κ), linker, scFv (VH, linker, VL), linker, scFc (hinge, CH2, CH3, linker, hinge, CH2, CH3). A TCE molecule of the present invention having an HLE moiety may also be in the following orientation: scFab (VL, either C κ

or C λ , linker, VH, CH1), linker, scFv (VH, linker, VL). A TCE molecule of the present invention having an HLE moiety may also be in the following orientation: scFv that binds CCR8 (VH, linker, VL), linker, scFv that binds CD3 (VH, linker, VL), scFc (hinge, CH2, CH3, linker, hinge, CH2, CH3). An scFc may also be referred to as Fc1 (hinge, CH2, CH3), linker, Fc2 (hinge, CH2, CH3, herein.

[0084] Figure 1 depicts examples of the structures of TCE molecules of the present invention.

[0085] It will be appreciated that a TCE molecule of the present invention may have at least one amino acid substitution, providing that the TCE molecule retains the same or better desired binding specificity (e.g., binding to CCR8 and/or CD3). Therefore, modifications to the TCE molecule structures are encompassed within the scope of the invention. Such modifications may include amino acid substitutions, which may be conservative or non-conservative that do not destroy the desired binding capability of a binding construct. Conservative amino acid substitutions may encompass non-naturally occurring amino acid residues, which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics and other reversed or inverted forms of amino acid moieties. A conservative amino acid substitution may also involve a substitution of a native amino acid residue with a normative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position.

[0086] A TCE molecule of the present invention may comprise a fragment of an amino acid sequence described herein.

[0087] A TCE molecule of the present invention can bind a target antigen (e.g. antigen expressed on a tumor cell) and CD3 expressed on T cells. A target antigen can be a human protein or a protein from another species, such as mouse, rat, rabbit, and/or cynomolgus monkey. A target antigen may be any protein expressed on tumor cells, in the case for treating cancer. Nonlimiting examples of target antigens include CCR8, claudin-6, and MAGE-B2.

[0088] In another embodiment, the present invention provides vectors comprising a nucleic acid encoding a polypeptide of the invention or a portion thereof. Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors.

[0089] The recombinant expression vectors of the invention can comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vectors include one or more regulatory sequences, selected on the basis

of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells (e.g., SV40 early gene enhancer, Rous sarcoma virus promoter and cytomegalovirus promoter), those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences, see Voss et al., 1986, Trends Biochem. Sci. 11:287, Maniatis et al., 1987, Science 236:1237, incorporated by reference herein in their entireties), and those that direct inducible expression of a nucleotide sequence in response to particular treatment or condition (e.g., the metallothionin promoter in mammalian cells and the tet-responsive and/or streptomycin responsive promoter in both prokaryotic and eukaryotic systems. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

[0090] In another embodiment, the present invention provides host cells into which a recombinant expression vector of the invention has been introduced. A host cell can be any prokaryotic cell or eukaryotic cell. Prokaryotic host cells include gram negative or gram positive organisms, for example *E. coli* or bacilli. Higher eukaryotic cells include insect cells, yeast cells, and established cell lines of mammalian origin. Examples of suitable mammalian host cell lines include Chinese hamster ovary (CHO) cells or their derivatives such as VEGGIE CHO and related cell lines which grow in serum-free media (see Rasmussen et al., 1998, Cytotechnology 28:31) or CHO strain DXB-11, which is deficient in DHFR (see Urlaub et al., 1980, Proc. Natl. Acad. Sci. USA 77:4216-20). Additional CHO cell lines include CHO-K1 (ATCC#CCL-61), EM9 (ATCC# CRL-1861), and UV20 (ATCC# CRL-1862). Additional host cells include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (see Gluzman et al., 1981, Cell 23:175), L cells, C127 cells, 3T3 cells (ATCC CCL 163), AM-1/D cells (described in U.S. Patent No. 6,210,924), HeLa cells, BHK (ATCC CRL 10) cell lines, the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) (see McMahan et al., 1991, EMBO J. 10:2821), human embryonic kidney cells such as 293, 293 EBNA or MSR 293, human epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels et al. (Cloning Vectors: A Laboratory Manual, Elsevier, New York, 1985).

[0091] Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as “flanking sequences” in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. The leader sequence may comprise an amino acid sequence given by SEQ ID NO: 213 (MDMRVPAQLLGLLLLWLRGA RC) which is encoded by SEQ ID NO: 214 (atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgc agatgc). The leader sequence may comprise an amino acid sequence given by SEQ ID NO: 215 (MAWALLLLTL LTQGTGSWA) which is encoded by SEQ ID NO: 216 (atggcctggg ctctgctgct cctcacctc ctactcagg gcacagggtc ctgggccc). The leader polynucleotide sequence may comprise a polynucleotide sequence given by SEQ ID NO: 594

(ATGGACATGAGAGTGCCTGCACAGCTGCTGGGCCTGCTGCTGCTGTGGCTGAGAGGCGCCAGATG)

[0092] Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Additional selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die), among other methods.

[0093] A polynucleotide encoding an amino acid sequence of a TCE molecule of the present invention can be any length as appropriate for the desired use or function, and can comprise one or more additional sequences, for example, regulatory sequences, and/or be part of a larger nucleic acid, for example, a vector. The skilled artisan will appreciate that, due to the degeneracy of the genetic code, each of the polypeptide sequences disclosed herein is encoded by a large number of other nucleic acid sequences. Mutations can also be introduced into a nucleic

acid without significantly altering the biological activity of a polypeptide that it encodes. For example, one can make nucleotide substitutions leading to amino acid substitutions at non-essential amino acid residues.

[0094] Transformed cells can be cultured under conditions that promote expression of the polypeptide, and the polypeptide recovered by conventional protein purification procedures. Polypeptides contemplated for use herein include substantially homogeneous recombinant mammalian polypeptides substantially free of contaminating endogenous materials. Cells containing the nucleic acid encoding the TCE molecules of the present invention also include hybridomas.

[0095] In some embodiments, a vector comprising a nucleic acid molecule as described herein is provided. In some embodiments, the invention comprises a host cell comprising a nucleic acid molecule as described herein. In some embodiments, a nucleic acid molecule encoding a TCE molecule as described herein is provided. In some embodiments, a pharmaceutical composition comprising at least one TCE molecule described herein is provided.

[0096] Glutamyl and asparagyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0097] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0098] Another type of covalent modification of the TCE molecules included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (*e.g.*, the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

[0099] Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment

of one of the sugars N-acetylglactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[00100] The TCR-CD3 complex is a heteromultimer comprising a heterodimer comprising TCR α and TCR β or TCR γ and TCR δ plus various CD3 chains from among the CD3 zeta (CD3 ζ) chain, CD3 epsilon (CD3 ϵ) chain, CD3 gamma (CD3 γ) chain, and CD3 delta (CD3 δ) chain.

[00101] The CD3 receptor complex is a protein complex and is composed of four chains. In mammals, the complex contains a CD3 γ (gamma) chain, a CD3 δ (delta) chain, and two CD3 ϵ (epsilon) chains. These chains associate with the T cell receptor (TCR) and the so-called ζ (zeta) chain to form the T cell receptor CD3 complex and to generate an activation signal in T lymphocytes. The CD3 γ (gamma), CD3 δ (delta), and CD3 ϵ (epsilon) chains are highly related cell-surface proteins of the immunoglobulin superfamily containing a single extracellular immunoglobulin domain. The intracellular tails of the CD3 molecules contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif or ITAM for short, which is essential for the signaling capacity of the TCR. The CD3 epsilon molecule is a polypeptide which in humans is encoded by the CD3E gene which resides on chromosome 11. The most preferred epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain. It is envisaged that the TCE molecules according to the present invention typically and advantageously show less unspecific T cell activation, which is not desired in specific immunotherapy. This translates to a reduced risk of side effects.

[00102] In some embodiments the effector cell protein can be the human CD3 epsilon (CD3 ϵ) chain, which can be part of a multimeric protein. Alternatively, the effector cell protein can be human and/or cynomolgus monkey TCR α , TCR β , TCR δ , TCR γ , CD3 beta (CD3 β) chain, CD3 gamma (CD3 γ) chain, CD3 delta (CD3 δ) chain, or CD3 zeta (CD3 ζ) chain.

[00103] Moreover, in some embodiments, a TCE molecule can also bind to a CD3 ϵ chain from a non-human species, such as mouse, rat, rabbit, new world monkey, and/or old world monkey species. Such species include, without limitation, the following mammalian species: *Mus musculus*; *Rattus*; *Rattus norvegicus*; the cynomolgus monkey, *Macaca fascicularis*; the hamadryas baboon, *Papio hamadryas*; the Guinea baboon, *Papio*; the olive baboon, *Papio anubis*; the yellow baboon, *Papio cynocephalus*; the Chacma baboon, *Papio ursinus*; *Callithrix jacchus*; *Saguinus Oedipus*; and *Saimiri sciureus*. Having a therapeutic molecule that has comparable activity in humans and species commonly used for preclinical testing, such as mice and monkeys, can simplify, accelerate, and ultimately provide improved outcomes in drug

development. In the long and expensive process of bringing a drug to market, such advantages can be critical.

[00104] As used interchangeably herein, "treatment" and/or "treating" and/or "treat" are intended to refer to all processes wherein there may be a slowing, interrupting, arresting, controlling, stopping, or reversing of the progression of the disorders described herein, but does not necessarily indicate a total elimination of all disorder symptoms. Treatment includes administration of a TCE molecule of the present invention for treatment of a disease or condition in a human that would benefit from activity of a TCE molecule of the present invention and includes: (a) inhibiting further progression of the disease; and (b) relieving the disease, i.e., causing regression of the disease or disorder or alleviating symptoms or complications thereof.

[00105] Suitable PD-L1 antagonist antibodies for use in combination with a TCE molecule of the present invention include, but are not limited to, atezolizumab, avelumab, or durvalumab. Examples of PD-1 antagonist antibodies suitable for use in the methods of the invention include, but are not limited to pembrolizumab, nivolumab, cemiplimab, pidilizumab, spartalizumab, camrelizumab, sintilimab, tislelizumab, toripalimab, dostarlimab, Antibody 20C1.006 (SEQ ID NOs: 72-81), Antibody 20C1.009 (SEQ ID NOs: 32-41 or SEQ ID NOs: 32-40 and SEQ ID NO: 212), Antibody 20A2.003 (SEQ ID NOs: 42-51), Antibody 20D4.006 (SEQ ID NOs: 52-61), or Antibody 20D4.17 (SEQ ID NOs: 62-71), and any of the PD-1 antagonist antibodies described in WO 2019/140196.

[00106] Therapeutically effective doses of a TCE molecule can be administered. The amount of TCE molecule that constitutes a therapeutically dose may vary with the indication treated, the weight of the patient, the calculated skin surface area of the patient. Dosing of a TCE molecule can be adjusted to achieve the desired effects. In many cases, repeated dosing may be required. Dosages and the frequency of administration may vary according to such factors as the route of administration, the particular TCE molecule employed, the nature and severity of the disease to be treated, whether the condition is acute or chronic, and the size and general condition of the subject.

[00107] As used herein, an "effective amount" means the amount of a TCE molecule of the present invention or pharmaceutical composition comprising such TCE molecule that will elicit the biological or medical response of or desired therapeutic effect on a tissue, system, animal, mammal, or human that is being sought by the researcher, medical doctor, or other clinician. An effective amount of the TCE molecule may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the TCE molecule to elicit a desired response in the individual. An effective amount is also one in which any toxic or

detrimental effect of the TCE molecule is outweighed by the therapeutically beneficial effects. Such benefit includes improving signs or symptoms of cancer. An effective amount can be readily determined by one skilled in the art, by the use of known techniques, and by observing results obtained under analogous circumstances. An effective amount of a TCE molecule of the present invention may be administered in a single dose or in multiple doses. In determining the effective amount for a patient, a number of factors are considered by the attending medical practitioner, including, but not limited to: the patient's size (e.g., weight or mass), body surface area, age, and general health; the specific disease or disorder involved; the degree of, or involvement, or the severity of the disease or disorder; the response of the individual patient; the particular compound administered; the mode of administration; the bioavailability characteristics of the preparation administered; the dose regimen selected; the use of concomitant medication; and other relevant circumstances known to medical practitioners.

[00108] A TCE molecule, or a pharmaceutical composition containing such a molecule, can be administered by any feasible method. Protein therapeutics will ordinarily be administered by a parenteral route, for example by injection, since oral administration, in the absence of some special formulation or circumstance, would lead to hydrolysis of the protein in the acid environment of the stomach. Subcutaneous, intramuscular, intravenous, intraarterial, intralesional, or peritoneal bolus injection are possible routes of administration. A TCE molecule can also be administered via infusion, for example intravenous or subcutaneous infusion.

[00109] TCE molecules can be administered in the form of a composition comprising one or more additional components such as a physiologically acceptable carrier, excipient or diluent. Optionally, the composition additionally comprises one or more physiologically active agents. In various particular embodiments, the composition comprises one, two, three, four, five, or six physiologically active agents in addition to one or more TCE molecules.

EXAMPLES

EXAMPLE: TCE Molecule Affinities

Claudin-6 TCE Molecule Affinities

[00110] Claudin-6 T cell engager (“TCE”) molecules are examined for affinities to human Claudin-6. TCE molecules are represented below in Table 1 by unique identifiers. For example, the TCE molecule “CL6 3C1 HL CC x I2C x scFc” refers to a TCE molecule having, from N-

terminus to C-terminus, an scFv with an engineered cysteine clamp (“CC”; clamp between VH44 and VL 100 (Kabat numbering)) that binds Claudin-6 (“CL6”) and has the VH N-terminal to the VL, an I2C scFv that targets CD3 (VH N-terminal to the VL), and an scFc. The TCE molecule “CL6 3C1 HL scFab x I2C x scFc” refers to a TCE molecule having an scFab that binds Claudin-6 having the VH N-terminal to the VL, an I2C scFv that targets CD3 (VH N-terminal to the VL), and an scFc. An “x” represents a linker. The CDR sequences for both CL6 3C1 molecules are identical. Figure 1 depicts a generic structure for each molecule. The human Claudin 6 sequence is given by UniProt entry P56747 and includes variants and isoforms thereof.

[00111] Cell-based affinity of TCE molecules is determined by nonlinear regression (one site - specific binding) analysis. CHO cells transfected with human Claudin-6 were incubated with decreasing concentrations of TCE molecules (up to 50 nM, step 1:1, 10 steps) for 16 h at 4° C. Bound TCE molecules are detected with Alexa Fluor 488-conjugated AffiniPure Fab Fragment Goat Anti-Human IgG (H+L). Fixed cells are detected with FACS flow and signals are detected by fluorescence cytometry. Respective equilibrium dissociation constant (Kd) values are calculated with the one site specific binding evaluation tool of the GraphPad Prism software. Mean Kd values and standard deviation are calculated with Microsoft Excel. Mean Kd values are calculated from three independent experiments.

[00112] According to procedures essentially as described above, the following affinities were obtained.

Table 1: Cell-based affinities of Claudin-6 TCE molecules to human Claudin-6.

TCE molecule	Mean Kd [nM]
CL6 3C1 HL CC scFv x I2C x scFc	7.77 ± 1.49
CL6 3C1 HL scFab x I2C x scFc	2.48 ± 0.24
CL6 3C1-01 HL (scFv) CC x I2C x scFc	2.09 ± 0.76
CL6 3C1-01 HL scFab x I2C x scFc	1.19 ± 0.09
CL6 3C1-03 HL CC scFv x I2C x scFc	7.42 ± 2.11
CL6 3C1-03 HL scFab x I2C x scFc	4.56 ± 1.42
CL6 3C1-04 HL CC(scFv) x I2C x scFc	24.82 ± 10.3
CL6 3C1-04 HL scFab x I2C x scFc	5.73 ± 2.38
CL6 3C1-04.1 HL CC scFv x I2C x scFc	12.94 ± 4.23
CL6 3C1-04.1 HL scFab x I2C x scFc	3.55 ± 0.91
CL6 3C1-05 HL CC scFv x I2C x scFc	24.39 ± 11.42

TCE molecule	Mean Kd [nM]
CL6 3C1-05 HL scFab x I2C x scFc	3.03 ± 0.73
CL6 3C1-05.1 HL CC scFv x I2C x scFc	2.70 ± 0.66
CL6 3C1-05.1 HL scFab x I2C x scFc	1.12 ± 0.49
CL6 3C1-06 HL CC scFv x I2C x scFc	17.61 ± 7.46
CL6 3C1-06 HL scFab x I2C x scFc	4.84 ± 2.17
CL6 3D4-01.1 LH CC scFv x I2C x scFc	5.83 ± 1.36
CL6 3D4-01.1 LH scFab x I2C x scFc	2.51 ± 1.05
CL6 3D4-02 LH CC scFv x I2C x scFc	4.23 ± 1.02
CL6 3D4-02 LH scFab x I2C x scFc	1.41 ± 0.42
CL6 3D4-03.1 LH CC scFv x I2C x scFc	11.83 ± 3.14
CL6 3D4-03.1 LH scFab x I2C x scFc	2.23 ± 0.96
CL6 3D4-04 LH CC scFv x I2C x scFc	17.00 ± 8.23
CL6 3D4-04 LH scFab x I2C x scFc	6.99 ± 2.04
CL6 3D4-04.G2 LH CC scFv x I2C x scFc	11.42 ± 3.08
CL6 3D4-04.G2 LH scFab x I2C x scFc	27.04 ± 2.52
CL6 3C1-02 HL CC scFv x I2C x scFc	5.45 ± 0.81
CL6 3C1-02 HL scFab x I2C x scFc	2.62 ± 0.30

[00113] As shown in Table 1, these data demonstrate that TCE molecules having an scFab target binder show higher affinity for human Claudin-6 compared to TCE molecules having an scFv target binder.

Mage-B2 TCE Molecule Affinities

[00114] Similarly, cell-based affinity of MAGE-B2 TCE molecules is determined by nonlinear regression (one site - specific binding) analysis. HLA-A*02:01 expressing T2 cells exogenously loaded with human MAGE-B2 peptide are incubated with decreasing concentrations of TCE molecules (up to 400 nM, 1:2 dilutions, 11 steps) for 16 hours at 4° C. Bound TCE molecules are detected with Alexa Fluor 488-conjugated AffiniPure Fab Fragment Goat Anti-Human IgG (H+L). Fixed cells are stained with DRAQ5, Far-Red Fluorescent Live-Cell Permeant DNA Dye, and signals are detected by fluorescence cytometry. Respective equilibrium dissociation constant (Kd) values are calculated with the one site specific binding evaluation tool

of the GraphPad Prism software. Mean Kd values and standard deviations are calculated with Microsoft Excel. Mean Kd values are calculated from three independent experiments.

[00115] Following procedures essentially as described above, the following data were obtained.

Table 2: Cell-based affinities of MAGE-B2 TCE molecules.

Construct	Mean Kd [nM]
MA 03-D8 AS CC scFv x I2C x scFc	0.54 ± 0.10
MA 03-D8 AS scFab x I2C x scFc	0.42 ± 0.11
MA 09-E2 CC scFv x I2C x scFc	0.70 ± 0.19
MA 09-E2 scFab x I2C x scFc	0.39 ± 0.03
MA 09-F12 CC scFv x I2C x scFc	0.53 ± 0.18
MA 09-F12 scFab x I2C x scFc	0.46 ± 0.13
MA 09-G10 CC scFv x I2C x scFc	0.83 ± 0.30
MA 09-G10 scFab x I2C x scFc	0.52 ± 0.10
MA 09-H10 CC scFv x I2C x scFc	0.62 ± 0.13
MA 09-H10 scFab x I2C x scFc	0.49 ± 0.18
MA 09-H7 CC scFv x I2C x scFc	0.79 ± 0.37
MA 09-H7 scFab x I2C x scFc	0.50 ± 0.11
MA 10-D3 CC scFv x I2C x scFc	1.10 ± 0.23
MA 10-D3 scFab x I2C x scFc	0.54 ± 0.10
MA 10-D6 CC scFv x I2C x scFc	0.67 ± 0.12
MA 10-D6 scFab x I2C x scFc	0.50 ± 0.10
MA 10-G10 AS CC scFv x I2C x scFc	1.75 ± 0.52
MA 10-G10 AS scFab x I2C x scFc	0.65 ± 0.10
MA 98-C7 CC scFv x I2C x scFc	0.72 ± 0.22
MA 98-C7 scFab x I2C x scFc	0.45 ± 0.08
MA 03-E11 AS CC scFv x I2C x scFc	4.21 ± 0.46
MA 03-E11 AS scFab x I2C x scFc	1.25 ± 0.15
MA 86-A4-N-F5 CC scFv x I2C x scFc	51.80 ± 12.18
MA 86-A4-N-F5 scFab x I2C x scFc	65.87 ± 15.79
MA 88-B3-F9 CC scFv x I2C x scFc	74.06 ± 36.22
MA 88-B3-F9 scFab x I2C x scFc	83.67 ± 8.70

Construct	Mean Kd [nM]
MA SG-F28 CC scFv x I2C x scFc	76.77 ± 18.34
MA SG-F28 scFab x I2C x scFc	62.81 ± 8.08

[00116] As shown in Table 2, these data demonstrate that TCE molecules having an scFab target binder show higher affinity for human MAGE-B2 compared to TCE molecules having an scFv target binder.

EXAMPLE: FACS-based cytotoxicity assay with unstimulated human PBMC

[00117] Human peripheral blood mononuclear cells (PBMC) are prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (buffy coats), a side product of blood banks collecting blood for transfusions. Buffy coats are supplied by a local blood bank and PBMC are prepared on the day after blood collection. After Ficoll density centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes are removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH₄Cl, 10 mM KHCO₃, 100 μM EDTA). Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells, and monocytes. PBMC are kept in culture at 37° C/5% CO₂ in RPMI medium (Gibco) with 10% FCS (Gibco).

[00118] Human T cells are isolated from PBMC using human Pan T cell isolation kit (Miltenyi Biotec, # 130-096-535) according to the manufacturer's protocol. T cells are isolated using LS Columns (Miltenyi Biotec, #130-042-401). T cells are cultured in RPMI complete medium (RPMI1640; Biochrom AG, #FG1215) supplemented with 10% FBS (Bio West, #S1810), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37° C.

[00119] For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC18 (DiO) (Thermo Fisher, #V22886) is used to label target antigen positive cells (Claudin-6 stable transfected CHO cells or DAN-G stable transfected MAGE-B2 cells) as target cells and distinguish them from effector cells. Briefly, cells are harvested, washed once with PBS and adjusted to 10⁶ cells/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μL/10⁶ cells). After incubation for 3 minutes at 37° C, cells are washed twice in complete RPMI medium and the cell number is adjusted to 1.25 x 10⁵ cells/mL. The vitality of cells is

determined using Nucleocounter NC-250 (Chemometec) and Solution18 Dye containing Acridine Orange and DAPI (Chemometec).

[00120] To quantify the lysis of target antigen positive cell lines in the presence of serial dilutions of TCE molecules, equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o CD14⁺ cells) are mixed, resulting in an E:T cell ratio of 10:1. 160 μ L of this suspension is transferred to each well of a 96-well plate. Forty μ L of serial dilutions of the corresponding TCE molecule, a negative control, or RPMI complete medium as an additional negative control are added. The TCE molecule-mediated cytotoxic reaction proceeds for 48 hours in a 7% CO₂ humidified incubator. Cells are transferred to a new 96-well plate and loss of target cell membrane integrity is monitored by adding propidium iodide (PI) at a final concentration of 1 μ g/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

[00121] Samples are measured by flow cytometry on an iQue Plus (Intellicyt, now Sartorius) instrument and analyzed by Forecyt software (Intellicyt). Target cells are identified as DiO-positive cells. PI-negative target cells are classified as living target cells. Percentage of cytotoxicity is calculated as dead target cells/target cells x 100. Using GraphPad Prism 7.04 software (Graph Pad Software, San Diego), the percentage of cytotoxicity is plotted against the corresponding TCE molecule concentrations. Dose response curves are analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC₅₀ values are calculated.

[00122] Following procedures essentially as described above, the following data were obtained.

Table 3. Claudin-6 TCE molecule mediated cytotoxicity.

TCE Molecule	EC₅₀ [pM]
CL6 3C1 HL CC scFv x I2C x scFc	2.35
CL6 3C1 HL scFab x I2C x scFc	0.13
CL6 3C1-01 HL CC scFv x I2C x scFc	1.86
CL6 3C1-01 HL scFab x I2C x scFc	0.11
CL6 3C1-03 HL CC scFv x I2C x scFc	12.80
CL6 3C1-03 HL scFab x I2C x scFc	0.45
CL6 3C1-04 HL CC scFv x I2C x scFc	33.7
CL6 3C1-04 HL scFab x I2C x scFc	0.67
CL6 3C1-04.1 HL CC scFv x I2C x scFc	15.43

TCE Molecule	EC₅₀ [pM]
CL6 3C1-04.1 HL scFab x I2C x scFc	0.38
CL6 3C1-05 HL CC scFv x I2C x scFc	18.75
CL6 3C1-05 HL scFab x I2C x scFc	0.42
CL6 3C1-05.1 HL CC scFv x I2C x scFc	5.27
CL6 3C1-05.1 HL scFab x I2C x scFc	0.11
CL6 3C1-06 HL CC scFv x I2C x scFc	36.7
CL6 3C1-06 HL scFab x I2C x scFc	0.58
CL6 3D4-01.1 LH CC scFv x I2C x scFc	25.9
CL6 3D4-01.1 LH scFab x I2C x scFc	1.41
CL6 3D4-02 LH CC scFv x I2C x scFc	4.69
CL6 3D4-02 LH scFab x I2C x scFc	0.52
CL6 3D4-03.1 LH CC scFv x I2C x scFc	23.3
CL6 3D4-03.1 LH scFab x I2C x scFc	1.03
CL6 3D4-04 LH CC scFv x I2C x scFc	37.2
CL6 3D4-04 LH scFab x I2C x scFc	3.15
CL6 3D4-04.G2 LH CC scFv x I2C x scFc	48.5
CL6 3D4-04.G2 LH scFab x I2C x scFc	11.99

[00123] These data demonstrate that the Claudin-6 TCE molecules having an scFab target binder demonstrated improved potency of Claudin-6 transfected CHO cells compared to TCE molecules having an scFv target binder.

[00124] Data demonstrating MAGE-B2 TCE molecule cytotoxicity is shown in Table 4.
Table 4. MAGE-B2 TCE molecule mediated cytotoxicity.

TCE Molecule	EC₅₀ [pM]
MA 03-D8 AS scFab x I2C x scFc	4.8
MA 03-D8 AS CC scFv x I2C x scFc	15.2
MA 09-E2 scFab x I2C x scFc	21.7
MA 09-E2 CC scFv x I2C x scFc	68.7
MA 09-F12 scFab x I2C x scFc	48.8
MA 09-F12 CC scFv x I2C x scFc	83.5
MA 09-G10 scFab x I2C x scFc	52.8

TCE Molecule	EC50 [pM]
MA 09-G10 CC scFv x I2C x scFc	90.8
MA 09-H10 scFab x I2C x scFc	40.5
MA 09-H10 CC scFv x I2C x scFc	103.4
MA 09-H7 scFab x I2C x scFc	74.6
MA 09-H7 CC scFv x I2C x scFc	227.2
MA 10-B5 scFab x I2C x scFc	11.7
MA 10-B5 CC scFv x I2C x scFc	33.3
MA 10-D3 scFab x I2C x scFc	60.8
MA 10-D3 CC scFv x I2C x scFc	196.9
MA 10-D6 scFab x I2C x scFc	27.7
MA 10-D6 CC scFv x I2C x scFc	45.0
MA 10-G10 AS scFab x I2C x scFc	32.9
MA 10-G10 AS CC scFv x I2C x scFc	141.0
MA 98-C7 scFab x I2C x scFc	9.9
MA 98-C7 CC scFv x I2C x scFc	70.5
MA 03-E11 AS scFab x I2C x scFc	60.6
MA 03-E11 AS CC scFv x I2C x scFc	212.4

[00125] These data demonstrate that the MAGE-B2 TCE molecules having an scFab target binder demonstrated increased lysis of DAN-G cells compared to TCE molecules having an scFv target binder.

[00126] In a similar experiment, a scFab-containing TCE molecule having a disulfide-bridge (cysteine clamp (“CC”); cysteines at Kabat residues VH44/VL100; CL6 3C1-02scFabCC x I2C x scFc) is tested for cytotoxic activity. These data (shown in Table 5) demonstrate that the scFab-containing TCE molecule having a disulfide bridge showed similar activity compared to the scFab-containing TCE molecule without this disulfide bridge. Both scFab-containing TCE molecules demonstrated increased cytotoxicity compared to TCE molecules having an scFv target binder.

Table 5. CL 3C1-02-based BiTE molecules.

CLDN6 BiTE molecules	EC50 [pM]
CL6 3C1-02 CC scFv x I2C x scFc	89
CL6 3C1-02 scFab x I2C x scFc	4.2
CL6 3C1-02 scFab CC x I2C x scFc	4.3

[00127] Data from TCE molecules binding a target antigen and CD3 is shown below in Table 6. The TCE molecules either contained a (G4S)₈ linker in a scFab(VH-CH1-(G4S)₈ linker-VL-Ck)-linker-aCd3scFv(VH-linker-VL)-linker-scFc(Fc-linker-Fc) orientation (top row), a (G4S)₆ linker (second row), a disulfide-bridge stabilized (Kabat VH44/VL100) scFv target binding moiety (third row), or a (G4S)₈ linker in a scFab(VH-CH1-linker-VL-Ck)-linker-aCd3scFv(VH-linker-VL)-linker-scFc(Fc-linker-Fc) orientation (bottom row).

Table 6. TCE molecule mediated cytotoxicity.

TCE Molecule	EC50 [pM]
HL scFab(G4S) ₈ x I2C x scFc	3.9
HL scFab(G4S) ₆ x I2C x scFc	7.5
HL CC scFv x I2C x scFc	40
LH scFab(G4S) ₈ x I2C x scFc	60

[00128] These data demonstrate that the scFab-containing TCE molecule having an scFab (G4S)₈ linker showed the highest cytotoxic activity compared to the other molecules tested. The scFab-containing TCE molecule with the VL-Ck-linker-VH-CH1-aCD3-scFc orientation demonstrated the least activity, which could be due to the orientation difference as compared to scFab-containing TCE molecule having the orientation VH-CH1-VL-Ck-aCD3-scFc.

EXAMPLE: Application of scFab moiety in TCE formats

[00129] Multitargeting TCE molecules are tested for cytotoxicity. As shown in the structures in Figure 2, tested TCE molecules have either two anti-target scFvs (CD22 11-C3 CC scFv x CD20 29-F5 CC scFv x I2C x scFc and CD20 99-E5 CC scFv x CD22 28-B7N655 CC scFv x I2C x scFc), an anti-target scFab and an anti-target scFv (CD20 99-E5 scFab x CD22 28-B7N655 CC scFv x I2C x scFc), or two anti-target scFabs (CD22 11-C3 scFab x CD20 29-F5 scFab x I2C x scFc). Tested TCE molecules have an anti-CD3 scFv ("I2C") and an scFc. 11-C3,

29-F5, 99-E5, and 28-B7N655 refer to target binders, such that 11-C3 scFab will have the same CDRs as 11-C3 scFv, for example. Cytotoxicity of Raji cells (double positive for CD20 and CD22) is essentially determined as described above, and the following data were obtained.

Table 7. TCE molecule mediated cytotoxicity (EC₅₀).

TCE molecule	Raji	CHO CD20	CHO CD22
CD22 11-C3 scFab x CD20 29-F5 scFab x I2C x scFc	872	14.5	17.0
CD22 11-C3 CC scFv x CD20 29-F5 CC scFv x I2C x scFc	2308	64.7	16.4
CD20 99-E5 scFab x CD22 28-B7N655 CC scFv x I2C x scFc	28.8	20.9	
CD20 99-E5 CC scFv x CD22 28-B7N655 CC scFv x I2C x scFc	35.4	52.4	

[00130] As shown in Table 7, TCE molecules having scFabs as both target binders (first row) have improved potency against single positive target cells (CD20 transfected CHO) and on double-positive Raji cells compared to TCE molecules having scFvs as both target binders (second row). In addition, TCE molecules having a CD20-binding scFab (third row) demonstrate improved potency for CD20 transfected CHO cells and double-positive Raji cells compared to TCE molecules having a CD20-binding scFv (fourth row).

EXAMPLE: Evaluation of TCE Molecules Protein Surface Hydrophobicity

[00131] To measure protein surface hydrophobicity, isolated and formulated TCE molecule monomer adjusted to a defined protein concentration is transferred into autosampler fitting sample vials and measured on a FPLC system. A Hydrophobic Interaction Chromatography (HIC) column is equilibrated with formulation buffer and a defined volume of protein solution applied at a constant formulation buffer flow. Detection is done by OD280 nm optical absorption.

[00132] Elution behavior is determined by peak shape respectively mathematically calculation of declining signal peak slope. Steeper slope / higher slope values indicate less

hydrophobic interaction of the protein surface compared to constructs with more flat elution behavior and lower slope value.

[00133] Following procedures essentially as described above, the following data were obtained. “I2C” refers to an scFv that binds CD3. “CC” refers to an scFv containing an engineered cysteine clamp between a cysteine at position 44 (VH) and a cysteine at position 100 (VL) (Kabat).

Table 8. HIC elution behavior of MAGE-B2 TCE molecules.

TCE molecule	HIC Elution Slope
MA 03-D8 AS CC scFv x I2C x scFc	49.69
MA 03-D8 AS scFab x I2C x scFc	50.4
MA 03-E11 AS CC scFv x I2C x scFc	25.35
MA 03-E11 AS scFab x I2C x scFc	45.93
MA 09-E2 CC scFv x I2C x scFc	21.55
MA 09-E2 scFab x I2C x scFc	39.58
MA 09-F12 CC scFv x I2C x scFc	25.39
MA 09-F12 scFab x I2C x scFc	35.03
MA 09-G10 CC scFv x I2C x scFc	37.3
MA 09-G10 scFab x I2C x scFc	40.26
MA 09-H10 CC scFv x I2C x scFc	29.02
MA 09-H10 scFab x I2C x scFc	40.21
MA 09-H7 CC scFv x I2C x scFc	35.56
MA 09-H7 scFab x I2C x scFc	43.47
MA 10-D3 CC scFv x I2C x scFc	16.23
MA 10-D3 scFab x I2C x scFc	35.17
MA 10-D6 CC scFv x I2C x scFc	7.4
MA 10-D6 scFab x I2C x scFc	27.65
MA 10-G10 AS CC scFv x I2C x scFc	51.54
MA 10-G10 AS scFab x I2C x scFc	43.73
MA 86-A4-N-F5 CC scFv x I2C x scFc	35.66
MA 86-A4-N-F5 scFab x I2C x scFc	60.06

MA 88-B3-F9 CC scFv x I2C x scFc	51.05
MA 88-B3-F9 scFab x I2C x scFc	54.89
MA 98-C7 CC scFv x I2C x scFc	44.38
MA 98-C7 scFab x I2C x scFc	52.04
MA SG-F28 CC scFv x I2C x scFc	19.77
MA SG-F28 scFab x I2C x scFc	30.47
MA 10-B5 CC scFv x I2C x scFc	16.81
MA 10-B5 scFab x I2C x scFc	42.19

Table 9. HIC elution behavior of CD20/CD22 TCE molecules.

TCE Molecule	HIC Elution Slope
CD22 11-C3 scFab x CD20 29-F5scFab x I2C x scFc	46.27
CD22 11-C3 CC scFv x CD20_29-F5_CC scFv x I2C x scFc	17.49
CD20 99-E5scFab x CD22 28-B7N655 CC scFv x I2C x scFc	17.4
CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv x I2C x scFc	10.99

Table 10. HIC elution behavior of Claudin-6 TCE molecules.

TCE Molecule	HIC Elution Slope
CL6 3C1 HL CC scFv x I2C x scFc	48.1
CL6 3C1 HL scFab x I2C x scFc	51.85
CL6 3C1-01 HL CC scFv x I2C x scFc	41.54
CL6 3C1-01 HL scFab x I2C x scFc	44.32
CL6 3C1-03 HL CC scFv x I2C x scFc	52.18
CL6 3C1-03 HL scFab x I2C x scFc	46.19
CL6 3C1-04 HL CC scFv x I2C x scFc	44.08
CL6 3C1-04 HL scFab x I2C x scFc	51.49
CL6 3C1-04.1 HL CC scFv x I2C x scFc	36.65
CL6 3C1-04.1 HL scFab x I2C x scFc	35.92

CL6 3C1-05 HL CC scFv x I2C x scFc	37.31
CL6 3C1-05 HL scFab x I2C x scFc	45.42
CL6 3C1-05.1 HL CC scFv x I2C x scFc	33.43
CL6 3C1-05.1 HL scFab x I2C x scFc	36.13
CL6 3C1-06 HL CC scFv x I2C x scFc	42.98
CL6 3C1-06 HL scFab x I2C x scFc	44.7
CL6 3D4-01.1 LH CC scFv x I2C x scFc	16.52
CL6 3D4-01.1 LH scFab x I2C x scFc	15.83
CL6 3D4-02 LH CC scFv x I2C x scFc	10.1
CL6 3D4-02 LH scFab x I2C x scFc	16.36
CL6 3D4-03.1 LH CC scFv x I2C x scFc	16.01
CL6 3D4-03.1 LH scFab x I2C x scFc	18.23
CL6 3D4-04 LH CC scFv x I2C x scFc	13.58
CL6 3D4-04 LH scFab x I2C x scFc	18.23
CL6 3D4-04.G2 LH CC scFv x I2C x scFc	15.43
CL6 3D4-04.G2 LH scFab x I2C x scFc	27.12
CL6 3C1-02 CC scFv x I2C x scFc	46.25
CL6 3C1-02 scFab x I2C x scFc	45.79

[00134] These data demonstrate the degree of interaction of the applied construct with the hydrophobic column matrix surface. In most cases, peak slopes for the scFab comprising TCE molecules are steeper and have higher mathematical values compared to the other tested TCE molecules. Constructs having a higher surface hydrophobicity will have a stronger interaction with the matrix compared to constructs with less surface hydrophobicity and will therefore elute over a bigger elution volume with less curve steepness.

EXAMPLE: Evaluation of TCE Molecules Aggregation Temperature

[00135] Rising temperatures may destabilize protein constructs, which will expose structures originally buried by protein folding. These structures can be sticky and can get in contact with other constructs resulting in aggregation and therefore a larger hydrodynamic radius. Molecules having higher aggregations temperature are more stable compared to molecules having lower aggregation temperatures.

[00136] To determine aggregation temperature of scFab-containing TCE molecules, isolated and formulated TCE molecule monomer adjusted to a defined protein concentration is pipetted in duplicates into a 96-well plate and covered with paraffin oil. The 96-well plate is transferred to a dynamic light scattering DLS reader capable of heating the plate at a defined rate in a defined temperature range. Measurement is performed from 40° C to 70° C at a defined rate of temperature increase. Detection is done by dynamic light scattering determining the hydrodynamic radius of the constructs over the temperature ramp. Temperature at the beginning of increase of hydrodynamic radius is defined as aggregation temperature. “I2C” refers to an scFv that binds CD3. “CC” refers to an scFv containing an engineered cysteine clamp (cysteine clamp between a cysteine at position 44 (VH) and a cysteine at position 100 (VL) (Kabat)) that binds a target (i.e. MAGE-B2 in Table 11).

Table 11. DLS aggregation temperature of MAGE-B2 (“MA”) TCE molecules.

TCE molecule	Mean Aggregation Temperature [°C]
MA 03-D8 AS CC scFv x I2C x scFc	53.57
MA 03-D8 AS scFab x I2C x scFc	57.86
MA 03-E11 AS CC scFv x I2C x scFc	54.51
MA 03-E11 AS scFabx I2C x scFc	57.96
MA 09-E2 CC scFv x I2C x scFc	52.09
MA 09-E2 scFab x I2C x scFc	57.83
MA 09-F12 CC scFv x I2C x scFc	53.45
MA 09-F12 scFab x I2C x scFc	58.44
MA 09-G10 CC scFv x I2C x scFc	49.84
MA 09-G10 scFab x I2C x scFc	58.56
MA 09-H10 CC scFv x I2C x scFc	55.14
MA 09-H10 scFab x I2C x scFc	55.42
MA 09-H7 CC scFv x I2C x scFc	53.11
MA 09-H7 scFab x I2C x scFc	58.64
MA 10-D3 CC scFv x I2C x scFc	52.67
MA 10-D3 scFab x I2C x scFc	58.01
MA 10-D6 CC scFv x I2C x scFc	52.19
MA 10-D6 scFab x I2C x scFc	58.23
MA 10-G10 AS CC scFv x I2C x scFc	54.11

TCE molecule	Mean Aggregation Temperature [°C]
MA 10-G10 AS scFab x I2C x scFc	57.79
MA 86-A4-N-F5 CC scFv x I2C x scFc	52.54
MA 86-A4-N-F5 scFab x I2C x scFc	58.47
MA 88-B3-F9 CC scFv x I2C x scFc	56.44
MA 88-B3-F9 scFab x I2C x scFc	57.7
MA 98-C7 CC x I2C scFv x scFc	56.96
MA 98-C7 scFab x I2C x scFc	57.17
MA SG-F28 CC scFv x I2C x scFc	53.36
MA SG-F28 scFab x I2C x scFc	58.48
MA 10-B5 CC scFv x I2C x scFc	52.6
MA 10-B5 scFab x I2C x scFc	58.22

Table 12. DLS aggregation temperature of CD20 and CD22 TCE molecules.

TCE molecule	Mean Aggregation Temperature [°C]
CD22 11-C3 scFab x CD20 29-F5 scFab x I2C x scFc	60.40
CD22 11-C3 CC scFv x CD20 29-F5 CC scFv x I2C x scFc	54.66
CD20 99-E5 scFab x CD22 28-B7N655 CC scFv x I2C x scFc	56.24
CD20 99-E5 CC scFv CD22 28-B7 N655 CC scFv x I2C x scFc	56.15

Table 13. DLS aggregation temperature of Claudin-6 TCE molecules.

	TCE molecule (xI2C x scFc)	Mean Aggregation Temperature [°C]
CL6 3C1	HL CC scFv	50.50
	HL scFab	55.98
	01 HL CC scFv	54.64
	01 HL scFab	56.77
	03 HL CC scFv	51.72
	03 HL scFab	56.45

	04 HL CC scFv	49.84
	04 HL scFab	56.48
	04.1 HL CC scFv	50.73
	04.1 HL scFab	56.37
	05 HL CC scFv	49.33
	05 HL scFab	56.29
	05.1 HL CC scFv	51.77
	05.1 HL scFab	55.94
	06 HL CC scFv	50.03
	06 HL scFab	55.94
CL6 3D4	01.1 LH CC scFv	51.61
	01.1 LH scFab	56.62
	02 LH CC scFv	52.76
	02 LH scFab	55.91
	03.1 LH CC scFv	49.60
	03.1 LH scFab	56.54
	04 LH CC scFv	53.38
	04 LH scFab	57.25
	04.G2 LH CC scFv	54.11
	04.G2 LH scFab	56.29
CL6 3C1	02 CC scFv	54.79
	02scFab	57.26

[00137] These data demonstrate that scFab TCE molecules show higher mean aggregation temperatures compared to the other tested TCE molecules (having an scFv target binder) and are therefore more stable than TCE molecules with an scFv target binder.

EXAMPLE: Cell-based CCR8 Binding Competition Assay

[00138] Effects of biochemical competition with CCR8 ligand CCL1 on CCR8-binding properties of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules are assessed by flow cytometry, based on an engineered variant of the human T lymphocyte cell line HuT 78 expressing native CCR8 but not expressing human CD3 epsilon chain. The cell line bore a defined knockout in the CD3E gene.

[00139] Fifty thousand cells are incubated with 200 nM recombinant human CCL1 (Abcam, cat. no. ab9854) (diluted in PBS/2% FCS) or with PBS/2% FCS in 50 μ l for 55 min at 4° C. Purified CCR8-binding TCE and scFab-containing CCR8-binding TCE molecules, diluted in PBS/2% FCS, are added to a final concentration of 100 nM in a total volume of 100 μ l, followed by incubation at 4° C for 45 minutes. For a negative control, PBS/2% FCS is added instead of purified CCR8-binding TCE or scFab-containing CCR8-binding TCE molecules. After three washes, bound molecules are detected for 45 minutes at 4° C with R-Phycoerythrin-conjugated, anti-human IgG, Fc gamma fragment-specific antibody (Jackson, cat. no. 109-116-098), diluted 1:50 in PBS/2% FCS. After three washes, samples are measured on a FACSCanto II instrument (Becton Dickinson). All conditions are performed in three replicates.

[00140] Data are analyzed by FlowJo software (FlowJo / Becton Dickinson), generating median values for PE signals (median PE). From the three replicates per condition, average median PE values (with standard deviations) as well as ratios of average median PE in CCL1-treated setting over average median PE in CCL1-untreated setting were calculated using Excel software (Microsoft).

[00141] According to procedures essentially as described above, the following data were obtained.

[00142] Table 14 shows averages (with standard deviations) of median values of PE-signals, and ratios of average median PE of CCL1-treated condition over CCL1-untreated condition. Identifiers of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules are indicated in the left column.

[00143] “I2E” represents an scFv that binds CD3. TCE1 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 113-128. TCE8 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 97-112. TCE2 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 49-64.

Table 14. CCR8 TCE molecule binding in the presence or absence of CCL1.

TCE molecule	Average Median PE, CCL1-treated (+CCL1)	Average Median PE, CCL1-untreated (-CCL1)	Ratio Average Median PE (+CCL1) / Average (-CCL1)
TCE1 scFab x I2E x scFc	27047.3 $\pm$ 231.3 3 7	27174.0 $\pm$ 376.7 0 2	1.00
TCE8 scFab x I2E x scFc	8799.00 $\pm$ 197.8 9	18919.6 $\pm$ 250.3 7 1	0.47

TCE2 scFab x I2E x scFc	1554.33 ± 15.17	2424.33 ± 108.19	0.64
TCE1 scFv CC x I2E x scFc	23129.0 ± 189.70	23195.6 ± 368.27	1.00
TCE8 scFv CC x I2E x scFc	7346.00 ± 195.16	15940.3 ± 108.13	0.46
Negative control	416.67 ± 58.93	374.67 ± 2.49	1.11

[00144] These data demonstrate that the presence of CCL1 did not affect binding of the CCR8-binding TCE molecule TCE1 or scFab-containing CCR8-binding TCE molecule TCE1. In contrast, CCL1 did block binding of TCE8 and TCE2 TCE molecules.

EXAMPLE: Evaluation of CCR8-binding TCE Molecule and scFab-Containing CCR8-Binding TCE Molecule Surface Hydrophobicity

[00145] To determine surface hydrophobicity of scFab-containing CCR8 binding TCE molecules, isolated and formulated CCR8-binding TCE molecule and scFab-containing CCR8-binding TCE molecule monomer adjusted to a defined protein concentration are transferred into autosampler fitting sample vials and measured on a FPLC system. A Hydrophobic Interaction Chromatography (HIC) column is equilibrated with formulation buffer and a defined volume of protein solution applied at a constant formulation buffer flow. Detection is done by OD280 nm optical absorption. Elution behavior is determined by peak shape respectively mathematically calculation of declining signal peak slope. Steeper slope / higher slope values indicate less hydrophobic interaction of the protein surface compared to constructs with more flat elution behavior and lower slope value. Following procedures essentially as described above, the following data were obtained.

[00146] TCE4 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 17-32. TCE1 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 113-128. TCE8 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 97-112. TCE2 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 49-64. TCE7 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 81-96. TCE5 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 33-48. TCE6 TCE molecule (either scFab-I2E-scFc or scFv CC x I2E x scFc) amino acid sequences are given by SEQ ID NOs: 65-80. "CC" denotes an engineered cysteine

clamp between cysteines at residue 44 of the heavy chain variable region and residue 100 of the light chain variable region of the anti-target scFv.

Table 15: HIC elution slopes of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules.

Construct	HIC Elution Slope
TCE4 scFab x I2E x scFc	50.29
TCE4 scFv CC x I2E x scFc	8.95
TCE1 scFab x I2E x scFc	50.52
TCE1 scFv CC x I2E x scFc	34.61
TCE3 scFab x I2E x scFc	44.97
TCE3 scFv CC x I2E x scFc	2.50
TCE8 scFab x I2E x scFc	31.71
TCE8 scFv CC x I2E x scFc	11.61
TCE2 scFab x I2E x scFc	53.70
TCE7 scFab x I2E x scFc	28.59
TCE7 scFv CC x I2E x scFc	18.44
TCE5 scFab x I2E x scFc	11.65
TCE5 scFv CC x I2E x scFc	9.87
TCE6 scFab x I2E x scFc	8.37
TCE6 scFv CC x I2E x scFc	8.66

[00147] These data demonstrate HIC elution peak slopes for the scFab-containing CCR8-binding TCE molecules are steeper and have higher mathematical values compared to the CCR8-binding TCE molecules having an scFv that binds CCR8.

EXAMPLE: CCR8 TCE Molecule Affinity

[00148] Cell-based affinity of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules is determined by nonlinear regression (one site - specific binding) analysis. CHO cells expressing human CCR8 (SEQ ID NO: 131), cynomolgus monkey CCR8 (SEQ ID NO: 129) or cynomolgus CCR8 (T4R; SEQ ID NO: 130) are incubated with decreasing concentrations of CCR8 bispecific constructs (50 – 3200 nM, step 1:2, 11 steps) for 16 hours at 4° C. Bound CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules are detected with Alexa Fluor 488-conjugated AffiniPure Fab Fragment Goat Anti-Human IgG (H+L). Fixed cells are stained with DRAQ5, Far-Red Fluorescent Live-Cell Permeant DNA Dye and signals are detected by fluorescence cytometry. Respective equilibrium dissociation constant (K_d) values are calculated with the one site specific binding evaluation tool of the GraphPad Prism software. Mean K_d values and affinity gaps are calculated with Microsoft Excel. Mean K_d

values are calculated from two or three independent experiments. The affinity gaps are determined by dividing the cyno Kd by the human Kd. Following procedures essentially as described above, the following data were obtained.

Table 16: Cell-based affinities of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules.

TCE Molecule	Cell based affinity hu CCR8 Mean Kd [nM]	Cell based affinity cyno CCR8 Mean Kd [nM]	Affinity gap Kdcy/Kdhu CCR8	Cell based affinity cy CCR8 (T4R) Mean Kd [nM]	Affinity gap Kdcy (T4R)/Kdhu CCR8
TCE4 scFab x I2E x scFc	11.41 ± 5.34	456.40 ± 383.53	40.00	1263.70 ± 1582.93	110.75
TCE4 scFv CC x I2E x scFc	33.24 ± 7.95	795.73 ± 901.90	23.94	267.90 ± 369.48	8.06
TCE1 scFab x I2E x scFc	0.88 ± 0.080	1.58 ± 0.38	1.80	138.50 ± 66.19	157.39
TCE1 scFv CC x I2E x scFc	0.96 ± 0.26	2.00 ± 0.55	2.08	186.21 ± 258.79	193.97
TCE3 scFab x I2E x scFc	12.84 ± 4.89	271.11 ± 219.01	21.11	5.96E+17 ± 1.03E+18	4.64E+16
TCE3 scFv CC x I2E x scFc	6.86 ± 2.47	704.62 ± 740.47	102.71	142.08 ± 110.91	20.71
TCE8 scFab x I2E x scFc	0.59 ± 0.18	442.57 ± 361.67	750.12	790.07 ± 399.5	1339.10
TCE8 scFv CC x I2E x scFc	2.20 ± 0.91	200.83 ± 157.75	91.29	305.07 ± 243.03	138.67
TCE7 scFab x I2E x scFc	0.88 ± 0.59	307.98 ± 238.88	349.98	706.15 ± 266.51	802.44
TCE7 scFv CC x I2E x scFc	1.13 ± 0.48	780.06 ± 831.30	690.32	322.55 ± 49.71	285.44
TCE5 scFab x I2E x scFc	0.83 ± 0.49	234.80 ± 94.47	282.89	197.45 ± 4.17	237.89
TCE5 scFv CC x I2E x scFc	0.63 ± 0.15	342.43 ± 253.83	543.54	275.10 ± 30.55	436.67
TCE6 scFab x I2E x scFc	0.88 ± 0.20	305.84 ± 241.93	347.55	310.10 ± 184.98	352.39
TCE6 scFv CC x I2E x scFc	0.61 ± 0.060	731.77 ± 530.08	1199.62	374.45 ± 188.59	613.85
TCE2 scFab x I2E x scFc	21.95 ± 1.76	551.74 ± 446.63	25.14	711.83 ± 710.91	32.43

[00149] These cell-based affinity measurements demonstrate that TCE molecules such as TCE1, with or without an scFab, have high affinity for both human CCR8 and cynomolgus monkey CCR8 without the T4R mutation. The affinity of the TCE1 TCE molecules was reduced against cynomolgus monkey cells having the T4R mutation.

[00150] In addition, the TCE molecule CCR8 TCE2 was not able to be produced in a sufficient amount. However, the TCE molecule having an scFab moiety (CCR8 TCE2 scFab) was able to be produced, demonstrating that the scFab moiety provides an advantage for molecule production.

EXAMPLE: Evaluation of CCR8-Binding TCE Molecule and scFab-Containing CCR8-Binding TCE Molecule Aggregation Temperature

[00151] To measure aggregation temperature, isolated and formulated CCR8-binding TCE molecule and scFab-containing CCR8-binding TCE molecule monomer adjusted to a defined

protein concentration are pipetted in duplicates into a 96-well plate and overlaid with paraffin oil. The 96-well plate is transferred to a dynamic light scattering DLS reader capable of heating the plate at a defined rate in a given temperature range. Measurement is performed from 40° C to 70° C at a defined rate of temperature increase. Detection is done by dynamic light scattering determining the hydrodynamic radius of the constructs over the temperature ramp. The temperature at begin of increase of hydrodynamic radius is defined as aggregation temperature. Following procedures essentially as described above, the following data were obtained.

Table 17. DLS aggregation temperature of CCR8 TCE molecules.

TCE Molecule	Aggregation temperature [°C]
TCE4 scFab x I2E x scFc	60.18
TCE4 scFv CC x I2E x scFc	56.83
TCE1 scFab x I2E x scFc	58.20
TCE1 scFv CC x I2E x scFc	53.60
TCE3 scFab x I2E x scFc	55.90
TCE3 scFv CC x I2E x scFc	48.01
TCE8 scFab x I2E x scFc	58.44
TCE8 scFv CC x I2E x scFc	53.82
TCE7 scFab x I2E x scFc	60.33
TCE7 scFv CC x I2E x scFc	49.92
TCE5 scFab x I2E x scFc	60.29
TCE5 scFv CC x I2E x scFc	46.25
TCE6 scFab x I2E x scFc	59.89
TCE6 scFv CC x I2E x scFc	53.27
TCE2 scFab x I2E x scFc	54.79

[00152] According to procedures essentially as described above, scFab-containing CCR8-binding TCE molecules demonstrated higher aggregation temperatures compared to the CCR8-binding TCE molecules having an scFv that binds CCR8. As described above, the TCE molecule CCR8 TCE2 was not able to be produced in a sufficient amount, whereas the TCE molecule having an scFab moiety (CCR8 TCE2 scFab) was able to be produced.

EXAMPLE: CCR8 Molecule Cytotoxicity Assay with Unstimulated Human PBMC

[00153] Human peripheral blood mononuclear cells (PBMC) are prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (buffy coats), a side product of blood banks collecting blood for transfusions. Buffy coats are supplied by a local blood bank and PBMC are prepared on the same day of blood collection. After Ficoll density

centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes are removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH_4Cl , 10 mM KHCO_3 , 100 μM EDTA). Platelets are removed via the supernatant upon centrifugation of PBMC at 100 x g. Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells and monocytes. PBMC are kept in culture at 37°C/5% CO_2 in RPMI medium (Gibco) with 10% FCS (Gibco).

[00154] For depletion of CD14^+ cells, human CD14 MicroBeads (Milteny Biotec, MACS, #130-050-201) are used. For depletion of NK cells, human CD56 MicroBeads (MACS, #130-050-401) are used. PBMC are counted and centrifuged for 10 minutes at room temperature with 300 x g. The supernatant is discarded, and the cell pellet resuspended in MACS isolation buffer [80 μL / 10^7 cells; PBS (Invitrogen, #20012-043), 0.5% (v/v) FBS (Gibco, #10270-106), 2 mM EDTA (Sigma-Aldrich, #E-6511)]. CD14 MicroBeads and CD56 MicroBeads (20 μL / 10^7 cells) are added and incubated for 15 minutes at 4 to 8° C. The cells are washed with MACS isolation buffer (1 - 2 mL/ 10^7 cells). After centrifugation (see above), supernatant is discarded, and cells are resuspended in MACS isolation buffer (500 μL / 10^8 cells). CD14/CD56 negative cells are isolated using LS Columns (Miltenyi Biotec, #130-042-401). PBMC without $\text{CD14}^+/\text{CD56}^+$ cells are cultured in RPMI complete medium i.e. RPMI1640 (Biochrom AG, #FG1215) supplemented with 10% FBS (Biochrom AG, #S0115), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37°C.

[00155] For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC₁₈ (DiO) (Molecular Probes, #V22886) is used to label human CCR8- or macaque CCR8-transfected CHO cells as target cells and distinguish them from effector cells. Briefly, cells are harvested, washed once with PBS and adjusted to 10^6 cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μL / 10^6 cells). After incubation for 3 minutes at 37° C, cells are washed twice in complete RPMI medium and the cell number adjusted to 1.25×10^5 cells/mL. The vitality of cells is determined using the NC-250 cell counter (Chemometec)

[00156] To quantify the lysis of cyno or human CCR8-transfected CHO cells in the presence of serial dilutions of CCR8-binding TCE molecule or scFab-containing CCR8-binding TCE molecule, equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o CD14^+ cells) are mixed, resulting in an E:T cell ratio of 10:1. 80 μL of this suspension is transferred to each well of a 96-well plate. 20 μL of serial dilutions of the CCR8-binding TCE molecule or scFab-containing CCR8-binding TCE molecule and a negative control (a CD3-based TCE molecule recognizing an irrelevant target antigen) or RPMI complete medium as an

additional negative control are added. The TCE molecule or scFab-containing TCE molecule-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO₂ humidified incubator. Cells are transferred to a new 96-well plate and loss of target cell membrane integrity is monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

[00157] Samples are measured by flow cytometry on an iQue Plus instrument and analyzed by Forecyt software (both from Intellicyt). Target cells are identified as DiO-positive cells. PI-negative target cells are classified as living target cells. Percentage of cytotoxicity is calculated as number of dead targets cells/number of target cells x 100. Using GraphPad Prism 5 software (Graph Pad Software, San Diego), the percentage of cytotoxicity is plotted against the corresponding TCE molecule or scFab-containing TCE molecule concentrations. Dose response curves are analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC₅₀ values are calculated.

[00158] Following procedures essentially as described above, data from a 48-hour FACS-based cytotoxicity assay of scFab-containing CCR8-binding TCE molecule with human CCR8 transfected CHO cells (clone # A2) and human CCR8 isoform A27G (SEQ ID NO: 132) transfected CHO cells as target cells and unstimulated human PBMC (CD14-/CD56-) as effector cells (E:T ratio 10:1) is shown below in Table 18.

Table 18: 48-hour FACS based cytotoxicity assay of scFab-containing CCR8-binding TCE molecules.

TCE Molecule	#A2 EC₅₀ [pM]	A27G EC₅₀ [pM]
CCR8 TCE1 scFab x I2E x scFc	14.39	15.68
CCR8 TCE8 scFab x I2E x scFc	7.26	5.93
CCR8 TCE2 scFab x I2E x scFc	290	342

[00159] These data demonstrate that binder TCE1 and TCE8 show comparable bioactivity in a one- to two-digit pM range.

[00160] Data from a 48-hour FACS-based cytotoxicity assay of bispecific constructs with Chinese cynomolgus CCR8 (SEQ ID NO: 129) transfected CHO cells (clone # G4) and the

mauritian cyno CCR8 isoform T4R (SEQ ID NO: 130) transfected CHO cells as target cells and unstimulated human PBMC (CD14-/CD56-) as effector cells (E:T ratio 10:1) is shown below in Table 19.

Table 19: 48-hour FACS based cytotoxicity assay of CCR8 scFab-containing CCR8-binding TCE molecules.

TCE Molecule	#G4 EC₅₀ [pM]	T4R EC₅₀ [pM]
CCR8 TCE1 scFab x I2E x scFc	3.91	X
CCR8 TCE8 scFab x I2E x scFc	X	X
CCR8 TCE2 scFab x I2E x scFc	X	X

[00161] These data demonstrate that only the tested TCE1 TCE molecule (having a scFab targeting CCR8) shows pM bioactivity on the chinese cynomolgus monkey CCR8 transfected CHO cell line. The other tested molecules demonstrated no activity (as depicted by “X” in the table).

[00162] Data from a 48-hour FACS-based cytotoxicity assay of CCR8-binding TCE molecule and scFab-containing CCR8-binding TCE molecule with HUT-78 (CD3+) as target cells and unstimulated human PBMC (CD14-/CD56-) as effector cells (E:T ratio 10:1) is shown below in Table 20. EC₅₀ values are determined by the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope.

Table 20: 48-hour FACS based cytotoxicity assay of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules.

TCE Molecule	EC₅₀ [pM]
CCR8 TCE4 scFab x I2E x scFc	1246
CCR8 TCE4 scFv x I2E x scFc	265
CCR8 TCE1 scFab x I2E x scFc	46.9
CCR8 TCE1 scFv x I2E x scFc	58.2
CCR8 TCE3 scFab x I2E x scFc	478

TCE Molecule	EC ₅₀ [pM]
CCR8 TCE3 scFv x I2E x scFc	28112
CCR8 TCE8 scFab x I2E x scFc	416
CCR8 TCE8 scFv x I2E x scFc	1565
CCR8 TCE5 scFab x I2E x scFc	506
CCR8 TCE5 scFv x I2E x scFc	2695
CCR8 TCE7 scFab x I2E x scFc	413
CCR8 TCE7 scFv x I2E x scFc	3269
CCR8 TCE6 scFab x I2E x scFc	576
CCR8 TCE6 scFv x I2E x scFc	354
CCR8 TCE2 scFab x I2E x scFc	3510

[00163] These data demonstrate that binder TCE1 shows high bioactivity on the endogenous cell line HUT-78 (CD3+).

EXAMPLE: Luciferase-Based Cytotoxicity Assay With Unstimulated Human PBMC

[00164] Isolation of effector cells and depletion of CD14⁺ and CD56⁺ cells are performed as described above. Target cells (described below) are harvested, spun down, and adjusted to 1.2x10⁵ cells/mL in complete RPMI medium. The vitality of cells is determined using Nucleocounter NC-250 (Chemometec) and Solution18 Dye containing Acridine Orange and DAPI (Chemometec).

[00165] To quantify the lysis of target cells in the presence of serial dilutions of CCR8-binding TCE molecules or scFab-containing CCR8-binding TCE molecules, equal volumes of luciferase-positive target cells and effector cells (i.e., PBMC w/o CD14⁺; CD56⁺ cells) are mixed, resulting in an E:T cell ratio of 10:1. 42 µL of this suspension is transferred to each well of a 384-well plate. 8 µL of serial dilutions of the corresponding CCR8-binding TCE molecule or scFab-containing CCR8-binding TCE molecule and a negative control (a CD3-based TCE molecule recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control are added. The TCE molecule cytotoxic reaction proceeds for 48 hours in a 5% CO₂ humidified incubator. Then, 25 µL substrate (Steady-Glo® Reagent, Promega) is transferred

to the 384-well plate. Only living luciferase-positive cells react to the substrate and create a luminescence signal. Samples are measured with a SPARK microplate reader (TECAN) and analyzed by Spark Control Magellan software (TECAN). Percentage of cytotoxicity was calculated as $(1 - \text{RLU}_{\text{Sample}} / \text{RLU}_{\text{Negative-Control}}) \times 100$. RLU mean relative light units. “Negative-Control” means cells without TCE molecule.

[00166] Using GraphPad Prism 7.04 software (Graph Pad Software, San Diego), the percentage of cytotoxicity is plotted against the corresponding multi-specific TCE molecule concentrations. Dose response curves are analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC_{50} values are calculated.

[00167] Following procedures essentially as described above, the following data were obtained. Data shown are of CCR8 scFab-containing CCR8-binding TCE molecules against the human CCR8 positive HUT-78 CD3 ϵ - ko cell line (parental cells and clones shown below) or the human CCR8 negative (ko) HUT-78 (CD3 ϵ +) cell line (monoplex clone 2E3; negative control) as target cells, and unstimulated human PBMC (CD14-/CD56-) as effector cells (E:T ratio 10:1).

Table 21: 48-hour Luciferase- based cytotoxicity assay of CCR8 scFab-containing CCR8-binding TCE molecules.

	CCR8 positive HUT-78				CCR8 negative HUT-78 (CD3 ϵ +) (CD3 ϵ +) Negative control
	Parental cells CCR8+ CD3 ϵ +	Monoplex clone 2B3 CD3 ϵ -	Monoplex clone 2E9 CD3 ϵ -	Monoplex clone 1F9 CD3 ϵ -	
Construct	EC_{50}				
TCE1 scFab x I2E x scFc	6.6	4.8	2.4	3.6	X
TCE8 scFab x I2E x scFc	93.1	50.7	32.6	40.1	X
TCE2 scFab x I2E x scFc	4279.4	943.3	1036.8	998.4	X

[00168] These data demonstrate that the TCE1 scFab-containing TCE molecule shows a superior bioactivity on the human CCR8 positive HUT-78 (CD3 ϵ -) cell lines compared to TCE8 and TCE2.

EXAMPLE: Bispecific Binding and Interspecies Cross-Reactivity

[00169] For confirmation of binding to human CCR8 and CD3 and to cyno CCR8 and CD3, TCE1 scFab-containing CCR8-binding TCE molecule, control TCE molecule (CD3-based TCE molecule recognizing an irrelevant target antigen), or anti-CCR8 antibodies clone L263G8 (BioLegend) and 433H (BD) are tested by flow cytometry using CHO cells transfected with human CCR8 and or macaque CCR8, the human CCR8 and CD3 positive human cell line HUT-78, the human CCR8 positive and CD3 negative HUT-78 cell line, CD3-expressing human T cell leukemia cell line HPB-all (DSMZ, Braunschweig, ACC483), and the cynomolgus CD3-expressing T cell line LnPx 4119.

[00170] Following procedures essentially as described above, the following data were obtained. A “-” indicates that no signal was detected. Data represent mean BL2 (channel in which the signal was detected) of the sample/mean BL2 of the secondary antibody control.

Table 22. Binding of TCE molecules to human and cynomolgus monkey CCR8 and CD3.

Cell line	CCR8 TCE1 scFab x I2E x scFc	Control TCE molecule	Anti CCR8 mAb (Clone L263G8)	Anti CCR8 mAb (433H)
hu CCR8+ CHO	42	1	40	-
Cy CCR8+ CHO	196	1	-	136
Cy CCR8 (T4R)+ CHO	1	1	-	106
Parental CHO	1	1	-	-
HUT-78 (CCR8+/CD3+)	62	72	9	-
HUT-78 (CCR8+/CD3-)	30	1	6	-
HPB-all	298	398	-	-
LnPx4119	33	75	-	-

[00171] These data demonstrate that the scFab-containing TCE1 TCE molecule bound human CCR8 and cynomolgus monkey CCR8 in human or cyno expressing CHO cells but did not bind the cynomolgus monkey CCR8 having a T4R mutation. These data also demonstrate that TCE1 binds CCR8 expressed on a naturally-expressing CCR8 cell line (HUT-78 CCR8+/CD3e-).

EXAMPLE: Epitope clustering of CCR8 TCE molecules

[00172] The extracellular domain of human CCR8 comprises three loops and a N-terminal peptide of 35 amino acids. For epitope mapping, the N-terminal peptide of human CCR8 (designated P₁₋₃₅ (SEQ ID NO: 133)) is divided into three consecutive segments (designated P₁₋₁₂ (SEQ ID NO: 134), P₁₃₋₂₄ (SEQ ID NO: 135), P₂₅₋₃₅ (SEQ ID NO: 136)). To cover

the adjacent N- or C-terminal regions of the consecutive segments two additional overlapping fragments (designated P_7-18 (SEQ ID NO: 137 and P_19-30 (SEQ ID NO: 138)) are made. At the C-terminal end of the full-length N-terminal peptide and all truncated N-terminal peptides of human CCR8 described above a V5 tag is fused via a G4S-linker. Following the V5 tag, chicken albumin is fused via a further G4S-linker followed by a FLAG tag, BAP (biotin acceptor protein) for in vivo biotinylation, and H3G, each fused via a SG-linker. All constructs described above are cloned into a pEFDHFR vector and transiently transfected into HEK 293 cells.

[00173] HEK 293 cells (1×10^8) are resuspended in 100 ml FreeStyle expression medium (Gibco 12338-018) and transfected with 4 ml OptiMEM (Gibco 31985-047), 100 μ l 293fectin (Invitrogen 12347-019) and 50 μ g DNA encoding either the full-length or truncated N-terminal CCR8 constructs according to the manufacturers protocol. Cells are grown in FreeStyle expression medium for 72 hours at 130 rpm in a humidified incubator with 8% CO₂. Cells are centrifuged at 1,500 rpm for 10 minutes and the supernatant is harvested. 10 ml of the supernatant of each of the transfected cells or 9 ml of HEK 293 cells as negative control are 20x concentrated with Amicon Ultra-15 tubes (UFC901008) to 500 μ L. For each of the full-length and truncated N-terminal CCR8 constructs as well as HEK 293 negative control, 18×10^6 washed streptavidin-beads (Streptavidin Microspheres, 6 μ m; Polysciences 24172-1) are resuspended in 500 μ L of the concentrated supernatant and incubated slowly shaking for one hour. Beads coupled with the respective antigen or negative control are washed and stored at 4°C overnight.

[00174] To verify expression and binding of the full-length and truncated N-terminal CCR8 constructs to streptavidin-beads, 2×10^5 beads per staining are incubated with 5 μ g/mL of an anti-FLAG antibody (clone M2, Sigma F3165/ F1804) and 5 μ g/mL of an anti-V5 antibody (clone SV5-Pk1; AbD Serotec, MCA 1360) and a 1:100 dilution of PE-labeled anti mouse Fcy secondary antibody (Jackson 115-116-071). Antigen-bound beads are incubated with three different anti-human CCR8 antibodies. Binding of two of the anti-human CCR8 antibodies (clone L263G8; BioLegend, 360602 and clone 433H; BD 747578; 5 μ g/ml each) is detected with a 1:100 dilution of a PE-labeled anti mouse Fcy secondary antibody (Jackson 115-116-071). Binding of anti-human CCR8 antibody (polyclonal; Abcam, ab140796) is detected with a 1:50 dilution of PE-labeled anti goat Fcy secondary antibody (Jackson 109-116-098).

[00175] To evaluate binding of CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules to the full-length and truncated N-terminal CCR8 constructs bound to streptavidin-beads, beads are incubated with 5 μ g/mL of the respective TCE molecule. Binding of these CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE

molecules is detected using 2 µg/ml of an anti-Histidin-antibody (clone AD1.1.10; AbD Serotec MCA 1396) and a 1:100 dilution of a PE-labeled anti mouse Fcy secondary antibody (Jackson 115-116-071). All antibodies, CCR8-binding TCE molecules, and scFab-containing CCR8-binding TCE molecules are diluted in PBS with 2% FBS and all incubations are performed at 4 °C for 45 minutes (primary antibodies) or for 30 minutes (secondary antibodies). Washes are performed using PBS with 2% FBS and the final suspension buffer prior to FACS analysis is also PBS with 2% FBS. Antibody and TCE binding is detected using an Intellicyte IQue. Changes in mean fluorescence are analyzed with an Intellicyte IQue and FlowJo. Binding to the various full-length and truncated N-terminal CCR8 constructs is reflected as a positive signal detected by flow cytometry.

[00176] Following procedures essentially as described above, expression and binding of the full-length and the various truncated N-terminal CCR8 constructs to streptavidin-beads could be verified by flow cytometry.

Table 23a. Flow Cytometry Binding Analysis of CCR8 Antibodies to Full-length or Truncated N-terminal Peptides of Human CCR8.

Sample	Peptide or controls							
	Beads (control)	HEK (control)	1-35	1-12	7-18	13-24	19-30	25-35
	Median Fluorescence of Sample/Median Fluorescence of Negative Control							
PBS	0.9	0.9	0.9	0.9	0.9	0.9	0.9	1.9
Flag	0.9	0.9	522.0	596.0	588.7	628.1	589.5	582.0
V5 Tag	0.9	0.9	952.6	1091.5	1085.9	1303.2	1016.2	1094.2
anti-CCR8 (clone L263G8)	1.2	0.9	751.2	0.9	0.9	284.8	0.9	0.9
anti-CCR8 (clone BV510)	1.8	0.9	290.2	0.9	0.9	300.3	0.9	0.9
anti-CCR8 (polyclonal)	0.9	1.0	259.7	0.9	222.6	385.6	0.9	0.9

[00177] These data demonstrate that anti-human CCR8 antibodies bound the full-length N-terminal peptide of human CCR8 P_1-35 indicating they recognized the N-terminal peptide of human CCR8. None of the antibodies showed binding to either streptavidin-beads alone or to the HEK 293 control. The anti-human CCR8 antibodies (clone L263G8 and clone 433H) showed the same binding pattern while the polyclonal anti-human CCR8 antibody showed additional binding to the overlapping fragment P_7-18.

[00178] As shown in Table 23, when binding to the truncated N-terminal peptides of CCR8 was evaluated, CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE

molecules showed two different binding patterns. For example, TCE4, TCE3 and TCE8 each bound to the truncated N-terminal peptide P_13-24. However, TCE1 bound to the truncated N-terminal peptide P_1-12.

Table 23b. Flow Cytometry Binding Analysis of CCR8 Antibodies and scFab-containing CCR8-binding TCE molecules to Full-length or Truncated N-terminal Peptides of Human CCR8.

Construct	Peptide or controls							
	Beads (control)	HEK (control)	1-35	1-12	7-18	13-24	19-30	25-35
	Median Fluorescence of Sample/Median Fluorescence of Negative Control							
PBS	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
CCR8 TCE1 scFab x I2E x scFc	1.2	1.1	470.8	413.5	1.0	1.1	1.1	1.1
CCR8 TCE1 scFv x I2E x scFc	1.1	1.0	381.8	306.2	1.0	1.1	1.1	1.0
CCR8 TCE4 scFab x I2E x scFc	1.0	1.0	1167.5	1.0	1.0	995.6	1.1	1.1
CCR8 TCE4 scFv x I2E x scFc	1.0	1.0	842.6	1.0	1.0	745.5	1.1	1.1
CCR8 TCE3 scFab x I2E x scFc	1.0	1.0	1281.6	1.0	1.0	1090.0	1.1	1.1
CCR8 TCE3 scFv x I2E x scFc	1.0	1.0	1265.9	1.1	1.0	1041.4	1.1	1.1
CCR8 TCE8 scFab x I2E x scFc	1.1	1.0	1298.3	1.0	1.0	435.6	1.1	1.1
CCR8 TCE8 scFv x I2E x scFc	1.0	1.0	1081.1	1.0	1.0	381.4	1.1	1.0
CCR8 TCE5 scFab x I2E x scFc	1.1	1.0	1370.6	1.0	1.0	500.4	1.1	1.1
CCR8 TCE5 scFv x I2E x scFc	1.1	1.0	1402.0	1.0	1.0	525.6	1.1	1.2
CCR8 TCE6 scFab x I2E x scFc	1.1	1.0	1289.8	1.0	1.0	441.6	1.0	1.1

Construct	Peptide or controls							
	Beads (control)	HEK (control)	1-35	1-12	7-18	13-24	19-30	25-35
	Median Fluorescence of Sample/Median Fluorescence of Negative Control							
CCR8 TCE6 scFv x I2E x scFc	1.5	1.1	1360.9	1.0	1.0	445.1	1.1	1.1
CCR8 TCE7 scFab x I2E x scFc	1.0	1.0	1578.8	1.0	1.0	536.0	1.1	1.1
CCR8 TCE7 scFv x I2E x scFc	1.1	1.0	1409.5	1.0	1.0	539.5	1.1	1.1
CCR8 TCE2 scFab x I2E x scFc	1.0	1.0	814.0	1.0	1.0	432.5	1.1	1.0
Negative control	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1

[00179] These data demonstrate that CCR8-binding TCE molecules and scFab-containing CCR8-binding TCE molecules bound to the full-length N-terminal CCR8 peptide P₁₋₃₅. All molecules except TCE1 bound to the truncated N-terminal CCR8 peptide P₁₃₋₂₄. Interestingly, TCE1 binds to the truncated N-terminal CCR8 peptide P₁₋₁₂, suggesting TCE1 binds a unique epitope on CCR8, which is thought to contribute to the high affinity and bioactivity of TCE1.

[00180] Additional scFvs representing a new sequence family that binds in the 1-12 amino acid epitope cluster have been generated and screened by phage display.

SEQUENCES

TCE3 CCR8 scFv and scFab HCDR1 (SEQ ID NO: 1)

SYVMH

TCE3 CCR8 scFv and scFab HCDR2 (SEQ ID NO: 2)

VISYDGSSQYYTDSVKG

TCE3 CCR8 scFv and scFab HCDR3 (SEQ ID NO: 3)

GRLATAILFDY

TCE3 CCR8 scFv and scFab LCDR1 (SEQ ID NO: 4)

KSSQSLLYSDGKTYLF

TCE3 CCR8 scFv and scFab LCDR2 (SEQ ID NO: 5)

EVSNRFS

TCE3 CCR8 scFv and scFab LCDR3 (SEQ ID NO: 6)

MQSIKLPLT

TCE3 CCR8 scFv VH (SEQ ID NO: 7)

QVQLVESGGGVVQGRSLRLSCEASGFTFSSYVMHWVRQAPGKCLEWVSVISYDGSSQ
 YYTDSVKGRFTISRDN SKNTLNLMNSLRAEDTAVYYCVRGRLATAILFDYWGQGLV
 TVSS

TCE3 CCR8 scFv VL (SEQ ID NO: 8)

EILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFWYLQRPQPPQLLIYEVS NRFS
 GVPDRFSGSGGTDFTLKISRVEAEDVGIYYCMQSIKLPLTFGCGTKVEIK

TCE3 CCR8 scFv (SEQ ID NO: 9)

QVQLVESGGGVVQGRSLRLSCEASGFTFSSYVMHWVRQAPGKCLEWVSVISYDGSSQ
 YYTDSVKGRFTISRDN SKNTLNLMNSLRAEDTAVYYCVRGRLATAILFDYWGQGLV
 TVSSGGGGQGGGGQGGGGQEILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFW
 YLQRPQPPQLLIYEVS NRFSGVPDRFSGSGGTDFTLKISRVEAEDVGIYYCMQSIKLPL
 TFGCGTKVEIK

TCE3 scFv (CCR8) x scFv (CD3) TCE (SEQ ID NO: 10)

QVQLVESGGGVVQGRSLRLSCEASGFTFSSYVMHWVRQAPGKCLEWVSVISYDGSSQ
 YYTDSVKGRFTISRDN SKNTLNLMNSLRAEDTAVYYCVRGRLATAILFDYWGQGLV
 TVSSGGGGQGGGGQGGGGQEILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFW

YLQRPGQPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQSIKLPL
TFGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPG
KGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCA
RAGNFGSSYISYWAYWGQGTLLTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPGG
TVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALT
LSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE3 scFv (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 11)

[illegible]

TCE3 CCR8 scFab VH and CH1 (SEQ ID NO: 12)

QVQLVESGGGVVQPGRSLRLSCEASGFTFSYVMHWVRQAPGKGLEWVSVISYDGSSQ
YYTDSVKGRFTISRDNKNTLNLQMNSLRAEDTAVYYCVRGRLATAILFDYWGGQTLV
TVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVTVPSSSLGTOTYICNVNHKPSNTKVKDKKVEPKSC

TCE3 CCR8 scFab VL and Ck (SEQ ID NO: 13)

EILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFWYLQRPQGPPQLLIYEVSNRFS
GVPDRFSGSGGTDFTLKISRVEADVGIYYCMQSIKLPLTFGGGTVKVEIKRTVAAPSVEI
FPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYSL
STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC

TCE3 CCR8 scFab (SEQ ID NO: 14)

QVQLVESGGGVVQPGRSLRLSCEASGFTFSSYVMHWVRQAPGKGLEWVSVISYDGS
YYTDSVKGRFTISRDNKNTLNLMNSLRAEDTAVYYCVRGLATAILFDYWGGTLV
TVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGQQGGG
GGQGGGGQGQQGGGQGGGGQGGGGQGGGGQEILMTQTPLSLSVTPGPASISCKSSQSLL
YSDGKTYLFWYLQRPGQPPLLIEVSNRFSGPSDFRFGSGSGTDFTLKISRVEAEDVGI
YYCMOSIKLPLTFGGGTKVEIKRTVAAPS VFIFPPSDEOLKSGTASVVCLLNNFYPREAK

TCE4 CCR8 scFv and scFab HCDR3 (SEQ ID NO: 19)

GRYFDWFLFDY

TCE4 CCR8 scFv and scFab LCDR1 (SEQ ID NO: 20)

KSSQSLLHSDGKTYLF

TCE4 CCR8 scFv and scFab LCDR2 (SEQ ID NO: 21)

EVSNRFS

TCE4 CCR8 scFv and scFab LCDR3 (SEQ ID NO: 22)

MQSLRLPLT

TCE4 CCR8 scFv VH (CCR8) (SEQ ID NO: 23)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LTVSS

TCE4 CCR8 scFv VL (CCR8) (SEQ ID NO: 24)

DTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFS
 GVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRLPLTFGCGTKVEIK

TCE4 CCR8 scFv (SEQ ID NO: 25)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LTVSSGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYL
 F WYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRL
 PLTFGCGTKVEIK

TCE4 scFv (CCR8) x scFv (CD3) TCE (SEQ ID NO: 26)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LTVSSGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYL
 F WYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRL
 PLTFGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY
 CARAGNFGSSYISYWAYWGQGT LTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSP
 GGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE4 CCR8 scFv (CCR8) x scFv (CD3) TCE x scFc (SEQ ID NO: 27)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGGQTL
 VTVSSGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLF
 WYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRL
 PLTFGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMN NLKTEDTAVYY
 CARAGNFGSSYISYWAYWGQGT LTVTVSSGGGGQGGGGQGGGGQGT VVTQEPSLTVSP
 GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFP
 PKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRC
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG
 NVFSCSV MHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
 QCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEV
 HNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
 GSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK

TCE4 CCR8 scFab VH and CH1 (SEQ ID NO: 28)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGGQTL
 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

TCE4 CCR8 scFab VL and Ck (SEQ ID NO: 29)

DTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFS
 GVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRLPLTFGGG TKVEIKRTVAAPSVFI
 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
 STLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

TCE4 CCR8 scFab (SEQ ID NO: 30)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGGQTL
 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ
 GGGQGGGGQGGGGQGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQS
 LLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDV
 GFYYCMQSLRLPLTFGGG TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGEC

TCE4 scFab (CCR8) x scFv (CD3) TCE (SEQ ID NO: 31)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGGQTL
 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ

GGGQGGGGQGGGGQGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQS
 LLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDV
 GFYYCMQSLRLPLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGECSSGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMNNLKTEDTAVYY
 CARAGNFGSSYISYWAYWGQGT LTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSP
 GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE4 CCR8 scFab (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 32)

QVQLVESGGGVVQGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT L
 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ
 GGGQGGGGQGGGGQGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQS
 LLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDV
 GFYYCMQSLRLPLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGECSSGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMNNLKTEDTAVYY
 CARAGNFGSSYISYWAYWGQGT LTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSP
 GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFP
 PKPKDTLMISRTPEVTCVVVDVSH EEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKS R WQQG
 NVFSCSV MHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
 QCPPELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSH EEPEVKFNWYVDGVEV
 HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
 GSFFLYSKLTV DKS R WQQGNVFSCSV MHEALHNHYTQKSLSLSPGK

TCE5 CCR8 scFv and scFab HCDR1 (SEQ ID NO: 33)

NAWMS

TCE5 CCR8 scFv and scFab HCDR2 (SEQ ID NO: 34)

RIKRKTDGGTTDYAAPVKG

TCE5 CCR8 scFv and scFab HCDR3 (SEQ ID NO: 35)

VTLV RGVIFDY

TCE5 CCR8 scFv and scFab LCDR1 (SEQ ID NO: 36)

RVSQSVSSSQA

GASSRAT

QQYGNSRT

EVQLVESGGGLVKPGGSLRLACAASGFIFSNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVTLVRGVIFDYWGQGT
LTVSS

EIVLTQFPGTLSPGESATLSCRVSQSVSSSQLAWYQQKPGQAPRLLIYGASSRATGIPD
RFSGSGSGTDFTLIISRLEPEDFAVYYCQQYGNSRTFGCGTKVEIK

EVQLVESGGGLVPGGSLRLACAAAGFIFSNAWMSWVRQAPGKCLEWVGRIKRTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVTLVRGVIFDYWGQGT
LTVTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLIISRLEPEDFAVYYCQQYGN
SRTFGC
GTKVEIK

[illegible]

EVQLVESGGGLVKPGGSLRLACAASGFIFSNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTSSGGGGGGGGGGGGGGGGGGQEIIVLTQFPGTSLSPGESATLSCRVSQSVSSSQLAWYQQ
KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLIISRLEPEDFAVYYCQQYGNRSRTFGC
GTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLLTVTSSGGGGGGGGGGGGGGGGGGQQTIVVTQEPSLTVSPGGTVTI
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGKAALTLTG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV

LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKG

TCE5 CCR8 scFab VH and CH1 (SEQ ID NO: 44)

EVQLVESGGGLVKPGGSLRLACAASGFIFSNAWMSWVRQAPGKGLEWVGRIKRKTDG
GTTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

TCE5 CCR8 scFab VL and Ck (SEQ ID NO: 45)

EIVLTQFPGTSLSPGESATLSCRVSQSVSSSQLAWYQQKPGQAPRLLIYGASSRATGIPD
RFSGSGSGTDFTLIISRLEPEDFAVYYCQQYGNSRTFGQGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLS
KADYEEKHKVYACEVTHOGLSPPVTKSFNRGEC

TCE5 CCR8 scFab (SEQ ID NO: 46)

EVQLVESGGGLVKPGGSLRLACAASGFIFSNAWMSWVRQAPGKGLEWVGRIKRTDGG
GTTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ
GGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
VSSSQLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLIISRLEPEDFAVYYC
QQYGNRSTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

TCE5 scFab (CCR8) x scFv (CD3) (SEQ ID NO: 47)

EVQLVESGGGLVKPGGSLRLACAASGFISSNAWMSWVRQAPGKGLEWVGRIKRTDGG
GTTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ
GGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
VSSQLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLIISRLEPEDFAVYYC
QQYGNRSTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGECSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYVYLLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLLTVTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
TCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLTG
VOPEDAEAYCYVLWYSNRWVFGSGTKLTVL

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSS

TCE2 CCR8 scFv VL (SEQ ID NO: 56)

DFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFWYLQKPGQPPHLLIYEVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP LTFGCGTKVEIN

TCE2 CCR8 scFv (SEQ ID NO: 57)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFW
YLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP
LTFGCGTKVEIN

TCE2 scFv (CCR8) x scFv (CD3) (SEQ ID NO: 58)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFW
YLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP
LTFGCGTKVEINSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAP
GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNMLKTEDTAVYYC
ARAGNFGSSYISYWAYWGQGTLLVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPG
GTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE2 scFv (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 59)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFW
YLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP
LTFGCGTKVEINSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAP
GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNMLKTEDTAVYYC
ARAGNFGSSYISYWAYWGQGTLLVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPG
GTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVH
NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF
FLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

TCE2 CCR8 scFab VH and CH1 (SEQ ID NO: 60)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
 KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

TCE2 scFab CCR8 VL and Ck (SEQ ID NO: 61)

DFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFWYLQKPGQPPHLLIYEVSNRFS
 GVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLPLTFGGGTKEINRTVAAPSVF
 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL
 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

TCE2 CCR8 scFab (SEQ ID NO: 62)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
 KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGGQGGGGQGGG
 GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLL
 HSDGKTYLFWYLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGL
 YYCMQTLKLPLTFGGGTKEINRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRKAV
 VQWKVDNALQSGNSQESVTEQDSKDYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
 PVTKSFNRGEC

TCE2 scFab (CCR8) x scFv (CD3) (SEQ ID NO: 63)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
 KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGGQGGGGQGGG
 GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLL
 HSDGKTYLFWYLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGL
 YYCMQTLKLPLTFGGGTKEINRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRKAV
 VQWKVDNALQSGNSQESVTEQDSKDYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
 PVTKSFNRGECSSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP
 GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYC
 ARAGNFGSSYISYWAYWGQGTLLTVSSGGGGGQGGGGQGGGGQQTIVTQEPSTVSPG
 GTVTITCGSSGTAVTSGNYPNWVQKKPGQAPRGLIGGTFLAPGTPARFSGSLSGGKAA
 LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE2 scFab (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 64)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
 KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGGQGGGGQGGG
 GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLL
 HSDGKTYLFWYLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGL
 YYCMQTLKLPLTFGGGTKEINRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRKAV
 VQWKVDNALQSGNSQESVTEQDSKDYSLSSTLTLSKADYEKHKVYACEVTHQGLSS

PVTKSFNRGECSSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP
 GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYC
 ARAGNFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQTQVVTQEPSLTVSPG
 GTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAA
 LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCSVMHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVH
 NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

TCE6 CCR8 scFv and scFab HCDR1 (SEQ ID NO: 65)
 NAWMS

TCE6 CCR8 scFv and scFab HCDR2 (SEQ ID NO: 66)
 RIKRKTDGGTTDYAAPVKG

TCE6 CCR8 scFv and scFab HCDR3 (SEQ ID NO: 67)
 VTLVRGIIFDY

TCE6 CCR8 scFv and scFab LCDR1 (SEQ ID NO: 68)
 RVSQSVSSQLA

TCE6 CCR8 scFv and scFab LCDR2 (SEQ ID NO: 69)
 GASSRAT

TCE6 CCR8 scFv and scFab LCDR3 (SEQ ID NO: 70)
 QQYGNSRT

TCE6 CCR8 scFv VH (SEQ ID NO: 71)
 EVQLVESGGGLVKPGGSLRLSCAASGFIFSNWMSWVRQAPGKCLEWVGRIKRKTDGG
 TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGIIFDYWGQGL
 VTVSS

TCE6 CCR8 scFv VL (SEQ ID NO: 72)
 EIVLTQSPGTLSPGESATLSCRVSQSVSSQLAWYQQKPGQAPRLLIYGASSRATGIPD
 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSRTFGCGTKVEIK

TCE6 CCR8 scFv (SEQ ID NO: 73)
 EVQLVESGGGLVKPGGSLRLSCAASGFIFSNWMSWVRQAPGKCLEWVGRIKRKTDGG
 TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGIIFDYWGQGL
 VTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
 KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSRTFGC
 GTKVEIK

TCE6 scFv (CCR8) x scFv (CD3) (SEQ ID NO: 74)

EVQLVESGGGLVKPGGSLRLSCAASGIFSNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGIHFDYWQGQTL
VTVSSGGGGGQGGGGQGGGGQEIVLTQSPGTLSPGESATLSCRVSQSVSSSQLAWYQQ
KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGNSTRFGC
GTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYQLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLLTVSSGGGGQGGGGQGGGGQQTVVTQEPSLTVSPGGTVTI
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLTG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE6 scFv (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 75)

[illegible]

TCE6 CCR8 scFab VH and CH1 (SEQ ID NO: 76)

EVQLVESGGGLVKPGGSLRLSCAASGIFISNAWMSWVRQAPGKGLEWVGRIKRTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGIIFDYWGQGT
LTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVTVPSSSLGTOTYICNVNHKPSNTKVDKKVEPKSC

TCE6 CCR8 scFab VL and Ck (SEO ID NO: 77)

EIVLTQSPGTLSPGESATLS $\overline{\text{CRV}}\text{SQSVSSQLAWYQQKPGQAPRLLIY}$ GASSRATGIPD
 RFGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSRTFGQGTKVEIKRTVAAPSVFIFPPSD
 EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLT
 SKADYEEKHKVYACEVTHOGLSSPVTKSFNRGEC

TCE6 CCR8 scFab (SEQ ID NO: 78)

[illegible]

RASQSVSSQLA

GASSRAT

QQYGNSRT

EVQLVESGGDLVKPGGSLRLSCAASGIFISNAWMSWVRQAPGKCLEWVGRIKRTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVSS

EIVLTQSPGTL^{SL}SPGESATL^{SC}RASQSVSSQLAWYQQKPGQT^{PR}LLIYGASSRATGIPD
R^{FS}GS^{GS}GTDF^{TL}TISRLEPEDFAVYYCQQY^{GN}SR^{TF}GC^{GT}KVEIK

EVQLVESGGDLVKPGGSLRLSCAASGFI¹SN²AWMSWVRQAPGKCLEWVGRIK³RKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVT⁴LV⁵RGVIFDYWGQGT
LTVTSSGGGGGQGGGGQGGGGQEIVLTQSPGTL⁶SLSPGESATLSCRASQSVSSSSQLAWYQQ
KPGQTPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSRTFGC
GTKVEIK

EVQLVESGGDLVKPGGSLRLSCAASGIFSNAWMSWVRQAPGKCLEWVGRIKRTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTSSGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGESATLSCRASQSVSSSQLAWYQQ
KPGQTPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSRTFGC
GTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLVTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGT VTI
TCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLTG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

[illegible]

EVQLVESGGDLVKPGGSLRLSCAASGFISSNAWMWVRQAPGKGLEWVGRIKRKTDGG
TTDYAAPVKGRTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVTLVRGVIFDYGQGGL
VTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDDKKVEPKSCGGGGQGGGGQG
GGGQGGGGQGGGGQGGGGQGGGGQGGGGQEIVLTQSPGTLSPGESATLSCRASQSV
SSSOLAWYQQKPGOTPRLLIYGASSRATGIPDRFGSGSGSGTDFTLTISRLEPEDFAVYYCO

QYGNsrTFGQgTKvEIKrtVAAPsvFIFPPsDEQLKSGTASvVCLLNNfYPReAKvQWk
VDNALQSGNSQESvTEQDSKdstYSLsSTLTLsKADyEKHKvYACEvTHQGLsSPvTKS
FNRGECSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLE
WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGN
FGSSYISYWAYWGQGLTVTVSSGGGGGQGGGGQGGGGQQTvVTQEPsLTVSPGGTVtIT
CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGtKFLAPGTPARfSGSLsSGKAALTLsGV
QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCpPCAPeLLGGPSvFLFPpKPKDTL
MISRTPEVTCVVVDVShEEpEVKfNWyVDGVEVhNAKTKPCEEQYgSTYRCvSVLTvL
HQDWLNgKEYKCKvSNKALPAPIEKtISKAKGQPREPQvYTLPPSREEMTKNqVSLtCL
VKGFyPSDIaVEWESNgQPENNYKtTPPVLDSDGSFFLYSKLTVDKSRWQQGNvFSCSV
MHEALHNHYtQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCPpCPA
PELLGGPSvFLFPpKPKDTLMISRTPEVTCVVVDVShEEpEVKfNWyVDGVEVhNAKTK
PCEEQYgSTYRCvSVLTvLHQDWLNgKEYKCKvSNKALPAPIEKtISKAKGQPREPQvY
TLPPSREEMTKNqVSLtCLVKGFyPSDIaVEWESNgQPENNYKtTPPVLDSDGSFFLYSK
LTVDKSRWQQGNvFSCSVMHEALHNHYtQKSLSLSPGK

TCE8 CCR8 scFv and scFab HCDR1 (SEQ ID NO: 97)

NAWMS

TCE8 CCR8 scFv and scFab HCDR2 (SEQ ID NO: 98)

RIKRRTDGGTTDYAAPVKD

TCE8 CCR8 scFv and scFab HCDR3 (SEQ ID NO: 99)

VTMVRGVIADY

TCE8 CCR8 scFv and scFab LCDR1 (SEQ ID NO: 100)

RASQSVSSGSLA

TCE8 CCR8 scFv and scFab LCDR2 (SEQ ID NO: 101)

GASSRAT

TCE8 CCR8 scFv and scFab LCDR3 (SEQ ID NO: 102)

QQYGSSRT

TCE8 CCR8 scFv VH (SEQ ID NO: 103)

EVQLVESGGGLVKPGGSLRLSCAASGFI¹FSNAWMSWVRQAPGKCLEWVARIKRRTDGG
TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT²VTMVRGVIADYWGQGT
LVTYSS

TCE8 CCR8 scFv VL (SEQ ID NO: 104)

EIVLTQSPGTL^{SL}SPGERATL^{SCR}ASQSVSSGSLAWYQQKLGQAPRLLIYGASSRATGIPD
RFGSGSGSDTFTLT^{IS}SLEPEDFAVYYCOOYGSSRTFGCGTKVELK

TCE8 CCR8 scFv (SEQ ID NO: 105)

EVQLVESGGGLVKPGGSLRLSCAASGFISSNAWMSWVRQAPGKCLEWVARIKRRTDGG
TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVMVRGVIADYWGQGT
LVTVSSGGGGQGGGGQGGGGQEIVLTQSPGTLSPGERATLSCRASQSVSSGSLAWYQ
QKLGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISPLEPEDIAVYYCQYGGSSRTFG
CGTKVELK

TCE8 scFv (CCR8) x scFv (CD3) (SEQ ID NO: 106)

EVQLVESGGGLVKPGGSLRLSCAASGFIFSNAMWSWVRQAPGKCLEWVARIKRRTDGG
 TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVMVRGVIADYWGQGT
 LVTVSSGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGERATLSCRASQSVSSGSLAWYQ
 QKLGGAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTSSLEPEDFAVYYCQQYGSSRTFG
 CGTKVELKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
 LEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARA
 GNFGSSYISYWAYWGQGT LVTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGTV
 TITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLS
 GVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

TCE8 scFv (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 107)

EVQLVESGGGLVKPGGSLRLSCAASGFIFSNAMWSWVRQAPGKCLEWVARIKRRTDGG
 TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVMVRGVIADYWGQGT
 LVTVSSGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGERATLSCRASQSVSSGSLAWYQ
 QKLGGAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTSSLEPEDFAVYYCQQYGSSRTFG
 CGTKVELKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
 LEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARA
 GNFGSSYISYWAYWGQGT LVTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGTV
 TITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLS
 GVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFPPKPKD
 TLMISRTPEVTCVVVDVSHREEPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLT
 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
 CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC
 SVMHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCP
 PPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHREEPEVKFNWYVDGVEVHNAK
 TKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY
 SKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK

TCE8 CCR8 scFab VH and CH1 (SEQ ID NO: 108)

EVQLVESGGGLVKPGGSLRLSCAASGFIFSNAMWSWVRQAPGKGLEWVARIKRRTDGG
 TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVMVRGVIADYWGQGT
 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKEPKSC

TCE8 CCR8 scFab VL and Cκ (SEQ ID NO: 109)

EIVLTQSPGTLSPGERATLSCRASQSVSSGSLAWYQQKLGGAPRLLIYGASSRATGIPD
 RFSGSGSGTDFTLTSSLEPEDFAVYYCQQYGSSRTFGQGTKVELKRTVAAPSVFIFPPSD
 EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT
 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

TCE8 CCR8 scFab (SEQ ID NO: 110)

EVQLVESGGGLVKPGGSLRLSCAASGFIFSNAMWSWVRQAPGKGLEWVARIKRRTDGG
 TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVMVRGVIADYWGQGT
 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCGGGGQGGGGQ
 GGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGERATLSCRASQ
 SVSSGSLAWYQQKLGGAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTSSLEPEDFAVYYC
 QQYGSSRTFGQGTKVELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW

KSSQSVLYSSNNKNYLA

WASTRES

QQYYSIPIT

EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMVTVSS

EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQPGQSPKLLISWASTR
ESGVDPDRFSGSGSGTDFLTINSLQAEDVAVYYCQQYYISIPITFGCGTKVEIK

EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSG
GGGQGGGGQGGGGQEI VMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQ
KPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFG
CGTKVEIK

EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVSSG
GGGQGGGGQGGGGQEI VMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQ
KPGQSPKLLISWASTRESGV PDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYY SIPITFG
CGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMNNLKTEDTAVYYCARA
GNFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQTVVTQEPSLTVSPGGTV
TITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLS
GVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVSSG
GGGQGGGGQGGGGQEI VMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQ
KPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYY SIPITFG
CGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMNNLKTEDTAVYYCARA
GNFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGTV
TITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLS
GVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSKLTVDKSRWQQGNV FSC
SYMHEALHNHYTOKSLSLSPGKGGGGGOGGGGOGGGGOGGGGOGGGGOGGGGOGGGGOCPPC

EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKGLEWVGRISKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGGGQ
GGGQGGGGQGGGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSN
NKNYLAWYHOKPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLOAEDVAVYY

Cynomolgus monkey chinese origin CCR8 (SEQ ID NO: 129)

Cynomolgus monkey Mauritian origin T4R CCR8 (SEQ ID NO: 130)

Human CCR8 (SEQ ID NO: 131)

Human A27G CCR8 (SEQ ID NO: 132)

CCR8 P 1-35 peptide (SEQ ID NO: 133)

MDYTLDSVTTVTDYYYPDIFSSPCDAELIOTNGK

CCR8 P_1-12 peptide (SEQ ID NO: 134)

MDYTLDLSTTV

CCR8 P_13-24 peptide (SEQ ID NO: 135)

TDYYYPDIFSSP

CCR8 P_25-35 peptide (SEQ ID NO: 136)

CDAELIQTNGK

CCR8 P_7-18 peptide (SEQ ID NO: 137)

LSVTTVTDYYYP

CCR8 P_19-30 peptide (SEQ ID NO: 138)

DIFSSPCDAELI

Antibody 20C1.009 LCDR1 (SEQ ID NO: 139)

RASQGISNWLA

Antibody 20C1.009 LCDR2 (SEQ ID NO: 140)

AASSLQS

Antibody 20C1.009 LCDR3 (SEQ ID NO: 141)

QQAESFPHT

Antibody 20C1.009 HCDR1 (SEQ ID NO: 142)

SYDMS

Antibody 20C1.009 HCDR2 (SEQ ID NO: 143)

LISGGGSQTYAESVKG

Antibody 20C1.009 HCDR3 (SEQ ID NO: 144)

PSGHYFYAMDV

Antibody 20C1.009 VL (SEQ ID NO: 145)DIQMTQSPSSVSASVGDRVITICRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFGSGSGTDFLTITSLQPEDFATYYCQQAESFPHTFGGGTKVEIK**Antibody 20C1.009 VH (SEQ ID NO: 146)**EVQLLESGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSQTY
YAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITV
VSS**Antibody 20C1.009 LC (SEQ ID NO: 147)**DIQMTQSPSSVSASVGDRVITICRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFGSGSGTDFLTITSLQPEDFATYYCQQAESFPHTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
L SKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Antibody 20C1.009 HC (SEQ ID NO: 148)

EVQLLESGLLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSQTY
 YAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQTTVT
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
 EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Antibody 20A2.3 LCDR1 (SEQ ID NO: 149)

SGDKLGDKYAS

Antibody 20A2.3 LCDR2 (SEQ ID NO: 150)

QDRKRPS

Antibody 20A2.3 LCDR3 (SEQ ID NO: 151)

QAFESSTEV

Antibody 20A2.3 HCDR1 (SEQ ID NO: 152)

NYGMH

Antibody 20A2.3 HCDR2 (SEQ ID NO: 153)

LIWYDASKKYAESVKG

Antibody 20A2.3 HCDR3 (SEQ ID NO: 154)

DPSSLTGSTGYYGMDV

Antibody 20A2.3 VL (SEQ ID NO: 155)

SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGIPER
 FSGSNSGNTATLTISGTQAMDEADYYCQAFESSTEVFGGGTKLTVL

Antibody 20A2.3 VH (SEQ ID NO: 156)

QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVALIWYDASK
 KYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCARDPSSLTGSTGYYGMDVW
 GQTTVTVSS

Antibody 20A2.3 LC (SEQ ID NO: 157)

SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGIPER
 FSGSNSGNTATLTISGTQAMDEADYYCQAFESSTEVFGGGTKLTVLGQPKAAPSVTLFPP
 SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS
 LTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS

Antibody 20A2.3 HC (SEQ ID NO: 158)

QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVALIWYDASK
 KYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCARDPSSLTGSTGYYGMDVW
 GQTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
 HTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
 AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE

PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Antibody 20D4.6 LCDR1 (SEQ ID NO: 159)
SGDALPKKYAY

Antibody 20D4.6 LCDR2 (SEQ ID NO: 160)
EDAKRPS

Antibody 20D4.6 LCDR3 (SEQ ID NO: 161)
YSTDASGNHRV

Antibody 20D4.6 HCDR1 (SEQ ID NO: 162)
DYSMS

Antibody 20D4.6 HCDR2 (SEQ ID NO: 163)
GINWNGGRTRYADAVKG

Antibody 20D4.6 HCDR3 (SEQ ID NO: 164)
EFNNFESNWFD

Antibody 20D4.6 VL (SEQ ID NO: 165)
SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKPGQAPVLVISED AKRPSGIPER
FSGSSSGTMATLTISGAQVEADYYCYSTDASGNHRVFSGGGLTKLTVL

Antibody 20D4.6 VH (SEQ ID NO: 166)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNGGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFD PWGQGT
LTVVSS

Antibody 20D4.6 LC (SEQ ID NO: 167)
SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKPGQAPVLVISED AKRPSGIPER
FSGSSSGTMATLTISGAQVEADYYCYSTDASGNHRVFSGGGLTKLTVLGQPKAAPSVTL
FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAASS
YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

Antibody 20D4.6 HC (SEQ ID NO: 168)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNGGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFD PWGQGT
LTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Antibody 20D4.17 LCDR1 (SEQ ID NO: 169)
SGDALPKKYAY

Antibody 20D4.17 LCDR2 (SEQ ID NO: 170)
EDAKRPS

Antibody 20D4.17 LCDR3 (SEQ ID NO: 171)
YSTDASGNHRV

Antibody 20D4.17 HCDR1 (SEQ ID NO: 172)
DYSMS

Antibody 20D4.17 HCDR2 (SEQ ID NO: 173)
GINWNAGRTRYADAVKG

Antibody 20D4.17 HCDR3 (SEQ ID NO: 174)
EFNNFESNWFD

Antibody 20D4.17 VL (SEQ ID NO: 175)
SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKPGQAPVLVISED AKRPSGIPER
FSGSSSGTMATLTISGAQVEADYYCYSTDASGNHRVFGGGTKLTVL

Antibody 20D4.17 VH (SEQ ID NO: 176)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNAGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFD PWGQGT
LTVSS

Antibody 20D4.17 LC (SEQ ID NO: 177)
SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKPGQAPVLVISED AKRPSGIPER
FSGSSSGTMATLTISGAQVEADYYCYSTDASGNHRVFGGGTKLTVLGQPKAAPSVTL
FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASS
YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

Antibody 20D4.17 HC (SEQ ID NO: 178)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNAGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFD PWGQGT
LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK
PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Antibody 20C1.006 LCDR1 (SEQ ID NO: 179)
RASQGISNWL

Antibody 20C1.006 LCDR2 (SEQ ID NO: 180)
AASSLQS

Antibody 20C1.006 LCDR3 (SEQ ID NO: 181)
QQAESFPH

Antibody 20C1.006 HCDR1 (SEQ ID NO: 182)

SYDMS

Antibody 20C1.006 HCDR2 (SEQ ID NO: 183)

LISGGGSNTYYAESVKG

Antibody 20C1.006 HCDR3 (SEQ ID NO: 184)

PSGHYFYAMDV

Antibody 20C1.006 VL (SEQ ID NO: 185)

DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFSGSGSGTDFLTISLQPEDFATYYCQQAESFPHTFGGGTKVEIK

Antibody 20C1.006 VH (SEQ ID NO: 186)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSNTY
YAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITV
VSS

Antibody 20C1.006 LC (SEQ ID NO: 187)

DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFSGSGSGTDFLTISLQPEDFATYYCQQAESFPHTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT
SKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Antibody 20C1.006 HC (SEQ ID NO: 188)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSNTY
YAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITV
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

G4S linker (SEQ ID NO: 189)

GGGGS

(G4S)₄ linker (SEQ ID NO: 190)

GGGGS GGGGS GGGGS GGGGS

I2C - HCDR1 (SEQ ID NO: 191)

KYAMN

I2C - HCDR2 (SEQ ID NO: 192)

RIRSKYNNYATYYADSVKD

I2C - HCDR3 (SEQ ID NO: 193)

HGNFGNSYISYWAY

I2C - LCDR1 (SEQ ID NO: 194)

GSSTGAVTSGNYPN

I2C – LCDR2 (SEQ ID NO: 195)

GTKFLAP

I2C - LCDR3 (SEQ ID NO: 196)

VLWYSNRWV

I2C – VH (SEQ ID NO: 197)

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN
YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAY
WGQGTLLTVSS

I2C – VL (SEQ ID NO: 198)

QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPG
TPARFSGSLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

I2E - HCDR1 (SEQ ID NO: 199)

KYAIN

I2E – HCDR2 (SEQ ID NO: 200)

RIRSKYNNYATYYADAVKD

I2E - HCDR3 (SEQ ID NO: 201)

AGNFGSSYISYWAY

I2E - LCDR1 (SEQ ID NO: 202)

GSSTGAVTSGNYPN

I2E - LCDR2 (SEQ ID NO: 203)

GTKFLAP

I2E - LCDR3 (SEQ ID NO: 204)

VLWYSNRWV

I2E – VH (SEQ ID NO: 205)

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY
ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYW
GQGTLLTVSS

I2E – VL (SEQ ID NO: 206)

QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGT
PARFSGSLSGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

G4Q Linker (SEQ ID NO: 207)

GGGGQ

(G4Q)4 Linker (SEQ ID NO: 208)

GGGGQGGGGQGGGGQGGGGQ

mCCR8 (SEQ ID NO: 209)

MDYTMENPNTMTDYYPDFFTAPCDAEFLLRGSMLYLAILYCVLFVLGLLGNSLVILVLV
 GCKKLRSITDIYLLNLAASDLLFVLSIPFQTHNLLDQWVFGTAMCKVVSGLYYIGFFSSM
 FFITLMSVDRYLAIVHAVYAIKVRTASVGTALSLTVWLA AVTATIPLMVFYQVASEDGM
 LQCFQFYEEQSLRWKLFTHFEINALGLLLFAILFCYVRILQQLRGCLNHNRTRAIKLVL
 TVVIVSLLFWVPFNV ALFLTSLHDLHILDGCATRQRLALAIHVTEVISFTHCCVNPVIYAFI
 GEKFKKHLMDVVFQKSCSHIFLYLGRQMPVGALERQLSSNQSSSHSSTLDDIL

Rat CCR8 (SEQ ID NO: 210)

MDYTLEPNVTMTDYYPDFFTTPCDTELLLRGGTLYLAVLYCILFVLGLLGNSLVILVLVA
 CKKLRSITDVYLLNLAASDLLFVLSIPFQTHNLLDQWVFGTVMCKVVSGLYYIGFFSSML
 FITLMSVDRYLAVVHPVHAIKVRTARVGTALSLAVWLA AIAATVPLMVFYQVSSSEDGM
 LQCFQLYDEQSLRWKLFTHFEVNALGLLLFAILFCYVRILQQLRGCLNHNRTRAIKLV
 LTIVVVSLLFWVPFNVVLFLTSLHDMHILEGCATRQRLALATHVTEVISFMHCCVNPVIY
 AFIGEKFKKHLVDVVFQKSCSHIFLYVGRQMPVGALERQLSSNQSSSHSSTLDYIL

hCCR4 (SEQ ID NO: 211)

MNPTDIADTTLDESIYSNYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVL
 VLFKYKRLRSMTDVYLLNLAISDLLFVFSLPFWGYAAADQWVFGGLGCKMISWMYLVG
 FYSGIFFVMLMSIDRYLAIVHAVFSLRARTLTYGVTSLATWSVAVFASLPGLFSTCYTE
 RNHTYCKTKYSLNSTTWKVLSSLEINILGLVIPLGIMLFCYSMIIRTLQHCKNEKKNKAV
 KMIFAVVVLFLGFWTPYNIVLFLETLVELEVLQDCTFERYLDYAIQATETLAFVHCCLNPI
 IYFFLGEKFRKYILQLFKTCRGLFVLCQYCGLLQIYSADTPSSSYTQSTMDHDLHDAL

Antibody 20C1.009 HC without C-terminal lysine (SEQ ID NO: 212)

EVQLLESGLLVQPGGSLRLSCAASGFTSSYDMSWVRQAPGKGLEWVSLISGGGSQTY
 YAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTIVT
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
 LGGPSTVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
 EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Leader sequence (SEQ ID NO: 213)

MDMRVPAQLL GLLLLWLRGA RC

DNA encoding leader sequence of SEQ ID NO: 213 (SEQ ID NO: 214)

atggacatga gaggctctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc agatgc.

Leader sequence (SEQ ID NO: 215)

MAWALLLLTL LTQGTGSWA

DNA encoding leader sequence of SEQ ID NO: 215 (SEQ ID NO: 216)

atggcctggg ctctgctgct cctcaccctc ctactcagg gcacagggtc ctgggcc

Table 24. TCE molecule sequences.

SEQ ID NO:	Designation	Sequence
CCR8 TCE 1.1 (CC EI GQ x I2E GQ x scFcmo delGK)		
217	HCDR1	NARMG
218	HCDR2	RIKSKTEGGTRDYAAPVKG
219	HCDR3	YSGV
220	LCDR1	KSSQSVLYSSNNKNYLA
221	LCDR2	WASTRES
222	LCDR3	QQYYSIPIT
223	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSS
224	VL	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA YHQPQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFGCGTKVEIK
225	SCFV	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSGGGGGQ GGGGQGGGGQEIIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLA YHQPQSPKLLISWASTRESGVPDRFSGS GSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFGCGTKVEIK
226	TCE 1.1	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSGGGGGQ GGGGQGGGGQEIIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLA YHQPQSPKLLISWASTRESGVPDRFSGS GSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFGCGTKVEIK SGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTVYLQMNSLKTEDTAVYYCARAGNFGSSYISYW AYWGQGLTVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLT VSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGG TKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVL WYSNRWVFGSGTKLTVL
227	TCE 1.1 HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSGGGGGQ GGGGQGGGGQEIIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLA YHQPQSPKLLISWASTRESGVPDRFSGS GSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFGCGTKVEIK SGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTVYLQMNSLKTEDTAVYYCARAGNFGSSYISYW AYWGQGLTVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLT VSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGG TKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVL WYSNRWVFGSGTKLTVLGGGGCPPCPAPPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSHREEPEVKFNWYVDGVEVH

		NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGQNVFSCSVMEALHNHYTQKSLSLSPGQGGQGGGGQGGGGQGGGGQGGGGQGGGGQCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGQNVFSCSVMEALHNHYTQKSLSLSPGK
CCR8 TCE 1.2 (CC EI GQ x I2E GQ x scFmod delGK_YTE)		
228	HCDR1	NARMG
229	HCDR2	RIKSKTEGGTRDYAAPVKG
230	HCDR3	YSGV
231	LCDR1	KSSQSVLYSSNNKNYLA
232	LCDR2	WASTRES
233	LCDR3	QQYYSIPIT
234	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSS
235	VL	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGSGGTDFLTINSLQAEDVAVYYCQQYYSIPITFGCGTKVEIK
236	SCFV	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGSGGTDFLTINSLQAEDVAVYYCQQYYSIPITFGCGTKVEIK
237	TCE 1.2	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGSGGTDFLTINSLQAEDVAVYYCQQYYSIPITFGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLYQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTLLTVSSGGGGQGGGGQGGGGQQT VVTQEPLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
238	TCE 1.2 HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGSGGTDFLTINSLQAEDVAVYYCQQYYSIPITFGCGTKVEIK

[illegible]

		REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
248	TCE 1.3	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSQAEDVAVYYCQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSSGGGGQE VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNSLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT VTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYCYLWYSNRWVF GSGTKLTVL
249	TCE 1.3 HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSQAEDVAVYYCQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSSGGGGQE VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNSLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT VTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYCYLWYSNRWVF GSGTKLTVLGGGGCPPCPAPPELLGGPSVFLFPPKPKDTLYIT REPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYF SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGQGGGG QGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG PKPKDTLYITREPEVTCVVVDVSHEEPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL

		YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
CCR8 TCE 1.4 (EI scFab x I2E GQ x scFmod delGK)		
250	HCDR1	NARMG
251	HCDR2	RIKSKTEGGTRDYAAPVKG
252	HCDR3	YSGV
253	LCDR1	KSSQSVLYSSNNKNYLA
254	LCDR2	WASTRES
255	LCDR3	QQYYSIPIT
256	VH-CH1	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSC
257	VL-Ck	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAW YHQKPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFGGGTKVEIKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
258	SCFAB	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
259	TCE 1.4	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT LTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG

		TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGT PARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GSGTKLTVL
260	TCE 1.4 HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGQE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT LTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGG TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGT PARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GSGTKLTVLGGGGCPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGQGGGG QGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGG PKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K

Table 25. MAGE-B2 (“MA”) and CD20xCD22 TCE molecule sequences.

MA 03-D8 AS CC scFv x I2C x scFc		
261	HCDR1	SHAMS
262	HCDR2	TISGSGGGTYAAASVKG
263	HCDR3	GKGVHLGFDY
264	LCDR1	GGNNIGSKSVH
265	LCDR2	DDNDRPS
266	LCDR3	QVWDYRTLWDV

267	VH	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSS
268	VL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADY YCQVWDYRTL DWVF GCGTKLTVL
269	SCFV	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIISR VEAGDEADY YCQVWDYRTL DWVF GCGTKLTVL
270	BISPECIFIC MOL.	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIISR VEAGDEADY YCQVWDYRTL DWVF GCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
271	BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIISR VEAGDEADY YCQVWDYRTL DWVF GCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
MA 03-D8 AS scFab x I2C x scFc		

272	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
273	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADY YCQVWDYRTLDWVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPPSKQ SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
274	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS RVEAGDEADYYCQVWDYRTLDWVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECS
275	scFab- BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS RVEAGDEADYYCQVWDYRTLDWVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTLLTVSSGGGGSGGGGSGGGGSQTIVV TQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
276	scFab-BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS

		RVEAGDEADYYCQVWDYRTLWDVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLSC AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYCKVSNKALPAIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLS LSPGK
MA 98-C7 CC scFv x I2C x scFc		
277	HCDR1	SHAMS
278	HCDR2	SISGSGGGTYAASVKG
279	HCDR3	GKGVHLGFDY
280	LCDR1	GGNNIGSKSVH
281	LCDR2	DDNDRPS
282	LCDR3	QVWDYSPLRHV
283	VH	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSS
284	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYSPLRHVFGCGTKLTVL
285	SCFV	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSPLRHVFGCGTKLTVL
286	BISPECIFIC MOL.	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSPLRHVFGCGTKLTVLSSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ

		MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
287	BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKG VHLGFDYWGQGLTVTVSSGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSPLRHVFGCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
MA 98-C7 scFab x I2C x scFc		
288	VH-CH1	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKG VHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
289	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYSPLRHVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
290	scFab	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKG VHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVLGQPKAAP

		SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECS
291	scFab- BISPECIFIC MOL.	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSSISGSGGGTYAAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSG VHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGT LVTVSSGGGSGGGGSGGGGSQTVV TQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAAL TSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
292	scFab-BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSSISGSGGGTYAAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSG VHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGT LVTVSSGGGSGGGGSGGGGSQTVV TQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAAL TSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD

		DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
MA 09-E2 CC scFv x I2C x scFc		
293	HCDR1	NAWMS
294	HCDR2	RIKSKTYGGTTDYAAPVKG
295	HCDR3	PSYSGSYNYFSVMDV
296	LCDR1	RTSQSISSYLN
297	LCDR2	AASSLQG
298	LCDR3	QQSYSSPFT
299	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSS
300	VL	DIQMTQSPSSLSASVGDRVITITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFLTITISLQPEDFATYYC QQSYSSPFTFGCGTKVEIK
301	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFLTITISLQPEDFATYYCQQSYSSPFTFGCGTKVEIK
302	BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFLTITISLQPEDFATYYCQQSYSSPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVT SSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
303	BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFLTITISLQPEDFATYYCQQSYSSPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVT SSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPELPGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP

		REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGG GGGSGGGSGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
MA 09-E2 scFab x I2C x scFc		
304	VH-CH1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC
305	VL-CL	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQSYSSPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
306	scFab	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGSGGGSGGGSGG GGGSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPFTFGPGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
307	scFab- BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGSGGGSGGGSGG GGGSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPFTFGPGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGS LKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGG QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP

		GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
308	scFab-BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISLQPEDFATYYCQQSYSSPFTFGPGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGS QTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVLGGGGDKHTCPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQ KSLSLSPGK
MA 03-E11 AS CC scFv x I2C x scFc		
309	HCDR1	SHAMS
310	HCDR2	AISGSGGGTYNAASVKG
311	HCDR3	GKGVHLGFDY
312	LCDR1	GGNNIGSKSVH
313	LCDR2	DDNDRPS
314	LCDR3	QVWDYYSNRAV
315	VH	EVQLLES GGGLVQPGGSLRLSCAASGFTFS SHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSS
316	VL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYYSNRAVFGCGTKLTVL
317	SCFV	EVQLLES GGGLVQPGGSLRLSCAASGFTFS SHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSGGGSGG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH

		WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYYSNRAVFGCGTKLTVL
318	BISPECIFIC MOL.	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYYSNRAVFGCGTKLTVLSSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
319	BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYYSNRAVFGCGTKLTVLSSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
MA 03-E11 AS scFab x I2C x scFc		
320	VH-CH1	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
321	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYYSNRAVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ

		SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
322	scFab	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECS
323	scFab- BISPECIFIC MOL.	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
324	scFab-BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLG

		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGIFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKTHCPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGIFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
MA 09-F12 CC scFv x I2C x scFc		
325	HCDR1	THKMGVD
326	HCDR2	LIYWNDKRYSPSLQS
327	HCDR3	RRYNWNYENWFD
328	LCDR1	QASQDISNYLN
329	LCDR2	AASSLQS
330	LCDR3	QQSYYYPTL
331	VH	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSS
332	VL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATY YCQQSYYYPTLFGCGTKVEIK
333	SCFV	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGCGTKVEIK
334	BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGCGTKVEIKSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGAALTLGVQPEDEAEYCYVWYSNRWVFGGGTKLTVL
335	BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGCGTKVEIKSGGGGSEV

		QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
CCR8 TCE		
336	CCR8 TCE LCDRI consensus	KSSQSVLYSSNNX ₁ NYLA; X ₁ is K or R
MA 09-F12 scFab x I2C x scFc		
337	VH-CH1	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSC
338	VL-CL	DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATY YCQQSYYYPTLFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
339	scFab	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGS GGSGGGSDIQMTQSPSSLSASVGDRTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISSLQPEDFATYYCQQSYYYPTLFGPGTKVEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFYPPREAKVQWKVDNALQSGN SQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
340	scFab- BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSAS

		TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISSLQPEDFATYYCQQSYYYPTLFGPGTKVEIKRTVAAPSVE IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGTLLTVVSSGGGSGGGGSGGGGSGTQVVT QEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
341	scFab-BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVLTMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGTLLTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISSLQPEDFATYYCQQSYYYPTLFGPGTKVEIKRTVAAPSVE IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGTLLTVVSSGGGSGGGGSGGGGSGTQVVT QEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
CCR8 TCE		
342	VL consensus	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNX₁NYLAWY X₂QKPGQX₃PKLLISWASTRESGVDRFSGSGSGTDFTLTINSLSL QAEDVAVYYCQQYYISIPITFGGGTKVEIKR, wherein X₁ is K or R, X₂ is H or Q, and/or X₃ is S or P

[illegible]

		GGGGS DKTH TCPC PAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
MA 09-G10 scFab x I2C x scFc		
354	VH-CH1	QITLKESGPTLVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
355	VL-CL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYFNWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQSYITPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
356	scFab	QITLKESGPTLVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQQSYITPFTFGPGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
357	scFab- BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQQSYITPFTFGPGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGGGSGTQVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
358	scFab-BiTE HLE	QITLKESGPTLVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN

		MDPVDTATYYCAYRRYNWNYENWFDPPWGQGTLLTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYITPFTFGPGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGTLLTVSSGGGSGGGGSGGGGSGTQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGKTLTVLGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS SLSPGK
MA 09-H7 CC scFv x I2C x scFc		
359	HCDR1	THKMGVD
360	HCDR2	LIYWNDKRYSPSLQS
361	HCDR3	RRYNWNYENWFDPP
362	LCDR1	QASQDISNYLN
363	LCDR2	AASSLQS
364	LCDR3	QQSYFPVVE
365	VH	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDTATYYCAYRRYNWNYENWFDPPWGQGTLLTVSS
366	VL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYY CQQSYFPVVEFGCGTKVEIK
367	SCFV	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDTATYYCAYRRYNWNYENWFDPPWGQGTLLTVSSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGCGTKVEIK
368	BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT

		NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKG LEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGGSGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
369	BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKG LEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGGSGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
MA 09-H7 scFab x I2C x scFc		
370	VH-CH1	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
371	VL-CL	DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYY CQQSYFPVVEFGPGTKVEIKRTVAAPSVEFIPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
372	scFab	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGA

		LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
373	scFab-BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWDDKRYSPSLQSRITITKDTSKNQVLTMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGGQTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGGSGTQTVVT QEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
374	scFab-BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWDDKRYSPSLQSRITITKDTSKNQVLTMT NMDPVDATATYYCAYRRYNWNYENWFDPPWGGQTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGGSGTQTVVT QEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPAP

		ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGK
MA 09-H10 CC scFv x I2C x scFc		
375	HCDR1	THKMGVD
376	HCDR2	LIYWND DKRYSPSLQS
377	HCDR3	RRYNWNYENWFD P
378	LCDR1	QASQDISNYLN
379	LCDR2	AASSLQS
380	LCDR3	QQSYTPPTT
381	VH	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTN MDPVDTATYYCAYRRYNWNYENWFD PWGQGLTVTVSS
382	VL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATY YCQQSYTPPTTFGCGTKVEIK
383	SCFV	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTN MDPVDTATYYCAYRRYNWNYENWFD PWGQGLTVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLT ISSLQPEDFATYYCQQSYTPPTTFGCGTKVEIK
384	BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTN MDPVDTATYYCAYRRYNWNYENWFD PWGQGLTVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLT ISSLQPEDFATYYCQQSYTPPTTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGG GSGGGGSGGGGSGTVVTQEPSLTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
385	BiTE HLE	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTN MDPVDTATYYCAYRRYNWNYENWFD PWGQGLTVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLT ISSLQPEDFATYYCQQSYTPPTTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGG GSGGGGSGGGGSGTVVTQEPSLTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG

		GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
MA 09-H10 scFab x I2C x scFc		
386	VH-CH1	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTNMDPVDTATYYCAYRRYNWNYENWFD PWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
387	VL-CL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQPEDFATY YCQQSYTPPTTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
388	scFab	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTNMDPVDTATYYCAYRRYNWNYENWFD PWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISSLQPEDFATY YCQQSYTPPTTFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDS TYSLSSLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
389	scFab-BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWND DKRYSPSLQSRLTITKDTSKNQVVL TMTNMDPVDTATYYCAYRRYNWNYENWFD PWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISSLQPEDFATY YCQQSYTPPTTFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDS TYSLSSLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF

		GNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
390	scFab-BiTE HLE	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KALEWLALIYWNDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISSLQPEDFATYYCQQSYTPPTTFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLS LSPGK
MA 10-D3 CC scFv x I2C x scFc		
391	HCDR1	NAWMS
392	HCDR2	RITSSRYGGTDDYAAPVKG
393	HCDR3	PSYSGSYNYFSVMDV
394	LCDR1	RTSQSISSYLN
395	LCDR2	AASSLQG
396	LCDR3	QQTYSMPFT
397	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTDDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SS
398	VL	DIQMTQSPSSLSASVGDRVITTCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQTYSMPFTFGCGTKVDIK

399	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRTS QSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVDIK
400	BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRTS QSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VL
401	BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRTS QSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGGSGGGGSDKTHCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK
MA 10-D3 scFab x I2C x scFc		
402	VH-CH1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC

403	VL-CL	DIQMTQSPSSLSASVGDRVITTCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGTDFTLTISLQPEDFATYYC QQTYSMPTFTGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSY SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
404	scFab	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSG GTDFTLTISLQPEDFATYYCQQTYSMPTFTGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC
405	scFab- BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSG GTDFTLTISLQPEDFATYYCQQTYSMPTFTGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTTLTVSSGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLGSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
406	scFab-BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSG GTDFTLTISLQPEDFATYYCQQTYSMPTFTGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTTLTVSSGGGSGGGGSGGG

		GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK
MA 10-D6 CC scFv x I2C x scFc		
407	HCDR1	NAWMS
408	HCDR2	RILNNAYGGTTDYAAPVKG
409	HCDR3	PSYSGSYNYFSVMDV
410	LCDR1	RTSQSISSYLN
411	LCDR2	AASSLQG
412	LCDR3	QQTYSMPFT
413	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWVGQGT VSS
414	VL	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQTYSMPFTFGCGTKVDIK
415	SCFV	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWVGQGT VSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVDIK
416	BISPECIFIC MOL.	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWVGQGT VSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVT VSSGGGGSGGGSGGGSGGGSTQTVVTQEPSLTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VL

417	BiTE HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNNYFSVMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITICRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
MA 10-D6 scFab x I2C x scFc		
418	VH-CH1	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNNYFSVMDVWGQGTITVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC
419	VL-CL	DIQMTQSPSSLSASVGDRVITICRTSQSISSYLNWYQQKGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQTYSMPTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY SLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC
420	scFab	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNNYFSVMDVWGQGTITVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITIC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYAC EVTHQGLSPVTKSFNRGEC

421	scFab-BISPECIFIC MOL.	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTTLTVSSGGGSGGGGSGGG GSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
422	scFab-BiTE HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTTLTVSSGGGSGGGGSGGG GSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK
MA 10-G10 AS CC scFv x I2C x scFc		
423	HCDR1	SHAMS

424	HCDR2	AISGSGGGTYNAASVKG
425	HCDR3	GKGVHLGFDY
426	LCDR1	GGNNIGSKSVH
427	LCDR2	DDNDRPS
428	LCDR3	QVWDYVAPRHV
429	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSS
430	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYVAPRHVFGCGTKLTVL
431	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYVAPRHVFGCGTKLTVL
432	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYVAPRHVFGCGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVS SGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
433	BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGT LVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYVAPRHVFGCGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVS SGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ

		YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
MA 10-G10 AS scFab x I2C x scFc		
434	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
435	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYVAPRHVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
436	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYVAPRHVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECS
437	scFab- BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYVAPRHVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGTLLTVSSGGGSGGGSGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
438	scFab-BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDNKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGP

		SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYVAPRHVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNKYYAASSYLSLTPEQWKS HKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSL SLSPGK
MA 86-A4-N-F5 CC scFv x I2C x scFc		
439	HCDR1	TYGMH
440	HCDR2	VISYDAETVKYAESVKG
441	HCDR3	GQLLTGY
442	LCDR1	RASQGISNYLA
443	LCDR2	AASTLQS
444	LCDR3	QKYNSAPFT
445	VH	QVQLVESGGGVVQPG RSLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDN SKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSS
446	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKV PKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYY CQKYNSAPFTFGCGTKVEIK
447	SCFV	QVQLVESGGGVVQPG RSLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDN SKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSGGGGSGGG GSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWY QQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQP EDVATYYCQKYNSAPFTFGCGTKVEIK
448	BISPECIFIC MOL.	QVQLVESGGGVVQPG RSLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDN SKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSGGGGSGGG

		GSGGGGSDIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWY QQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFLTITSSLP EDVATYYCQKYNAPFTFGCGTKVEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVA RIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGGSGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
449	BiTE HLE	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDN SKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSGGGGSGGG GSGGGGSDIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWY QQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFLTITSSLP EDVATYYCQKYNAPFTFGCGTKVEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVA RIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGGSGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN HYTQKSLSLSPGKGGGGSGGGGGSGGGGGSGGGGGSGGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHE ALHNHYTQKSLSLSPGK
MA 86-A4-N-F5 scFab x I2C x scFc		
450	VH-CH1	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSTYGMHWVRQAP GKGLEWVAVISYDAETVKYAESVKGRFTISRDN SKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSC
451	VL-CL	DIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWYQQKPGKV PKLLIYAASLTQSGVPSRFSGSGSGTDFLTITSSLPEDVATYY CQKYNAPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
452	scFab	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSTYGMHWVRQAP GKGLEWVAVISYDAETVKYAESVKGRFTISRDN SKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV

		DKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCRASQGISNYLA WYQQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSL QPEDVATYYCQKYNSAPFTFGPGTKVEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDYSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVT KSFNRGEC
453	scFab-BISPECIFIC MOL.	QVQLVESGGGVVQPGRLRLSCAASGFTFSTYGMHWVRQAP GKGLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGGQTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCRASQGISNYLA WYQQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSL QPEDVATYYCQKYNSAPFTFGPGTKVEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDYSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVT KSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFT FNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYIS YWAYWGGQTLVTVSSGGGGSGGGGSGGGGSGTQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTCLTVL
454	scFab-BiTE HLE	QVQLVESGGGVVQPGRLRLSCAASGFTFSTYGMHWVRQAP GKGLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGGQTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCRASQGISNYLA WYQQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSL QPEDVATYYCQKYNSAPFTFGPGTKVEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDYSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVT KSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFT FNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYIS YWAYWGGQTLVTVSSGGGGSGGGGSGGGGSGTQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTCLTVLGGGDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSG GGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD

		GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
MA 88-B3-F9 CC scFv x I2C x scFc		
455	HCDR1	DYYMS
456	HCDR2	YISKSSYTVTYADAVKG
457	HCDR3	YNYGHFDY
458	LCDR1	GGNNIGSKSVH
459	LCDR2	DDADRP
460	LCDR3	QVWDASAGYGVV
461	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVSYISKSSYTVTYADAVKGRFTISRDNKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSS
462	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVLVYDDADRPSPGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDASAGYGVVFGCGTKLTVL
463	SCFV	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVSYISKSSYTVTYADAVKGRFTISRDNKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSSGGGGSGG GGSGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHW YQQKPGQAPVLVYDDADRPSPGIPERFSGSNSGNTATLTISRV EAGDEADYYCQVWDASAGYGVVFGCGTKLTVL
464	BISPECIFIC MOL.	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVSYISKSSYTVTYADAVKGRFTISRDNKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSSGGGGSGG GGSGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHW YQQKPGQAPVLVYDDADRPSPGIPERFSGSNSGNTATLTISRV EAGDEADYYCQVWDASAGYGVVFGCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
465	BiTE HLE	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVSYISKSSYTVTYADAVKGRFTISRDNKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSSGGGGSGG GGSGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHW YQQKPGQAPVLVYDDADRPSPGIPERFSGSNSGNTATLTISRV EAGDEADYYCQVWDASAGYGVVFGCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR

		CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK
MA 88-B3-F9 scFab x I2C x scFc		
466	VH-CH1	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGGQTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
467	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDADRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
468	scFab	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGGQTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDADRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
469	scFab-BISPECIFIC MOL.	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGGQTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDADRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQTLTVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDADRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS

		TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
470	scFab-BiTE HLE	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KGLEWVSYISKSSYTVTYADAVKGRFTISRDNANKSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGTLLTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVLLVYDDADRP SGIPERFSGSNSGNTATLTISR VEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKYAASSYLSLTPEQWKS HKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLSL AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTLLTVSSGGGGSGGGGSGGGGSGTQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLS SLSPGK
MA SG-F28 CC scFv x I2C x scFc		
471	HCDR1	SNPYYWS
472	HCDR2	YISYSGITNYNPSLKS
473	HCDR3	EKMWFGLNYYYGMDV
474	LCDR1	RSSQSLLHRSGYNYLD
475	LCDR2	LGSNRAS
476	LCDR3	MQALQTPWT
477	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYNPSLKS RVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGLNYYYGMDVWGQGTTVTVS S
478	VL	DIVMTQTPLSLPVTGPGEPAISCRSSQSLLHRSGYNYLDWYLQ KPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLKISRVEAGD VGVYYCMQALQTPWTFGCGTKVEIK
479	SCFV	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYNPSLKS RVTMSVDTSKNQFSLKLTS

		LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTITVTS SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGCGTKVEIK
480	BISPECIFIC MOL.	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTVMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTITVTS SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGCGTKVEIK SGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSLTVSPGGTV TLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFG GGTKLTVL
481	BiTE HLE	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTVMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTITVTS SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGCGTKVEIK SGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSLTVSPGGTV TLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFG GGTKLTVLGGGGDKHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSGDSFLLYSLKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGG GSGGGGSGGGGSGGGGSDKHTCPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFLLYSLKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
MA SG-F28 scFab x I2C x scFc		
482	VH-CH1	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTVMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTITVTS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSC
483	VL-CL	DIVMTQTPLSLPVTGPGEASISCRSSQSLLHRSGYNYLDWYLQ KPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAGD

		VG VYYCMQALQTPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC
484	scFab	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKGLEWIGYISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLLQKPGQSPQLLIYLGNSRASGVPDRFSGS GSGTDFTLKISRVEAGDVGVYYCMQALQTPWTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC
485	scFab- BISPECIFIC MOL.	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKGLEWIGYISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLLQKPGQSPQLLIYLGNSRASGVPDRFSGS GSGTDFTLKISRVEAGDVGVYYCMQALQTPWTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGECSGGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSG GGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLGVSQ PEDEAEYYCVLWYSNRWVFGGGTKLTVL
486	scFab-BiTE HLE	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKGLEWIGYISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLLQKPGQSPQLLIYLGNSRASGVPDRFSGS GSGTDFTLKISRVEAGDVGVYYCMQALQTPWTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGECSGGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSG GGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWV

		QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKT HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
MA 03-G10 AS CC scFv x I2C x scFc		
487	HCDR1	SYAMS
488	HCDR2	AISGSGGGTYAASVKG
489	HCDR3	GKGVHLGFDY
490	LCDR1	GGNNIGSKSVH
491	LCDR2	DDNDRPS
492	LCDR3	QVWDYSGQRQV
493	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSS
494	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYSGQRQVFGCGTKLTVL
495	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSGGGGSG GGGSGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSGQRQVFGCGTKLTVL
496	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSGGGGSG GGGSGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSGQRQVFGCGTKLTVLSSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVS SGGGGSGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
497	BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSGGGGSG GGGSGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH

		WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGCKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNGNSYISYWAYWGQGTLLTVSSGGGGSGGGGSGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
MA 03-G10 AS scFab x I2C x scFc		
498	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKG VHLGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
499	VL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVL
500	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKG VHLGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVL
501	scFab-BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKG VHLGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLO

		MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
502	scFab-BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KGLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCVMHEALHNHYTQKSLSLSPGK
MA 10-B5 CC scFv x I2C x scFc		
503	HCDR1	NAWMS
504	HCDR2	RIRSRSYGGTTDYAAPVKG
505	HCDR3	PSYSGSYNYFSVMDV
506	LCDR1	RTSQSISSYLN
507	LCDR2	AASSLQG
508	LCDR3	QQTYSMPFT
509	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRSRSYGGTTDYAAPVKGGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSS
510	VL	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQTYSMPFTFGCGTKVEIK
511	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRSRSYGGTTDYAAPVKGGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRT

		SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPTFGCGTKVEIK
512	BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTITLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VL
513	BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTITLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTIVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTIVLHQQDWLNGKEYKCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCVMHEALHNHYTQKSLSLSPGK
MA 10-B5 scFab x I2C x scFc		
514	VH-CH1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC
515	VL-CL	DIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQTYSMPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV

		VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY SLSSLTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
516	scFab	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQQYSMPFTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSSLTLTLKADYEKHKVYAC EVTHQGLSSPVTKSFNREGC
517	scFab- BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQQYSMPFTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSSLTLTLKADYEKHKVYAC EVTHQGLSSPVTKSFNREGCSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
518	scFab-BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQQYSMPFTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSSLTLTLKADYEKHKVYAC EVTHQGLSSPVTKSFNREGCSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA

		PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS SLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH YTQKSLSLSPGK
CD22 11-C3 CC scFv x I2C x scFc		
519	HCDR1	SFYWS
520	HCDR2	RISSSGDVDYNPSLKS
521	HCDR3	EGGFYY
522	LCDR1	RASQSVSSSYLA
523	LCDR2	GASSRAT
524	LCDR3	QQYGSSPIT
525	VH	QVQLQESGPGLVKPSSETLSLTCTVSGGSISFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSS
526	VL	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQQYGSSPITFGCGTKLEIK
527	SCFV	QVQLQESGPGLVKPSSETLSLTCTVSGGSISFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSGGGGSGGGGSGGG GSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGCGTKLEIK
528	BISPECIFIC MOL.	QVQLQESGPGLVKPSSETLSLTCTVSGGSISFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSGGGGSGGGGSGGG GSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLGTVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
529	BiTE HLE	QVQLQESGPGLVKPSSETLSLTCTVSGGSISFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSGGGGSGGGGSGGG GSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPG

		GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK
CD20 29-F5 CC scFv x I2C x scFc		
530	HCDR1	GYYS
531	HCDR2	EINHRGSTNYPNPSLKS
532	HCDR3	GYSSSWYTG YVFDY
533	LCDR1	TGTSSDVFGYDYVS
534	LCDR2	DVSNRPS
535	LCDR3	SSYKSSSTVV
536	VH	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKS RVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSS
537	VL	QSALTQPASVSGSPGQSITISCTGTSSDVFGYDYVSWYQQHPG KAPKLMYDVSNRPSGVSNRFGSGKSGNAASLTISGLQAEDEA DYCYSSYKSSSTVVFGCGTKLTVL
538	SCFV	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKS RVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSGGG SGGGSGGGSGSALTQPASVSGSPGQSITISCTGTSSDVFGY DYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSGKSGNAA SLTISGLQAEDEADYCYSSYKSSSTVVFGCGTKLTVL
539	BISPECIFIC MOL.	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKS RVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSGGG SGGGSGGGSGSALTQPASVSGSPGQSITISCTGTSSDVFGY DYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSGKSGNAA SLTISGLQAEDEADYCYSSYKSSSTVVFGCGTKLTVLSSGGGS EVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTV SSGGSGGGSGGGSGSQT VVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

540	BiTE HLE	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYNPSLKSRTVISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYVFDYWGQGLTVTVSSGGG GSGGGGSGGGGSQSALTQPASVSGSPGQSITISCTGTSSDVFY DYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNAA SLTISGLQAEDEADYYCSSYKSSSTVVFGCGTKLTVLSGGGG EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTV SSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSL LGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGS GGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
CD22 28-B7 N655 CC scFv x I2C x scFc		
541	HCDR1	SYGIS
542	HCDR2	WISAYSGNAIYAQKLQG
543	HCDR3	DPDYYGSGSYSDY
544	LCDR1	RASQSVSSNLA
545	LCDR2	GASSRAT
546	LCDR3	QQYHSWPLLT
547	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAP GQCLEWMGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYME LRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSS
548	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQA PRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYC QQYHSWPLLTFGCGTKVEIK
549	SCFV	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAP GQCLEWMGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYME LRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSG GGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSV SSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFT LTISLQSEDFAVYYCQQYHSWPLLTFGCGTKVEIK
550	BISPECIFIC MOL.	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAP GQCLEWMGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYME LRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSG GGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSV SSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFT LTISLQSEDFAVYYCQQYHSWPLLTFGCGTKVEIKSGGGGSE

		VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
551	BiTE HLE	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAP GQCLEWMGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYME LRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSG GGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSV SSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFT LTISSLQSEDFAVYYCQQYHSWPLLTFGCGTKVEIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
CD20 99-E5 CC scFv x I2C x scFc		
552	HCDR1	SYWMH
553	HCDR2	YITPSTGYTEYNQKFKG
554	HCDR3	VHDYDrameY
555	LCDR1	KASQDINKYIA
556	LCDR2	YTSTLQP
557	LCDR3	LQYASYPFT
558	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDrameYWGQGTTVTVSS
559	VL	DIQMTQSPSSLSASVGDRVTITCKASQDINKYIAWYQQKPGKG PKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIATYYC LQYASYPFTFGCGTRLEIK
560	SCFV	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDrameYWGQGTTVTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIK

561	BISPECIFIC MOL.	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTITVTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG GSGGGGSGGGGSGTVVTQEPSLTVSPGGTVTLTCGSSTGAVT SGNYPNWVQQKPGQAPRGLIGGTFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
562	BiTE HLE	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTITVTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG GSGGGGSGGGGSGTVVTQEPSLTVSPGGTVTLTCGSSTGAVT SGNYPNWVQQKPGQAPRGLIGGTFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGS GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
CD20 99-E5 scFab x I2C x scFc		
563	VH-CH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTITVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
564	VL-CL	DIQMTQSPSSLSASVGDRVITITCKASQDINKYIAWYQQKPGKG PKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIATYYC LQYASYPFTFGQGTREIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
565	scFab	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME

		LSSLTSED TAVYYC ARVHDY DRA MEYWGQ GTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDIA TYYCLQYASYPFTFGQGRLEIKRTVAAPS VFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
566	scFab- BISPECIFIC MOL.	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYC ARVHDY DRA MEYWGQ GTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDIA TYYCLQYASYPFTFGQGRLEIKRTVAAPS VFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGSGT VVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
567	scFab-BiTE HLE	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYC ARVHDY DRA MEYWGQ GTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDIA TYYCLQYASYPFTFGQGRLEIKRTVAAPS VFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGSGT VVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY

		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
CD20 29-F5 scFab x I2C x scFc		
568	VH-CH1	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
569	VL-CL	QSALTQPASVSGSPGQSITISCTGTSSDVFGYDYVSWYQQHPG KAPKLMYDVSNRPSGVSNRFSGSKSGNAASLTISGLQAEDEA DYCYSSYKSSSTVVFSGGGLTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS
570	scFab	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSGSALTQPASVSGSPGQSITISCTGTSSDVFG YDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNA ASLTISGLQAEDEADYCYSSYKSSSTVVFSGGGLTKLTVLGQPKA APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
571	scFab- BISPECIFIC MOL.	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSGSALTQPASVSGSPGQSITISCTGTSSDVFG YDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNA ASLTISGLQAEDEADYCYSSYKSSSTVVFSGGGLTKLTVLGQPKA APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ

		APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
572	scFab-BiTE HLE	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSGQSALTQPASVSGSPGQSITISCTGTSSDVFG YDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNA ASLTISGLQAEDEADYYCSSYKSSSTVVFGGGTKLTVLGQPKA APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP VKAGVETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGQT VVTQEPSLTVSPGGTVLTCGSSTGAVTSGNYPNWVQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG KGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
CD22 11-C3 scFab x I2C x scFc		
573	VH-CH1	QVQLQESGPGLVKLPSETLSLTCTVSGGSISFYWSWIRQPPGK GLEWIGRISSSGDV DYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSC
574	VL-CL	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
575	scFab	QVQLQESGPGLVKLPSETLSLTCTVSGGSISFYWSWIRQPPGK GLEWIGRISSSGDV DYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGG

		GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
576	scFab- BISPECIFIC MOL.	QVQLQESGPGLVKPSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW GQGLTVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVL
577	scFab-BiTE HLE	QVQLQESGPGLVKPSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW GQGLTVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGG GGSGGGGSGGGGSGGGGSGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA

		LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGQNVFSCSVMHEALHNHYTQKSLSLSPGK
578	CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTTVTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSQVQLVQ SGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEW MGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSD DTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSGGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISSLQS EDFAVYYCQQYHSWPLLTFGCGTKVEIK
579	CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv x I2C	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTTVTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSQVQLVQ SGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEW MGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSD DTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSGGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISSLQS EDFAVYYCQQYHSWPLLTFGCGTKVEIKSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWV ARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGSGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
580	CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv x I2C x scFc	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTTVTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSQVQLVQ SGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEW MGWISAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSD DTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSGGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISSLQS EDFAVYYCQQYHSWPLLTFGCGTKVEIKSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWV ARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGSGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGAAL

		T L S G V Q P E D A E Y Y C V L W Y S N R W V F G G G T K L T V L G G G G D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K P C E E Q Y G S T Y R C V S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K G G G G S G G G G S G G G G S G G G G S G G G G S G G G G S D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K P C E E Q Y G S T Y R C V S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K
581	CD22 11-C3 CC scFv x CD20 29-F5 CC scFv	Q V Q L Q E S G P G L V K P S E T L S L T C T V S G G S I S S F Y W S W I R Q P P G K C L E W I G R I S S S G D V D Y N P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T A V Y Y C A R E G G F Y W G Q G T L V T V S S G G G G S G G G G S G G G G S E I V L T Q S P G T L S L S P G E R A T L S C R A S Q S V S S S Y L A W Y Q Q K P G Q A P R L L I Y G A S S R A T G I P D R F S G S G S G T D F T L T I S R L E P E D F A V Y Y C Q Q Y G S S P I T F G C G T K L E I K S G G G G S Q V Q L Q Q W G A G L L K P S E T L S L T C A V Y G G S F S G Y Y W S W I R Q P P G K C L E W I G E I N H R G S T N Y N P S L K S R V T I S G D T S K N Q F S L K L S S V N A A D T A V Y Y C A R G Y S S S W Y T G Y V F D Y W G Q G T L V T V S S G G G G S G G G G S G G G G S Q S A L T Q P A S V S G S P G Q S I T I S C T G T S S D V F G Y D Y V S W Y Q Q H P G K A P K L M I Y D V S N R P S G V S N R F S G S K S G N A A S L T I S G L Q A E D E A D Y Y C S S Y K S S S T V V F G C G T K L T V L
582	CD22 11-C3 CC scFv x CD20 29-F5 CC scFv x I2C	Q V Q L Q E S G P G L V K P S E T L S L T C T V S G G S I S S F Y W S W I R Q P P G K C L E W I G R I S S S G D V D Y N P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T A V Y Y C A R E G G F Y W G Q G T L V T V S S G G G G S G G G G S G G G G S E I V L T Q S P G T L S L S P G E R A T L S C R A S Q S V S S S Y L A W Y Q Q K P G Q A P R L L I Y G A S S R A T G I P D R F S G S G S G T D F T L T I S R L E P E D F A V Y Y C Q Q Y G S S P I T F G C G T K L E I K S G G G G S Q V Q L Q Q W G A G L L K P S E T L S L T C A V Y G G S F S G Y Y W S W I R Q P P G K C L E W I G E I N H R G S T N Y N P S L K S R V T I S G D T S K N Q F S L K L S S V N A A D T A V Y Y C A R G Y S S S W Y T G Y V F D Y W G Q G T L V T V S S G G G G S G G G G S G G G G S Q S A L T Q P A S V S G S P G Q S I T I S C T G T S S D V F G Y D Y V S W Y Q Q H P G K A P K L M I Y D V S N R P S G V S N R F S G S K S G N A A S L T I S G L Q A E D E A D Y Y C S S Y K S S S T V V F G C G T K L T V L S G G G G S E V Q L V E S G G G L V Q P G G S L K L S C A A S G F T F N K Y A M N W V R Q A P G K G L E W V A R I R S K Y N N Y A T Y Y A D S V K D R F T I S R D D S K N T A Y L Q M N N L K T E D T A V Y Y C V R H G N F G N S Y I S Y W A Y W G Q G T L V T V S S G G G G S G G G G S G G G G S Q T V V T Q E P S L T V S P G G T V T L T C S S T G A V T S G N Y P N W V Q Q K P G Q A P R G L I G G T K F L A P G T P A R F S G S L L G G K A A L T L S G V Q P E D E A E Y Y C V L W Y S N R W V F G G G T K L T V L
583	CD22 11-C3 CC scFv x CD20 29-F5 CC scFv x I2C x scFc	Q V Q L Q E S G P G L V K P S E T L S L T C T V S G G S I S S F Y W S W I R Q P P G K C L E W I G R I S S S G D V D Y N P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T A V Y Y C A R E G G F Y W G Q G T L V T V S S G G G G S G G G G S G G G G S E I V L T Q S P G T L S L S P G E R A T L S C R A S Q S V S S S Y L A W Y Q Q K P G Q A P R L L I Y G A S S R A T G I P D R F S G S G S G T D F T L T I S R L E P E D F A V Y Y C Q Q Y G S S P I T F G C G T K L E I K S G G G G S Q V Q L Q Q W G A G L L K P S E T L S L T C A V Y G G S F S G Y Y W S W I R Q P P G K C L E W I G E I N H R G S T

		NYNPSLKSRTISGDTSKNQFSLKLSSVNAADTAVYYCARGY SSSWYTGYVFDYWGQGLTVTVSSGGGGSGGGGSQSA LTQPASVSGSPQSITISCTGTSSDVFGYDYVSWYQQHPGKAP KLMIYDVSNRPSGVSNRFSKSGNAASLTISGLQAEDEADYY CSSYKSSSTVVFQCGTKLTVLSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGG GSQTVVTQEPLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK
584	CD20 99-E5 scFab x CD22 28-B7 N655 CC scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRA MEYWGQGT TVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISLQPEDIA TYYCLQYASYPFTFGQGRLEIKRTVAAPS VFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDS TYSLSSTLTL SKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC SGGGSQVQLVQSGAEVKKPGASVKVSCK ASGYTFTSYGISWVRQAPGQC LEWMGWISAYSGNAIYAQKL QGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGS GSYSDYWGQGLTVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPAT LSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASS RATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQYH SWPLL TFGCGTKVEIK
585	CD20 99-E5 scFab x CD22 28-B7 N655 CC scFv x I2C	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRA MEYWGQGT TVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISLQPEDIA TYYCLQYASYPFTFGQGRLEIKRTVAAPS VFIF

		PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSSGGGSQVQLVQSGAEVKKPGASVKVSCK ASGYTFTSYGISWVRQAPGQCLEWMGWISAYSGNAIYAQKL QGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGS GSYSDYWGGQTLVTVSSGGGSGGGGSGGGGSEIVLTQSPAT LSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASS RATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQYHSWPLL TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSKAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGGQTLVTVSSGGGSGGGGSGGGGSGTQVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
586	CD20 99-E5 scFab x CD22 28-B7 N655 CC scFv x I2C x scFc	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDVAVYYCARVHDYDRA MEYWGQGTITVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQTQSPSSLSASVGDRTITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDVATYYCLQYASYPFTFGQGRLEIKRTVAAPSIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSSGGGSQVQLVQSGAEVKKPGASVKVSCK ASGYTFTSYGISWVRQAPGQCLEWMGWISAYSGNAIYAQKL QGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGS GSYSDYWGGQTLVTVSSGGGSGGGGSGGGGSEIVLTQSPAT LSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASS RATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQYHSWPLL TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSKAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGGQTLVTVSSGGGSGGGGSGGGGSGTQVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGG GSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF

		LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
587	CD22 11-C3 scFab x CD20 29-F5 scFab	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSSGGGSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYY WSWIRQPPGKLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKN QFSLKLSSVNAADTAVYYCARGYSSSWYTGYYFDYWGQGLT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGG SGGGSGGGGSGGGGSGGGGSGGGSQSALTQPASVSGSPGQSITISC TGTSSDVFGYDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRF SGSKSGNAASLTISGLQAEDEADYYCSSYKSSSTVVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVAPTECS
588	CD22 11-C3 scFab x CD20 29-F5 scFab x I2C	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSSGGGSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYY WSWIRQPPGKLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKN QFSLKLSSVNAADTAVYYCARGYSSSWYTGYYFDYWGQGLT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGG SGGGSGGGGSGGGGSGGGGSGGGSQSALTQPASVSGSPGQSITISC TGTSSDVFGYDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRF SGSKSGNAASLTISGLQAEDEADYYCSSYKSSSTVVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLV QPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRS KYNNAATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA

		VYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGS GGGGSQTVVTQEPLSTVSPGGTVTLTCGSSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVL
589	CD22 11-C3 scFab x CD20 29-F5 scFab x I2C x scFc	QVQLQESGPGLVKPSSETLSLTCTVSGGSISFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSSGGGSGVQLQWAGLLKPSETLSLTCAVYGGSFSGYY WSWIRQPPGKLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKN QFSLKLSSVNAADTAVYYCARGYSSSWYTG YVFDYWGQGL TVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSGGGGSGSALTQPAVSGSPGQSITISC TGTSSDVFGYDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRF SGSKSGNAASLTISGLQAEDEADYYCSSYKSSSTVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLV QPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRS KYNKYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGS GGGGSQTVVTQEPLSTVSPGGTVTLTCGSSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDGSEFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQ KSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSGSEFLYSLKLTVDKSRWQQGNVFCFSVMHEALH NHYTQKSLSLSPGK

DNA encoding CCR8 TCE 1.1 HLE of SEQ ID NO: 227 (SEQ ID NO: 590)

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ACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGAAAACCGAGGACACCGCC
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TCTAGCGGCGGAGGTGGACAAGGTGGTGGCGGACAAGGCGGCGGTGGTCAAGAGAT
TGTGATGACCCAGTCTCCTGACAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCAT
CAACTGCAAGTCCAGCCAGTCCGTGCTGTACTCCTCCAACAACAAGAACTACCTGGC
CTGGTATCACCAGAAGCCAGGCCAGTCTCCAAAGCTGCTGATCTCCTGGGCCTCCAC
CAGAGAAAGCGGCGTGCCCGATAGATTCTCCGGCTCTGGCTCTGGCACCGACTTCAC
CCTGACCATCAATTCCTGCAGGCCGAGGATGTGGCTGTGTACTATTGCCAGCAGTA
CTACAGCATCCCATCACCTTCGGCTGCGGCACCAAGGTGGAAATCAAGTCCGGAGG
TGGAGGGCAGGAAGTGCAGCTGGTTGAATCTGGCGGCGGATTGGTTCAGCCTGGCG
GATCTCTGAAGCTGTCTTGTGCCGCCCTCTGGCTTCACCTTCAACAAATACGCCATCAA
CTGGGTCCGACAGGCCCTGGCAAAGGACTGGAATGGGTGCGCCCGGATCAGATCCA
AGTACAACAACCTACGCTACCTACTACGCCGACGCCGTGAAGGACCGGTTACCATCT
CCAGAGATGACTCCAAGAACACCGTGTACCTGCAGATGAACAACCTCAAGACCGAG
GACACCGCCGTGTACTACTGTGCCAGAGCCGGCAACTTCGGCTCCTCTACATCAGC
TACTGGGCCTATTGGGGCCAGGGCACACTGGTCACAGTTAGTTCAGGTGGCGGTGGA
CAGGGCGGCGGAGGTGAGGTGGCGGAGGCCAGCAAACAGTGGTCAACCAAGAGC
CTAGCCTGACCGTTTCTCCTGGCGGCACCGTGACCATCACCTGTGGATCTTCTACCGG
CGCTGTGACCTCCGGCAACTACCCTAATTGGGTGCAGAAGAAGCCCGGCCAGGCTCC
TAGAGGACTGATCGGAGGCACCAAGTTTCTGGCTCCCGGCACTCCTGCCAGATTCTC
CGGTTCTCTGTCTGGCGGAAAGGCCGCTCTGACATTGTCTGGCGTGCAGCCTGAGGA
TGAGGCTGAGTACTATTGCGTGCTGTGGTACTCCAACAGATGGGTGTTCCGGCTCCGG
CACCAAGCTGACAGTTCTCGGCGGAGGTGGATGCCCTCCTTGTCTGCTCCTGAATT
GCTCGGCGGACCCCTCCGTGTTCTCTGTTTCTCCAAAGCCTAAGGACACCCTGATGAT
CTCTCGTACGCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCACGAGGAACCCGA
AGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACAAAGC
CCTGCGAGGAACAGTACGGCTCCACCTACAGATGCGTGTCCGTGCTGACAGTGCTGC
ACCAGGATTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTG
CCTGCTCCTATCGAAAAGACCATCTCCAAGGCCAAGGGCCAGCCTAGAGAGCCCCA
GGTTTACACCCTGCCTCCAAGCAGAGAAGAGATGACCAAGAACCAGGTGTCCCTGA
CCTGCCTGGTCAAGGGCTTCTACCCTTCCGATATCGCCGTGGAATGGGAGAGCAATG
GACAGCCCCGAGAACAACTACAAGACCACACCTCCTGTGCTGGACTCCGACGGCTCAT
TCTTCTGTACTCCAAGCTGACCGTGGACAAGTCCAGATGGCAGCAGGGCAACGTGT
TCTCCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTGT
CTCTGTCCCTGGAGGCGGAGGACAAGGCGGAGGTGGTCAAGGTGGTGGTGGCCAA
GGCGGAGGCGGACAAGGCGGCGGAGGACAAGGTGGCGGTGGACAGTGTCTCCATG
TCCAGCACCTGAGCTTCTCGGAGGCCCTTCTGTGTTTCTGTTCCACCTAAGCCAAAG
GATACACTCATGATCAGCCGCACACCTGAAGTCACATGTGTCTGTCGTGGATGTCTCT
CATGAAGAACCAGAAGTCAAGTTTAATTGGTATGTGATGGCGTCGAGGTCCACAAT
GCTAAGACCAAGCCTTGTGAAGAACAATATGGCAGCACCTATCGCTGTGTGTCTGTC
CTGACCGTCTGCATCAAGACTGGCTCAATGGGAAAGAATACAAATGCAAAGTCTCT
AACAAAGCTCTGCCCCGACCAATCGAGAAAACCATCAGCAAGGCTAAAGGACAGCC
TCGCGAGCCTCAAGTGTATACCCTGCCACCTTCTCGCGAGGAAATGACAAAAAATCA
AGTCTCCCTCACCTGTCTCGTGAAGGGATTCTATCCCAGCGACATTGCCGTCGAGTG
GGAGTCTAATGGCCAGCCTGAAAACAATTATAAGACAACCCACCTGTCTCTGGACA
GCGACGGCTCATTTTTTCTCTACTCTAAACTCACCGTGGATAAGAGCCGGTGGCAAC
AGGGAAATGTGTTTCAAGCTGTAGCGTGATGCATGAAGCTCTCCACAACCATTATACAC
AGAAGAGTCTGAGCCTGTCTCCTGGCAAATGA

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DNA encoding CCR8 TCE 1.2 HLE of SEQ ID NO: 238 (SEQ ID NO: 591)

GAGGTGCAGCTGGTGGAAATCTGGCGGAGGACTTGTGAAGCCTGGCGGCTCTCTGAG
ACTGTCTTGTGCCGCTTCTGGCTTACCTTCAGCAACGCCAGAATGGGCTGGGTCCG
ACAGGCTCCTGGAAAGTGTCTGGAATGGGTGCGACGGATCAAGTCCAAGACCGAAG
GCGGCACCAGAGACTACGCCGCTCCTGTGAAGGGCAGATTCACCATCTCTCGGGACG
ACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGAAAACCGAGGACACCGCC
GTGTACTACTGCACCTCTTACTCTGGCGTGTGGGGCCAGGGCACAATGGTCACAGTT
TCTAGCGGCGGAGGTGGACAAGGTGGTGGCGGACAAGGCGGCGGTGGTCAAGAGAT
TGTGATGACCCAGTCTCCTGACAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCAT
CAACTGCAAGTCCAGCCAGTCCGTGCTGTACTCCTCCAACAACAAGAACTACCTGGC
CTGGTATCACCAGAAGCCAGGCCAGTCTCCAAAGCTGCTGATCTCCTGGGCCTCCAC
CAGAGAAAGCGGCGTGCCCGATAGATTCTCCGGCTCTGGCTCTGGCACCGACTTCAC
CCTGACCATCAATTCCCTGCAGGCCGAGGATGTGGCTGTGTACTATTGCCAGCAGTA
CTACAGCATCCCATCACCTTCGGCTGCGGCACCAAGGTGGAAATCAAGTCCGGAGG
TGGAGGGCAGGAAGTGCAGCTGGTTGAATCTGGCGGCGGATTGGTTCAGCCTGGCG
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CTGGGTCCGACAGGCCCTGGCAAAGGACTGGAATGGGTGCGCCGGATCAGATCCA
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GACACCGCCGTGTACTACTGTGCCAGAGCCGGCAACTTCGGCTCCTCCTACATCAGC
TACTGGGCCTATTGGGGCCAGGGCACACTGGTCACAGTTAGTTCAGGTGGCGGTGGA
CAGGGCGGCGGAGGTGAGGGTGGCGGAGGCCAGCAAACAGTGGTCACCCAAGAGC
CTAGCCTGACCGTTTCTCCTGGCGGCACCGTGACCATCACCTGTGGATCTTCTACCGG
CGCTGTGACCTCCGGCAACTACCCTAATTGGGTGCAGAAGAAGCCCGGCCAGGCTCC
TAGAGGACTGATCGGAGGCACCAAGTTTCTGGCTCCCGGCACTCCTGCCAGATTCTC
CGTTCTCTGTCTGGCGGAAAGGCCGCTCTGACATTGTCTGGCGTGCAGCCTGAGGA
TGAGGCTGAGTACTATTGCGTGCTGTGGTACTCCAACAGATGGGTGTTGGCTCCGG
CACCAAGCTGACAGTTCTCGGCGGAGGTGGATGCCCTCCTTGCTCTGCTCCTGAATT
GCTCGGCGGACCCCTCCGTGTTCTGTTTCTCCAAAGCCTAAGGACACCCTGTACATC
ACCCGCGAGCCTGAAGTGACCTGCGTGTTGGTGGATGTGTCCCACGAGGAACCCGA
AGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACAAAGC
CCTGCGAGGAACAGTACGGCTCCACCTACAGATGCGTGTCGGTGCTGACAGTGCTGC
ACCAGGATTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTG
CCTGCTCCTATCGAAAAGACCATCTCCAAGGCCAAGGGCCAGCCTAGAGAGCCCCA
GGTTTACACCCTGCCTCCAAGCAGAGAAGAGATGACCAAGAACCAGGTGTCCCTGA
CCTGCCTGGTCAAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATG
GACAGCCCCGAGAACAACCTACAAGACCACACCTCCTGTGCTGGACTCCGACGGCTCAT
TCTTCCTGTACTCCAAGCTGACCGTGGACAAGTCCAGATGGCAGCAGGGCAACGTGT
TCTCCTGTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTGT
CTCTGTCCCTGGAGGCGGAGGACAAGGCGGAGGTGGTCAAGGTGGTGGTGGCCAA
GGCGGAGGCGGACAAGGCGGCGGAGGACAAGGTGGCGGTGGACAGTGTCTCCATG
TCCAGCACCTGAGCTTCTCGGAGGCCCTTCTGTGTTTCTGTTCCACCTAAGCCAAAG
GATACACTCTACATCACCCGCGAGCCTGAAGTCACATGTGTCTGTCGTGGATGTCTCT
CATGAAGAACCAGAAGTCAAGTTTAATTGGTATGTGATGGCGTCGAGGTCCACAAT
GCTAAGACCAAGCCTTGTGAAGAACAATATGGCAGCACCTATCGCTGTGTGTCTGTC
CTGACCGTCTGTCATCAAGACTGGCTCAATGGGAAAGAATACAAATGCAAAGTCTCT
AACAAAGCTCTGCCCCGACCAATCGAGAAAACCATCAGCAAGGCTAAAGGACAGCC
TCGCGAGCCTCAAGTGTATACCCTGCCACCTTCTCGCGAGGAAATGACAAAAAATCA
AGTCTCCCTCACCTGTCTCGTGAAGGGATTCTATCCCAGCGACATTGCCGTCGAGTG
GGAGTCTAATGGCCAGCCTGAAAACAATTATAAGACAACCCACCTGTCCTGGACA

GCGACGGCTCATTTTTCTCTACTCTAAACTCACCGTGGATAAGAGCCGGTGGCAAC
AGGGAAATGTGTTTACGCTGTAGCGTGATGCATGAAGCTCTCCACAACCATTATACAC
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DNA encoding CCR8 TCE 1.3 HLE of SEQ ID NO: 249 (SEQ ID NO: 592)

GAGGTGCAGCTGGTGAATCTGGCGGAGGACTTGTGAAGCCTGGCGGCTCTCTGAG
ACTGTCTTGTGCCGCTTCTGGCTTCACCTTCAGCAACGCCAGAATGGGCTGGGTCCG
ACAGGCTCCTGGAAAAGGACTGGAATGGGTCTGGACGGATCAAGTCCAAGACCGAAG
GCGGCACCAGAGACTACGCCGCTCCTGTGAAGGGCAGATTCACCATCTCTCGGGACG
ACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGAAAACCGAGGACACCGCC
GTGTACTACTGCACCTCTTACTCTGGCGTGTGGGGCCAGGGCACAATGGTCAAGTT
TCTTCCGCCTCCACCAAGGGACCCAGCGTTTTCCCTCTGGCTCCATCCTCCAAGTCTA
CCTCTGGCGGAACAGCTGCTCTGGGCTGCCTGGTCAAGGACTACTTTCCTGAGCCTG
TGACCGTGTCTGGAATCTGGCGCTCTGACATCTGGCGTGCACACCTTTCAGCTGT
GCTGCAGTCTCCTCCGGCCTGTACTCTCTGTCTCTGTCTGTGACCGTGCCTTCCAGCTCT
CTGGGAACCCAGACCTACATCTGCAATGTGAACCACAAGCCTTCCAACACCAAGGTG
GACAAGAAGGTGGAACCCAAGTCTTGTGGCGGAGGCGGACAAGGTGGTGGTGGTCA
AGGTGGCGGAGGACAAGGCGGTGGCGGCCAAGGCGGAGGTGGACAAGGCGGCGGA
GGCCAAGGTGGCGGCGGTCAAGGCGGCGGTGGTCAAGAAATTGTGATGACCCAGTC
TCCTGACAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCATCAACTGCAAGTCCAG
CCAGTCCGTGCTGTACTCCTCCAACAACAAGAACTACCTGGCCTGGTATCACCAGAA
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GCCCCACAGATTTTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCAATTCC
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ACCTTCGGAGGTGGCACCAAGGTGCGAGATCAAGAGAACCCTGGCCGCTCCTTCCGTG
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TGCTGAACAACCTTCTACCCTCGGGAAGCCAAGGTGCAGTGGAAGTGGATAACGCC
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CTACAGCCTGTCTCCACACTGACCCTGTCCAAGGCCGACTACGAGAAGCACAAGGT
GTACGCCTGCGAAGTGACCCATCAGGGCCTGTCTAGCCCTGTGACCAAGTCTTTCAA
CCGGGGCGAGTGTTCCGGAGGTGGAGGGCAGGAAGTGCAGCTGGTTGAATCTGGCG
GCGGATTGGTTCAGCCTGGCGGATCTCTGAAGCTGTCTTGTGCCGCCTCTGGCTTCAC
CTTCAACAAATACGCCATCAACTGGGTCCGACAGGCCCTGGCAAAGGACTGGAAT
GGGTCGCCCCGATCAGATCCAAGTACAACAACCTACGCTACCTACTACGCCGACGCCG
TGAAGGACCGGTTACCATCTCCAGAGATGACTCCAAGAACACCGTGTACCTGCAGA
TGAACAACCTCAAGACCGAGGACACCGCCGTGTACTACTGTGCCAGAGCCGGCAAC
TTCGGCTCCTCCTACATCAGCTACTGGGCCTATTGGGGCCAGGGCACACTGGTCACA
GTTAGTTCAGGTGGCGGTGGACAGGGCGGCGGAGGTGAGGGTGGCGGAGGCCAGCA
AACAGTGGTCAACCAAGAGCCTAGCCTGACCGTTTCTCCTGGCGGCACCGTGACCAT
CACCTGTGGATCTTCTACCGGCGCTGTGACCTCCGGCAACTACCCTAATTGGGTGCA
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CCGGCACTCCTGCCAGATTCTCCGGTTCTCTGTCTGGCGGAAAGGCCGCTCTGACATT
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CAGATGGGTGTTCCGGCTCCGGCACCAAGCTGACAGTTCTCGGCGGAGGTGGATGCCC
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CCTAAGGACACCTGATGATCTCTCGTACGCCTGAAGTGACCTGCGTGGTGGTGGAT
GTGTCCCACGAGGAACCCGAAGTGAAGTTC AATTGGTACGTGGACGGCGTGGAAGT
GCACAACGCCAAGACAAAGCCCTGCGAGGAACAGTACGGCTCCACCTACAGATGCG
TGTCCTGTGCTGACAGTGCTGCACCAGGATTGGCTGAACGGCAAAGAGTACAAGTGC
AAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAAAAGACCATCTCCAAGGCCAAG

GGCCAGCCTAGAGAGCCCCAGGTTTACACCCTGCCTCCAAGCAGAGAAGAGATGAC
CAAGAACCAGGTGTCCCTGACCTGCCTGGTCAAGGGCTTCTACCCCTCCGATATCGC
CGTGGAATGGGAGAGCAATGGACAGCCGAGAACAACCTACAAGACCACACCTCCTG
TGCTGGACTCCGACGGCTCATTCTTCCTGTACTCCAAGCTGACCGTGGACAAGTCCA
GATGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGAGGCCCTGCACAATC
ACTACACCCAGAAGTCCCTGTCTCTGTCCCCTGGAGGCGGAGGACAAGGCGGAGGT
GGTCAAGGTGGTGGTGGCCAAGGCGGAGGCGGACAAGGCGGCGGAGGACAAGGTG
GCGGTGGACAGTGTCTCCATGTCCAGCACCTGAGCTTCTCGGAGGCCCTTCTGTGTT
TCTGTTCCACCTAAGCCAAAGGATACACTCATGATCAGCCGCACACCTGAAGTCAC
ATGTGTCGTCGTGGATGTCTCTCATGAAGAACCAGAAGTCAAGTTTAATTGGTATGT
CGATGGCGTCGAGGTCCACAATGCTAAGACCAAGCCTTGTGAAGAACAAATATGGCA
GCACCTATCGCTGTGTGTCTGTCTGACCGTCTGCATCAAGACTGGCTCAATGGGA
AAGAATACAAATGCAAAGTCTCTAACAAAGCTCTGCCCCGACCAATCGAGAAAACC
ATCAGCAAGGCTAAAGGACAGCCTCGCGAGCCTCAAGTGTATAACCTGCCACCTTCT
CGCGAGGAAATGACAAAAAATCAAGTCTCCCTCACCTGTCTCGTGAAGGGATTCTAT
CCCAGCGACATTGCCGTCGAGTGGGAGTCTAATGGCCAGCCTGAAAACAATTATAA
GACAACCCACCTGTCTGGACAGCGACGGCTCATTTTTTCTCTACTCTAACTCACC
GTGGATAAGAGCCGGTGGCAACAGGGAAATGTGTTCAAGTGTAGCGTGTATGCATGA
AGCTCTCCACAACCATTATACACAGAAGAGTCTGAGCCTGTCTCCTGGCAAATGA

DNA encoding the CCR8 TCE 1.4 HLE of SEQ ID NO: 260 (SEQ ID NO: 593)

GAGGTGCAGCTGGTGGAAATCTGGCGGAGGACTTGTGAAGCCTGGCGGCTCTCTGAG
ACTGTCTTGTGCCGCTTCTGGCTTACCTTCAGCAACGCCAGAATGGGCTGGGTCCG
ACAGGCTCCTGGAAAAGGACTGGAATGGGTTCGGACGGATCAAGTCCAAGACCGAAG
GCGGCACCAGAGACTACGCCGCTCCTGTGAAGGGCAGATTCACCATCTCTCGGGACG
ACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGAAAACCGAGGACACCGCC
GTGTACTACTGCACCTCTTACTCTGGCGTGTGGGGCCAGGGCACAATGGTCAACAGTT
TCTTCCGCCTCCACCAAGGGACCCAGCGTTTTTCCCTCTGGCTCCATCCTCCAAGTCTA
CCTCTGGCGGAACAGCTGCTCTGGGCTGCCTGGTCAAGGACTACTTTCTGAGCCTG
TGACCGTGTCTGGAACCTCTGGCGCTCTGACATCTGGCGTGCACACCTTTCCAGCTGT
GCTGCAGTCTCCTCCGGCCTGTACTCTCTGTCTCTGTCTGACCGTGCCTTCCAGCTCT
CTGGGAACCCAGACCTACATCTGCAATGTGAACCACAAGCCTTCCAACACCAAGGTG
GACAAGAAGGTGGAACCCAAGTCTTGTGGCGGAGGCGGACAAGGTGGTGGTGGTCA
AGGTGGCGGAGGACAAGGCGGTGGCGGCCAAGGCGGAGGTGGACAAGGCGGCGGA
GGCCAAGGTGGCGGCGGTCAAGGCGGCGGTGGTCAAGAAATTGTGATGACCCAGTC
TCCTGACAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCATCAACTGCAAGTCCAG
CCAGTCCGTGCTGTACTCCTCCAACAACAAGAACTACCTGGCCTGGTATCACCAGAA
GCCAGGCCAGTCTCCAAAGCTGCTGATCTCCTGGGCCTCTACCAGAGAATCCGGCGT
GCCCCACAGATTTTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCAATTCC
CTGCAGGCCGAGGATGTGGCTGTGTACTATTGCCAGCAGTACTACAGCATCCCCATC
ACCTTCGGAGGTGGCACCAAGGTTCGAGATCAAGAGAACCGTGGCCGCTCCTTCCGTG
TTCATCTTCCCACCTTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCTGTCTGTGCTG
TGCTGAACAACTTCTACCTCGGGAAGCCAAGGTGCAGTGGAAAGTGGATAACGCC
CTGCAGTCCGGCAACTCCCAAGAGTCTGTGACCGAGCAGGACTCCAAGGACAGCAC
CTACAGCCTGTCTCCACACTGACCCTGTCCAAGGCCGACTACGAGAAGCACAAGGT
GTACGCCTGCGAAGTGACCCATCAGGGCCTGTCTAGCCCTGTGACCAAGTCTTTCAA
CCGGGGCGAGTGTTCGGGAGGTGGAGGGCAGGAAGTGCAGCTGGTTGAATCTGGCG
GCGGATTGGTTCAGCCTGGCGGATCTCTGAAGCTGTCTTGTGCCGCTCTGGCTTCAC
CTTCAACAAATACGCCATCAACTGGGTCCGACAGGCCCTGGCAAAGGACTGGAAT
GGGTCGCCCGGATCAGATCCAAGTACAACAACCTACGCTACCTACTACGCCGACGCCG

TGAAGGACCGGTTACCATCTCCAGAGATGACTCCAAGAACACCGTGTACCTGCAGA
TGAACAACCTCAAGACCGAGGACACCGCCGTGTACTACTGTGCCAGAGCCGGCAAC
TTCGGCTCCTCCTACATCAGCTACTGGGCTATTGGGGCCAGGGCACACTGGTCACA
GTTAGTTTCAGGTGGCGGTGGACAGGGCGGCGGAGGTCAGGGTGGCGGAGGGCCAGCA
AACAGTGGTCAACCAAGAGCCTAGCCTGACCGTTTCTCCTGGCGGCACCGTGACCAT
CACCTGTGGATCTTCTACCGGCGCTGTGACCTCCGGCAACTACCCTAATTGGGTGCA
GAAGAAGCCCGGCCAGGCTCCTAGAGGACTGATCGGAGGCACCAAGTTTCTGGCTC
CCGGCACTCCTGCCAGATTCTCCGGTTCTGTCTGGCGGAAAGGCCGCTCTGACATT
GTCTGGCGTGCAGCCTGAGGATGAGGCTGAGTACTATTGCGTGCTGTGGTACTCCAA
CAGATGGGTGTTTCGGCTCCGGCACCAAGCTGACAGTTCTCGGCGGAGGTGGATGCCC
TCCTTGTCTGCTCCTGAATTGCTCGGCGGACCCCTCCGTGTTCTGTTTCTCCAAAG
CCTAAGGACACCTGTACATCACCCGCGAGCCTGAAGTGACCTGCGTGGTGGTGGAT
GTGTCCACGAGGAACCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGT
GCACAACGCCAAGACAAAGCCCTGCGAGGAACAGTACGGCTCCACCTACAGATGCG
TGTCCTGTGCTGACAGTGTGACACAGGATTGGCTGAACGGCAAAGAGTACAAGTGC
AAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAAAAGACCATCTCCAAGGCCAAG
GGCCAGCCTAGAGAGCCCCAGGTTTACACCTGCCTCCAAGCAGAGAAGAGATGAC
CAAGAACCAGGTGTCCCTGACCTGCCTGGTCAAGGGCTTCTACCTTCCGATATCGC
CGTGGGAATGGGAGAGCAATGGACAGCCGAGAACAATAAGACCACACCTCCTG
TGCTGGACTCCGACGGCTCATTCTTCTGTACTCCAAGCTGACCGTGGACAAGTCCA
GATGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGAGGCCCTGCACAATC
ACTACACCCAGAAGTCCCTGTCTGTCTGCTCCCTGGAGGCGGAGGACAAGGCGGAGGT
GGTCAAGGTGGTGGTGGCCAAGGCGGAGGCGGACAAGGCGGCGGAGGACAAGGTG
GCGGTGGACAGTGTCTCCATGTCCAGCACCTGAGCTTCTCGGAGGCCCTTCTGTGTT
TCTGTTCCACCTAAGCCAAAGGATACACTCTACATCACCCGCGAGCCTGAAGTCAC
ATGTGTCGTCGTGGATGTCTCTCATGAAGAACCAGAAGTCAAGTTTAATTGGTATGT
CGATGGCGTCGAGGTCCACAATGCTAAGACCAAGCCTTGTGAAGAACAATATGGCA
GCACCTATCGCTGTGTGTCTGTCTGACCGTCTGCATCAAGACTGGCTCAATGGGA
AAGAATACAAATGCAAAGTCTCTAACAAAGCTCTGCCCCGACCAATCGAGAAAACC
ATCAGCAAGGCTAAAGGACAGCCTCGCGAGCCTCAAGTGTATACCTGCCACCTTCT
CGCGAGGAAATGACAAAAAATCAAGTCTCCCTCACCTGTCTCGTGAAGGGATTCTAT
CCCAGCGACATTGCCGTCGAGTGGGAGTCTAATGGCCAGCCTGAAAACAATTATAA
GACAACCCACCTGTCTGACAGCGACGGCTCATTTTTTCTCTACTCTAACTCACC
GTGGATAAGAGCCGGTGGCAACAGGGAAATGTGTTTCAGCTGTAGCGTGATGCATGA
AGCTCTCCACAACCATTATACACAGAAGAGTCTGAGCCTGTCTCCTGGCAAATGA

Leader polynucleotide sequence (SEQ ID NO: 594)

ATGGACATGAGAGTGCCTGCACAGCTGCTGGGCCTGCTGCTGCTGTGGCTGAGAGGC
GCCAGATG

Table 26. Anti-CCR8 molecule sequences.

SEQ ID NO:	Designation	Sequence
595	MPK20298-A4 SCFV huCCR8 HV hv cdr1	NNGMH
596	MPK20298-A4 SCFV huCCR8 HV hv cdr2	VISNDGSNKYYADSVKG
597	MPK20298-A4 SCFV huCCR8 HV hv cdr3	VYYGSGIYYKNRNYGMDV
598	MPK20298-A4 SCFV huCCR8 LV lv cdr1	GGNNIGSQNVH

SEQ ID NO:	Designation	Sequence
599	MPK20298-A4 SCFV huCCR8 LV lv_cdr2	RDSNRPS
600	MPK20298-A4 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
601	MPK20299-D2 SCFV huCCR8 HV hv_cdr1	NYGMH
602	MPK20299-D2 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
603	MPK20299-D2 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
604	MPK20299-D2 SCFV huCCR8 LV lv_cdr1	GGHNIGSKGVH
605	MPK20299-D2 SCFV huCCR8 LV lv_cdr2	RNSNRPS
606	MPK20299-D2 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
607	MPK20299-F11 SCFV huCCR8 HV hv_cdr1	NYGMH
608	MPK20299-F11 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
609	MPK20299-F11 SCFV huCCR8 HV hv_cdr3	VYYGSGSYKKRYYYGMDV
610	MPK20299-F11 SCFV huCCR8 LV lv_cdr1	GGNNIGSQNVH
611	MPK20299-F11 SCFV huCCR8 LV lv_cdr2	RDSNRPS
612	MPK20299-F11 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
613	MPK20298-H6 SCFV huCCR8 HV hv_cdr1	SSGMH
614	MPK20298-H6 SCFV huCCR8 HV hv_cdr2	VISYDGTNKYYADSVKG
615	MPK20298-H6 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
616	MPK20298-H6 SCFV huCCR8 LV lv_cdr1	GGHNIGSKGVH
617	MPK20298-H6 SCFV huCCR8 LV lv_cdr2	RNSNRPS
618	MPK20298-H6 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
619	MPK20297-A4 SCFV huCCR8 HV hv_cdr1	NYGMH
620	MPK20297-A4 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
621	MPK20297-A4 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
622	MPK20297-A4 SCFV huCCR8 LV lv_cdr1	GGHNIGSQNVH
623	MPK20297-A4 SCFV huCCR8 LV lv_cdr2	RDSNRPS
624	MPK20297-A4 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
625	MPK20299-H8 SCFV huCCR8 HV hv_cdr1	NYGMH
626	MPK20299-H8 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
627	MPK20299-H8 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
628	MPK20299-H8 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
629	MPK20299-H8 SCFV huCCR8 LV lv_cdr2	RNSNRPS
630	MPK20299-H8 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
631	MPK20300-C11 SCFV huCCR8 HV hv_cdr1	SYGMH
632	MPK20300-C11 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
633	MPK20300-C11 SCFV huCCR8 HV hv_cdr3	VYYGSGSYKKRYYYGMDV
634	MPK20300-C11 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
635	MPK20300-C11 SCFV huCCR8 LV lv_cdr2	RDINRPS
636	MPK20300-C11 SCFV huCCR8 LV lv_cdr3	QVWDSSVV
637	MPK20298-B1 SCFV huCCR8 HV hv_cdr1	NYGMH
638	MPK20298-B1 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
639	MPK20298-B1 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
640	MPK20298-B1 SCFV huCCR8 LV lv_cdr1	EGNNIGSKNVH
641	MPK20298-B1 SCFV huCCR8 LV lv_cdr2	RNSNRPS

SEQ ID NO:	Designation	Sequence
642	MPK20298-B1 SCFV huCCR8 LV lv_cdr3	QAWDSSTVV
643	MPK20297-E5 SCFV huCCR8 HV hv_cdr1	NNGMH
644	MPK20297-E5 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYTDSVKG
645	MPK20297-E5 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
646	MPK20297-E5 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
647	MPK20297-E5 SCFV huCCR8 LV lv_cdr2	RDSNRPS
648	MPK20297-E5 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
649	MPK20299-A3 SCFV huCCR8 HV hv_cdr1	NYGMH
650	MPK20299-A3 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
651	MPK20299-A3 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
652	MPK20299-A3 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
653	MPK20299-A3 SCFV huCCR8 LV lv_cdr2	RNSNRPS
654	MPK20299-A3 SCFV huCCR8 LV lv_cdr3	QAWDSSTVV
655	MPK20297-B4 SCFV huCCR8 HV hv_cdr1	RNGMH
656	MPK20297-B4 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
657	MPK20297-B4 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNNYYYGMDV
658	MPK20297-B4 SCFV huCCR8 LV lv_cdr1	GGNNIGSQNVH
659	MPK20297-B4 SCFV huCCR8 LV lv_cdr2	RDSNRPS
660	MPK20297-B4 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
661	MPK20298-F6 SCFV huCCR8 HV hv_cdr1	RNGMH
662	MPK20298-F6 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
663	MPK20298-F6 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
664	MPK20298-F6 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
665	MPK20298-F6 SCFV huCCR8 LV lv_cdr2	RDSNRPS
666	MPK20298-F6 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
667	MPK20299-H3 SCFV huCCR8 HV hv_cdr1	NYGMH
668	MPK20299-H3 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
669	MPK20299-H3 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
670	MPK20299-H3 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
671	MPK20299-H3 SCFV huCCR8 LV lv_cdr2	RNSNRPS
672	MPK20299-H3 SCFV huCCR8 LV lv_cdr3	QIWDSSSTVV
673	MPK20298-B9 SCFV huCCR8 HV hv_cdr1	RNGMH
674	MPK20298-B9 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
675	MPK20298-B9 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKNYYYGMDV
676	MPK20298-B9 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
677	MPK20298-B9 SCFV huCCR8 LV lv_cdr2	RDSNRPS
678	MPK20298-B9 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
679	MPK20299-E2 SCFV huCCR8 HV hv_cdr1	NNGMH
680	MPK20299-E2 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYTDSVKG
681	MPK20299-E2 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
682	MPK20299-E2 SCFV huCCR8 LV lv_cdr1	EGNNIGSQNVH
683	MPK20299-E2 SCFV huCCR8 LV lv_cdr2	RDSNRPS
684	MPK20299-E2 SCFV huCCR8 LV lv_cdr3	QVWDGSAVV
685	MPK20299-D6 SCFV huCCR8 HV hv_cdr1	SYGMH
686	MPK20299-D6 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
687	MPK20299-D6 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV

SEQ ID NO:	Designation	Sequence
688	MPK20299-D6 SCFV huCCR8 LV lv cdr1	EGNNIGSQNVH
689	MPK20299-D6 SCFV huCCR8 LV lv cdr2	RDSNRPS
690	MPK20299-D6 SCFV huCCR8 LV lv cdr3	QVWDGSAVV
691	MPK20299-A4 SCFV huCCR8 HV hv cdr1	NYGFH
692	MPK20299-A4 SCFV huCCR8 HV hv cdr2	VISYDGSNRYADSVKG
693	MPK20299-A4 SCFV huCCR8 HV hv cdr3	VYYGSGTYYKNRYYYGMDV
694	MPK20299-A4 SCFV huCCR8 LV lv cdr1	GGHNIGSKGVH
695	MPK20299-A4 SCFV huCCR8 LV lv cdr2	RNSNRPS
696	MPK20299-A4 SCFV huCCR8 LV lv cdr3	QAWDSGTVV
697	MPK20300-G5 SCFV huCCR8 HV hv cdr1	NYGFH
698	MPK20300-G5 SCFV huCCR8 HV hv cdr2	VISYDGSNRYADSVKG
699	MPK20300-G5 SCFV huCCR8 HV hv cdr3	VYYGSGTYYKNRYYYGMDV
700	MPK20300-G5 SCFV huCCR8 LV lv cdr1	GANNIGSKNVH
701	MPK20300-G5 SCFV huCCR8 LV lv cdr2	RDFNRPS
702	MPK20300-G5 SCFV huCCR8 LV lv cdr3	QVWDSSTGNVV
703	MPK20299-C3 SCFV huCCR8 HV hv cdr1	NYGFH
704	MPK20299-C3 SCFV huCCR8 HV hv cdr2	VISYDGSNKYYADSVKG
705	MPK20299-C3 SCFV huCCR8 HV hv cdr3	VYYGSGSYKNRYYYGMDV
706	MPK20299-C3 SCFV huCCR8 LV lv cdr1	GGNNIGSKNVH
707	MPK20299-C3 SCFV huCCR8 LV lv cdr2	RDSNRPS
708	MPK20299-C3 SCFV huCCR8 LV lv cdr3	QVWDSSTVV
709	MPK20299-B7 SCFV huCCR8 HV hv cdr1	NYGMH
710	MPK20299-B7 SCFV huCCR8 HV hv cdr2	VISYDGSNKYYADSVKG
711	MPK20299-B7 SCFV huCCR8 HV hv cdr3	VYYGSGIYYKKRYYYGMDV
712	MPK20299-B7 SCFV huCCR8 LV lv cdr1	GGNNIGSKNVH
713	MPK20299-B7 SCFV huCCR8 LV lv cdr2	RDSNRPS
714	MPK20299-B7 SCFV huCCR8 LV lv cdr3	QVWDSSSAHVI
715	MPK20299-A5 SCFV huCCR8 HV hv cdr1	GYGMH
716	MPK20299-A5 SCFV huCCR8 HV hv cdr2	VISYDGSNKYYADSVKG
717	MPK20299-A5 SCFV huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
718	MPK20299-A5 SCFV huCCR8 LV lv cdr1	GGNNLGSKNVH
719	MPK20299-A5 SCFV huCCR8 LV lv cdr2	RNSNRPS
720	MPK20299-A5 SCFV huCCR8 LV lv cdr3	QVWDSSTVV
721	MPK20299-D1 SCFV huCCR8 HV hv cdr1	NNGMH
722	MPK20299-D1 SCFV huCCR8 HV hv cdr2	VISYDGSNKYYADSVKG
723	MPK20299-D1 SCFV huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
724	MPK20299-D1 SCFV huCCR8 LV lv cdr1	GGNRIGSKNVH
725	MPK20299-D1 SCFV huCCR8 LV lv cdr2	RDSNRPS
726	MPK20299-D1 SCFV huCCR8 LV lv cdr3	QVWDSSTVV
727	MPK20299-C5 SCFV huCCR8 HV hv cdr1	NYGFH
728	MPK20299-C5 SCFV huCCR8 HV hv cdr2	VISYDGSNRYADSVKG
729	MPK20299-C5 SCFV huCCR8 HV hv cdr3	VYYGSGTYYKNRYYYGMDV
730	MPK20299-C5 SCFV huCCR8 LV lv cdr1	GGHNIGSKGVH
731	MPK20299-C5 SCFV huCCR8 LV lv cdr2	RNSNRPS
732	MPK20299-C5 SCFV huCCR8 LV lv cdr3	QVWDSSTVV
733	MPK20299-B5 SCFV huCCR8 HV hv cdr1	NYGMH

SEQ ID NO:	Designation	Sequence
734	MPK20299-B5 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
735	MPK20299-B5 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
736	MPK20299-B5 SCFV huCCR8 LV lv_cdr1	GGHNIGSKGVH
737	MPK20299-B5 SCFV huCCR8 LV lv_cdr2	RNSNRPS
738	MPK20299-B5 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
739	MPK20299-G9 SCFV huCCR8 HV hv_cdr1	NNGMH
740	MPK20299-G9 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVRG
741	MPK20299-G9 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
742	MPK20299-G9 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
743	MPK20299-G9 SCFV huCCR8 LV lv_cdr2	RNSNRPS
744	MPK20299-G9 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
745	MPK20299-G5 SCFV huCCR8 HV hv_cdr1	NNGMH
746	MPK20299-G5 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVRG
747	MPK20299-G5 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
748	MPK20299-G5 SCFV huCCR8 LV lv_cdr1	EGNNIGSKNVH
749	MPK20299-G5 SCFV huCCR8 LV lv_cdr2	RDSNRPS
750	MPK20299-G5 SCFV huCCR8 LV lv_cdr3	QVWDSSAVV
751	MPK20298-C10_SCFV huCCR8 HV hv_cdr1	SSGMH
752	MPK20298-C10_SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
753	MPK20298-C10_SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNNYYGMDV
754	MPK20298-C10_SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
755	MPK20298-C10_SCFV huCCR8 LV lv_cdr2	RNSNRPS
756	MPK20298-C10_SCFV huCCR8 LV lv_cdr3	QAWDSSTVV
757	MPK20298-B5 SCFV huCCR8 HV hv_cdr1	NYGMH
758	MPK20298-B5 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
759	MPK20298-B5 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
760	MPK20298-B5 SCFV huCCR8 LV lv_cdr1	GGNNIGSQNVH
761	MPK20298-B5 SCFV huCCR8 LV lv_cdr2	RDSNRPS
762	MPK20298-B5 SCFV huCCR8 LV lv_cdr3	QVWDSSAVV
763	MPK20299-F2 SCFV huCCR8 HV hv_cdr1	SSGMH
764	MPK20299-F2 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
765	MPK20299-F2 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
766	MPK20299-F2 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
767	MPK20299-F2 SCFV huCCR8 LV lv_cdr2	RDSNRPS
768	MPK20299-F2 SCFV huCCR8 LV lv_cdr3	QAWDSGTVV
769	MPK20298-D4 SCFV huCCR8 HV hv_cdr1	NYGMH
770	MPK20298-D4 SCFV huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
771	MPK20298-D4 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKKRYYYGMDV
772	MPK20298-D4 SCFV huCCR8 LV lv_cdr1	GGNNIGGKNVH
773	MPK20298-D4 SCFV huCCR8 LV lv_cdr2	RDSNRPS
774	MPK20298-D4 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
775	MPK20297-F5 SCFV huCCR8 HV hv_cdr1	RNGMH
776	MPK20297-F5 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG

SEQ ID NO:	Designation	Sequence
777	MPK20297-F5 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNNYYYYGMDV
778	MPK20297-F5 SCFV huCCR8 LV lv_cdr1	GGNNIGSKNVH
779	MPK20297-F5 SCFV huCCR8 LV lv_cdr2	RNSNRPS
780	MPK20297-F5 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
781	MPK20299-D9 SCFV huCCR8 HV hv_cdr1	RNGMH
782	MPK20299-D9 SCFV huCCR8 HV hv_cdr2	VISNDGSNKYYADSVKG
783	MPK20299-D9 SCFV huCCR8 HV hv_cdr3	VYYGSGIYYKNNYYYYGMDV
784	MPK20299-D9 SCFV huCCR8 LV lv_cdr1	GGNNIESKNVH
785	MPK20299-D9 SCFV huCCR8 LV lv_cdr2	RDSNRPS
786	MPK20299-D9 SCFV huCCR8 LV lv_cdr3	QVWDSSTVV
787	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC huCCR8 HV hv_cdr1	NARMG
788	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC huCCR8 HV hv_cdr2	RIKSKTEGGTRDYAAPVKG
789	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC huCCR8 HV hv_cdr3	YSGV
790	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC huCCR8 LV lv_cdr1	KSSQSVLYSSNNRNYLA
791	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC huCCR8 LV lv_cdr2	WASTRES
792	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC huCCR8 LV lv_cdr3	QQYYSIPIT
793	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr1	NYGFH
794	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr2	VISYDGSNRYYASSVKG
795	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr3	VYYGSGTYYKNRYYYGMDV
796	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr1	GGHNIGSKGVH
797	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr2	RAANRPS
798	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr3	QAFDAGTVV

SEQ ID NO:	Designation	Sequence
799	anti-huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr1	NYGFH
800	anti-huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr2	VISYAGSNRYYAASVKG
801	anti-huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr3	VYYGSGTYYKNRYYYGMDV
802	anti-huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr1	GGHNIGSKGVH
803	anti-huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr2	RQSNRPS
804	anti-huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr3	QAFDAGTVV
805	anti-huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr1	NYGFH
806	anti-huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr2	VISYSGSNRYYADSVKG
807	anti-huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_HC huCCR8 HV hv_cdr3	VYYGSGTYYKNRYYYGMDV
808	anti-huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr1	GGHNIGSKGVH
809	anti-huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr2	RQSNRPS
810	anti-huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_LC huCCR8 LV lv_cdr3	QAFDAGTVV

SEQ ID NO:	Designation	Sequence
811	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb LC huCCR8 LV lv cdr1	GGHNIGSKGVH
812	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb LC huCCR8 LV lv cdr2	RNSNRPS
813	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb LC huCCR8 LV lv cdr3	QVWDISTVV
814	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb HC huCCR8 HV hv cdr1	NCGMH
815	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb HC huCCR8 HV hv cdr2	VISYDGGNKYHADSVKG
816	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb HC huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
817	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb LC huCCR8 LV lv cdr1	GGHNIGSKGVH
818	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb LC huCCR8 LV lv cdr2	RNSNRPS
819	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb LC huCCR8 LV lv cdr3	QVWDSSTVV
820	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb HC huCCR8 HV hv cdr1	NCGMH
821	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb HC huCCR8 HV hv cdr2	VISYDGGNKYYADSVKG
822	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb HC huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
823	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb LC huCCR8 LV lv cdr1	GGNNIGSKNVH
824	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb LC huCCR8 LV lv cdr2	RDSNRPS
825	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb LC huCCR8 LV lv cdr3	QVWDSNTVV
826	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb HC huCCR8 HV hv cdr1	NNGMH
827	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb HC huCCR8 HV hv cdr2	VISNDGSNKYYADSVRG
828	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb HC huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
829	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb LC huCCR8 LV lv cdr1	GGNNIGSKNVH
830	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb LC huCCR8 LV lv cdr2	RNSNRPS
831	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb LC huCCR8 LV lv cdr3	QVWDSSTVV
832	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb HC huCCR8 HV hv cdr1	TYGMH
833	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb HC huCCR8 HV hv cdr2	VISYDGSNKYYADSVKG

SEQ ID NO:	Designation	Sequence
834	Hu anti-huCCR8 LIBC317977-1 HulgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGSYKKNNYYYGMDV
835	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGGKNVH
836	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_LC huCCR8 LV lv_cdr2	RDSNRPS
837	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
838	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_HC huCCR8 HV hv_cdr1	SYGFH
839	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_HC huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
840	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGTYYKNRYYYGMDV
841	Hu anti-huCCR8 LIBC319840-1 HulgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
842	Hu anti-huCCR8 LIBC319840-1 HulgG1z mAb_LC huCCR8 LV lv_cdr2	RDSNRPS
843	Hu anti-huCCR8 LIBC319840-1 HulgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
844	Hu anti-huCCR8 LIBC319840-1 HulgG1z mAb_HC huCCR8 HV hv_cdr1	NNGMH
845	Hu anti-huCCR8 LIBC319840-1 HulgG1z mAb_HC huCCR8 HV hv_cdr2	VISNDGSNKYYPDVSVKG
846	Hu anti-huCCR8 LIBC319840-1 HulgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGNYYKNRYYYGMDV
847	Hu anti-huCCR8 LIBC320212-1 HulgG1z mAb_LC huCCR8 LV lv_cdr1	EGNNIGSQNVH
848	Hu anti-huCCR8 LIBC320212-1 HulgG1z mAb_LC huCCR8 LV lv_cdr2	RDSNRPS
849	Hu anti-huCCR8 LIBC320212-1 HulgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDGSAVV
850	Hu anti-huCCR8 LIBC320212-1 HulgG1z mAb_HC huCCR8 HV hv_cdr1	SSGMH
851	Hu anti-huCCR8 LIBC320212-1 HulgG1z mAb_HC huCCR8 HV hv_cdr2	VISHDGSNKYYADSVKG
852	Hu anti-huCCR8 LIBC320212-1 HulgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
853	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_LC huCCR8 LV lv_cdr1	GGHNIGSKGVH
854	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_LC huCCR8 LV lv_cdr2	RNSNRPS
855	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
856	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_HC huCCR8 HV hv_cdr1	DCGMH

SEQ ID NO:	Designation	Sequence
857	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISYDGGNKYYADSVKG
858	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
859	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
860	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr2	RSSNRPS
861	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr3	QIWDSSSTVV
862	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr1	SYGMH
863	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISFDGNNKYYADSVKG
864	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGSYYYKNRYYYGMDV
865	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
866	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr2	RDSNRPS
867	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
868	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr1	SNGMH
869	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISNDGSNKYYGDSVKG
870	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYRNRYYYGMDV
871	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
872	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr2	RNTNRPS
873	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
874	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr1	GYGMH
875	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
876	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
877	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
878	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr2	RNTNRPS
879	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV

SEQ ID NO:	Designation	Sequence
880	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr1	GYGMH
881	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
882	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
883	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGDKNVH
884	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr2	RNNVRPS
885	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
886	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr1	NFGMH
887	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISYDGGNKYYADSVKG
888	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGSYKKRYYYGMDV
889	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
890	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr2	RDSNRPS
891	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
892	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr1	SCGMH
893	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr2	VISYDGTNKYYADSVKG
894	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKKNYYGMDV
895	huCCR8_32360_huIgG1z mAb_HC huCCR8 HV hv_cdr1	NARMG
896	huCCR8_32360_huIgG1z mAb_HC huCCR8 HV hv_cdr2	RIKSKTEGGTRDYAAPVKG
897	huCCR8_32360_huIgG1z mAb_HC huCCR8 HV hv_cdr3	YSGV
898	huCCR8_32360_huIgG1z mAb_LC huCCR8 LV lv_cdr1	KSSQSVLYSSNNKNYLA
899	huCCR8_32360_huIgG1z mAb_LC huCCR8 LV lv_cdr2	WASTRES
900	huCCR8_32360_huIgG1z mAb_LC huCCR8 LV lv_cdr3	QQYYSIPIT
901	MPK20298-A4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDNS KNTLYLQMNSLRTEDTAVYYCAKV

SEQ ID NO:	Designation	Sequence
		YYGSGIYYKNRNYYGMDVWGQGT TVSS
902	MPK20298-A4_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPDRFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTK LTVL
903	MPK20299-D2_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSS
904	MPK20299-D2_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTITRAQ AGDEADYYCQVWDSSTTVFGGGTK LTVL
905	MPK20299-F11_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAPS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLFLQMNSLRAEDTAVYFCARVY YGSYSYYKKRYYYGMDVWGQGT TVSS
906	MPK20299-F11_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTQ LTVL
907	MPK20298-H6_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISYDGTNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVSS
908	MPK20298-H6_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTQ LTVL
909	MPK20297-A4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNYGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT TVSS

SEQ ID NO:	Designation	Sequence
910	MPK20297-A4_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGHN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTQ LTVL
911	MPK20299-H8_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSS
912	MPK20299-H8_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKAGQAPVQVIYRNS NRPSGIPARFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTK LTVL
913	MPK20300-C11_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKRNRYYYGMDVWGQGT TVTVSS
914	MPK20300-C11_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARIPCGGNNI GSKNVHWYQQKPGQAPVLVIYRDIN RPSGIPERFSGSNSGNTATLTISRAQA GDEADYYCQVWDSSVFGGGTKLT VL
915	MPK20298-B1_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSS
916	MPK20298-B1_SCFV LV huCCR8	SYELTQPPSVSVALGQTARLTCEGNN IGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISR VQAGDEADYYCQAWDSSTTVFGGGTQ LTVL
917	MPK20297-E5_SCFV HV huCCR8	QVQLVESGGGLVKPGGSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT TVTVSS
918	MPK20297-E5_SCFV LV huCCR8	SYELTQPLSVSEALGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSNSGNAATLTISRVEA

SEQ ID NO:	Designation	Sequence
		GDEADYYCQVWDSSTHVVFGGGTQLTVL
919	MPK20299-A3_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGIYYKKRYYYGMDVWGQGT TVSS
920	MPK20299-A3_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRNSN RPSGIPERFSGSNSGNTATLTISGTQA MDEADYYCQAWDSNVVFGGGTQLTVL
921	MPK20297-B4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWRQVPGRLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGIYYKNYYYGMDVWGQGT TVSS
922	MPK20297-B4_SCFV LV huCCR8	SYELTQPLSVSVALGQTARITCGGNNI IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPDRFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTQLTVL
923	MPK20298-F6_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWRQVPGRLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGIYYKNRYYYGMDVWGQGT TVSS
924	MPK20298-F6_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAQA GDEAEYYCQVWDSSTVVFGGGTELT VL
925	MPK20299-H3_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGIYYKKRYYYGMDVWGQGT TVSS
926	MPK20299-H3_SCFV LV huCCR8	SYELTQPLSVSVALGQTARITCGGNNI IGSKNVHWYQQKPGQAPVLAIRNS NRPSGIPERFTGSNSGNTATLTISRAQ AGDESDYYCQIWDSSTVVFGGGTKL TVL

SEQ ID NO:	Designation	Sequence
927	MPK20298-B9_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKKNYYYGMDVWGQGT TVSS
928	MPK20298-B9_SCFV LV huCCR8	SYELTQPPSVSVALGQTARISCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAQA GDEAEYYCQVWDSSTVVFGGGTQLT VL
929	MPK20299-E2_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT TVSS
930	MPK20299-E2_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCEGNNI GSQNVHWYQQKPGQAPVLV MYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDGSAVVFGGGTK LTVL
931	MPK20299-D6_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSIGIYYKKRYYYGMDVWGQGT TVSS
932	MPK20299-D6_SCFV LV huCCR8	SYELTQPLSVSVALGQTARITCEGNNI GSQNVHWYQQKPGQAPVLV MYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDGSAVVFGGGTQ LTVL
933	MPK20299-A4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV YYGSGTYKKNRYYYGMDVWGQGT TVTVSS
934	MPK20299-A4_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISGTQ AMDEADYYCQAWDSGTVVFGGGTQ LTVL
935	MPK20300-G5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV

SEQ ID NO:	Designation	Sequence
		YYGSGTYYKNRYYYGMDVWGQGT TVTVSS
936	MPK20300-G5_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARITCGANN IGSKNVHWYQQKPGQPPVLVIYRDF NRPSGIPERFSASNSGNTATLTISRQ AGDEADYYCQVWDSSTGNVVFGGG TKLTVL
937	MPK20299-C3_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFIFSNYGFHWVRQTPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDN NTLYLQMNSLRGEDTAVYYCARVY YGSGSYKKNRYYYGMDVWGQGT TVTVSS
938	MPK20299-C3_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAQA GDEADYYCQVWDSSTVVFGGGTELT VL
939	MPK20299-B7_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGIYYKKRYYYGMDVWGQGT TVTVSS
940	MPK20299-B7_SCFV LV huCCR8	SYELTQSSSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRVEA GDEADYYCQVWDSSSAHVIFGGG TKLTVL
941	MPK20299-A5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
942	MPK20299-A5_SCFV LV huCCR8	SYELTQPPSGSV ALGQTARITCGGNN LGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGG TKLTVL
943	MPK20299-D1_SCFV HV huCCR8	QVQLVESGGGLVKPGGSLRLSCAAS GFTFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS

SEQ ID NO:	Designation	Sequence
944	MPK20299-D1_SCFV LV huCCR8	SYELTQPPSVSVVALGQTARITCGGNRI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAQA GDEAEYYCQVWDSSTTVFGGGKLT VL
945	MPK20299-C5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSS
946	MPK20299-C5_SCFV LV huCCR8	SYELTQLPSVSVVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTE LTVL
947	MPK20299-B5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGIYYKNRYYYGMDVWGQGT TVSS
948	MPK20299-B5_SCFV LV huCCR8	SYELTQPPSVSVVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTQ LTVL
949	MPK20299-G9_SCFV HV huCCR8	QVQLVESGGDLVQPGRSLRLSCAAS GFTFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
950	MPK20299-G9_SCFV LV huCCR8	SYELTQPLSVSVVALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTLSRVQ AGDEADYYCQVWDSSTTVFGGGK LTVL
951	MPK20299-G5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
952	MPK20299-G5_SCFV LV huCCR8	SYELTQPPSVSVVALGQTARLTCEGNN IGSKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLAISRAQ

SEQ ID NO:	Designation	Sequence
		AGDESDYYCQVWDSSAVVFGGGTK LTVL
953	MPK20298-C10_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNYYYGMDVWGQGT TVSS
954	MPK20298-C10_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLAIRNS NRPSGIPERFTGSNSGNTATLTISGTQ AMDEADYYCQAWDSSTVVFGGGTK LTVL
955	MPK20298-B5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSS
956	MPK20298-B5_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDSSAVVFGGGTQ LTVL
957	MPK20299-F2_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTLSSSGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVSS
958	MPK20299-F2_SCFV LV huCCR8	SYELTQPPSVSVALGQTARISCGGNNI GSKNVHWYQQKPGQAPVLVMIYRDS NRPSGIPERFSGNSGNTATLTISGTQ AMDEADYYCQAWDSGTVVFGGGTK LTVL
959	MPK20298-D4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSS
960	MPK20298-D4_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGGKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDESDYYCQVWDSSTVVFGGGTQ LTVL

SEQ ID NO:	Designation	Sequence
961	MPK20297-F5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNYYGMDVWGQGT VTVSS
962	MPK20297-F5_SCFV LV huCCR8	SYELTQPLSVSVLALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAG AGDEADYYCQVWDSSTVVFGGGTK LTVL
963	MPK20299-D9_SCFV HV huCCR8	QVQLVESGGGLVKPGGSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNYYGMDVWGQGT VTVSS
964	MPK20299-D9_SCFV LV huCCR8	SYELTQPPSVSVLALGQTARISCGGNNI ESKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAGA GDEAEYYCQVWDSSTVVFGGGTQLT VL
965	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC HV huCCR8	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISRD DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVTVSS
966	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC LV huCCR8	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNRNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSTDF LTINSLQAEDVAVYYCQQYYSIPITFG GGTKVEIKR
967	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYYASSVKGRFTISRDNS KNTLYLQMNSLRGEDTALYYCARV YYGSGTYKNNRYYYGMDVWGQGT TVTVSS
968	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC LV huCCR8	SYELTQPPSVSVLALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRAA NRPSGIPERFSGSNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFGGGTQ LTVLG
969	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q _M99E_W109F_S111A)_huIgG1z (mAb)_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYAGSNRYYYAASVKGRFTISRDNS KNTLYLQMNSLRGEDTALYYCARV

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		YYGSGTYYKNRYYYGMDVWGQGT TVTVSS
970	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_LC LV huCCR8	SYELTQPPSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRQS NRPSGIPERFSGSNSGNTATLTISGTQ AEDEADYYCQAFDAGTVVFGGGTQ LTVLG
971	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYSGSNRYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSS
972	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_LC LV huCCR8	SYELTQPPSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRQS NRPSGIPERFSGSNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFGGGTQ LTVLG
973	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb _LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDISTVVFGGGT TVLG
974	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb _HC HV huCCR8	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSNCGMHWVRQAPGKGLEWVA VISYDGGNKYHADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
975	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb _LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGKTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGT LTVLG
976	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb _HC HV huCCR8	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSNCGMHWVRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
977	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb _LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQKRPQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSNTVVFGGGT LTVLG

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978	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYSCAKV YYGSGIYYKNNYYYGMDVWGQGT TVVSS
979	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSVVALGQTARITCGGNN IGSKNVHWYQQKAGQAPVQVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLG
980	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFNTYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KSTLYLQMNSLRAEDTAVYYCARVY YGSGSYKKNYYYGMDVWGQGT TVVSS
981	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSVVALGQTARITCGGNN IGGKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDESDYYCQVWDSSTVVFGGGTT TVLG
982	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_HC HV huCCR8	QVQVVESGGGVVQPGRSLRLSCAAS GFTLSSYGFWVRQTPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITAVYYCARVY YSGTYYKNRYYYGMDVWGQGT TVVSS
983	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSEALGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGNTATLTISRAQA GDEADYYCQVWDSSTVVFGGGTKV TVLG
984	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFINNGMHWVRQAPGKGLDWVA VISNDGSNKYYPDsvKGRFTISRDN KNTLYLQMNSLRAEDSAVYYCAKV YYGSGNYYKNNYYYGMDVWGQGT TVTVSS
985	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSVVALGQTARITCEGNNI GSQNVHWYQQKPGQAPVLVMYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDGSAVVFGGGTT LTVLG
986	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_HC HV huCCR8	QMQVVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISHDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLGGEDITAVYYCAKV

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		YYGSGIYYKNRYYYGMDVWGQGT VIVSS
987	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTE LTVLG
988	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSDCGMHWVRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQTDLSRTEDTAVYYCAKVY YGSGIYYKNRYYYGMDVWGQGTTV TVSS
989	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTGRITCGGNN IGSKNVHWYQQKPGQAPVLVIYRSS NRPSGIPERFSGSNSGNTATLTISRAQ AGDESDYYCQIWDSSTTVFGGGTKL TVLG
990	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC HV huCCR8	QVQVVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISFDGNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKNRYYYGMDVWGQGT TVTVST
991	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQRPGQAPVLVIYRDS NRPSGIPERLSGSKAGNTATLTISRAH AGDEADYYCQVWDSSTTVFGGGTE LTVQG
992	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAVS GFTFSSNGMHWVRQAPGKGLEWVA VISNDGSNKYYGDSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYRNYYYYGMDVWGQGT TVVSS
993	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTTVFGGGTKLT VLG
994	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC HV huCCR8	QVQVVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFPISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VAVSS

SEQ ID NO:	Designation	Sequence
995	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTVVFGGGTKLT VLG
996	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC HV huCCR8	QVQVVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VAVSS
997	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC LV huCCR8	SYDLTQPLSVSV ALGQTARITCGGNN IGDKNVHWYQQKPGQAPVLVIYRNN VRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLG
998	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GLNFSNFGMHWRQAPGKGLDWVA VISYDGGNKYYADSVKGRFTVSRDN SKNTLFLQMNSLRAEDTALYYCAKV YYGSGSYKKRYYYGMDVWGQGT TVTVSS
999	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGAK LTVLG
1000	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSSCGMHWRQAPGKGLEWVA VISYDGTNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNYYYYGMDVWGQGT TVTVSS
1001	huCCR8_32360_huIgG1z mAb_HC HV huCCR8	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISRD DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVTVSS
1002	huCCR8_32360_huIgG1z mAb_LC LV huCCR8	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNKNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSGTDFT LTINSLQAEDVAVYYCQQYYIPITFG GGTKVEIKR

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1003	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGK
1004	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC Constant	TVAAPSVFIFPPSDEQLKSGTASVCL LNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFN RGE
1005	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGK
1006	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1007	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_ M99E_W109F_S111A)_huIgG1z (mAb)_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV L

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		DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1008	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1009	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1010	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1011	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1012	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK

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1013	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1014	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVV DSDGSFFLYSKLTVDKSRWQQGNV SCSVMHEALHNHYTQKSLSLSPGK
1015	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1016	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVV DSDGSFFLYSKLTVDKSRWQQGNV SCSVMHEALHNHYTQKSLSLSPGK
1017	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1018	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN

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		STYRVVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV L DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1019	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1020	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV L DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1021	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1022	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV L DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1023	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS

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1024	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
1025	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1026	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
1027	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1028	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:	Designation	Sequence
		DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1029	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1030	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1031	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1032	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1033	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS

SEQ ID NO:	Designation	Sequence
1034	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
1035	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1036	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
1037	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1038	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:	Designation	Sequence
		DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1039	huCCR8_32360_huIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPK KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1040	huCCR8_32360_huIgG1z mAb_LC Constant	TVAAPSVEFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFN RGE
1041	MPK20298-A4_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKRNYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGGNNIGSQ VHWYQQKPGQAPVLVIYRDSNRPSG IPDRFSGSKSGNTATLTISRAQAGDEA DYQCQVWDSSTVVFGGGTKLTVL
1042	MPK20299-D2_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSVALGQTARITCGGHNIGSKGV HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTITRAQAGDEAD YYCQVWDSSTVVFGGGTKLTVL

SEQ ID NO:	Designation	Sequence
1043	MPK20299-F11_SCFV	QVQLVESGGGVVQPGRSLRLSCAPS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLFLQMNSLRAEDTAVYFCARVY YGSYSYKKRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGNNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGNTATLTISRAQAGDEA DYCYQVWDSSTVVFGGGTQLTVL
1044	MPK20298-H6_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISYDGTNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGHNIGSKG VHWYQQKPGQAPVLVIYRNSNRPSG IPERFSGSNSGNTATLTISRAQAGDEA DYCYQVWDSSTVVFGGGTQLTVL
1045	MPK20297-A4_SCFV	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNYGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGHNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGNTATLTISRAQAGDEA DYCYQVWDSSTVVFGGGTQLTVL
1046	MPK20299-H8_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSYIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSVAPGQTARITCGNNIGSKNV HWYQQKAGQAPVQVIYRNSNRPSGI PARFSGSNSGNTATLTISRAQAGDEA DYCYQVWDSSTVVFGGGTKLTVL
1047	MPK20300-C11_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKKNRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYEL TQPPSVSVAPGQTARIPCGNNIGSK NVHWYQQKPGQAPVLVIYRDINRPS

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		GIPERFSGSNSGNTATLTISRAGDE ADYYCQVWDSSVVFGGGTCLTVL
1048	MPK20298-B1_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGGSGGGGSSYELTQ PPSVSV ALGQTARLTCEGNNIGSKN HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTISRQAGDEAD YYCQAWDSSTVVFGGGTCLTVL
1049	MPK20297-E5_SCFV	QVQLVESGGGLVKPGGSLRLSCAVS GFNFSNNGMHWRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYSGIYYKKRYYYGMDVWGQGT VTVSSGGGGSGGGGSGGGGSSYELT QPLSVSEALGQTARITCGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSNSGNAATLTISRVEAGDEA DYYCQVWDSSSDHVVFGGGTCLTV L
1050	MPK20299-A3_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGGSGGGGSSYELTQ PPSVSVAPGQTARITCGNNIGSKN HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTISGTQAMDEAD YYCQAWDSNVVFGGGTCLTVL
1051	MPK20297-B4_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGIYYKNYYGMDVWGQGT VTVSSGGGGSGGGGSGGGGSSYELT QPLSVSV ALGQTARITCGNNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPDRFSGSKSGNTATLTISRAGDEA DYYCQVWDSSSTVVFGGGTCLTVL

SEQ ID NO:	Designation	Sequence
1052	MPK20298-F6_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGGSGGGSSYELT QPPSVSVAPGQTARITCGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTCLTVL
1053	MPK20299-H3_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGGSGGGSSYELTQ PLSVSVALGQTARITCGNNIGSKNV HWYQQKPGQAPVLAIYRNSNRPSGIP ERFTGSNSGNTATLTISRAQAGDESD YYCQIWDSSTVVFGGGTCLTVL
1054	MPK20298-B9_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGGSGGGSSYELT QPPSVSVALGQTARISCGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTCLTVL
1055	MPK20299-E2_SCFV	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT VTVSSGGGGSGGGGSGGGSSYELT QPPSVSVALGQTARITCEGNNIGSQN VHWYQQKPGQAPVLVMYRDSNRPS GIPERFSGSKSGNTATLAISRAQAGDE SDYYCQVWDGSAVVFGGGTKLTVL
1056	MPK20299-D6_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGGSGGGSSYELTQ PLSVSVALGQTARITCEGNNIGSQNV HWYQQKPGQAPVLVMYRDSNRPSGI

SEQ ID NO:	Designation	Sequence
		PERFSGSKSGNTATLAISRAQAGDES DYCYQVWDGSAVVFGGGTQLTVL
1057	MPK20299-A4_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYNRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYEL TQPPSVSV ALGQTARITCGHNIGSK GVHWYQQKPGQAPVLVIYRNSNRPS GIPERFSGSNSGNTATLTISGTQAMDE ADYYCQAWDSGTVVFGGGTQLTVL
1058	MPK20300-G5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYNRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYEL TQPPSVSV ALGQTARITCGANNIGSK NVHWYQQKPGQPPVLVIYRDFNRPS GIPERFASNSGNTATLTISRQAGDE ADYYCQVWDSSTGNVFGGGTKLT VL
1059	MPK20299-C3_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFIFSNYGFHWVRQTPGKGLEWVA ISYDGSNKYYADSVKGRFTISRDN NTLYLQMNSLRGEDTAVYYCARV YGSYSYKNRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYELT QPPSVSVAPGQTARITCGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAGAGDEA DYCYQVWDSSTVVFGGGTELTVL
1060	MPK20299-B7_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARV YSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ SSSVSVAPGQTARITCGNNIGSKNV HWYQQKPGQAPVLVIYRDSNRPSGIP ERFSGSKSGTTATLTISRVEAGDEAD YYCQVWDSSSAHVIFGGGKLTVL

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1061	MPK20299-A5_SCFV	QVQLVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSGSVALGQTARITCGNNLGSKN VHWYQQKPGQAPVLVIYRNSNRPSG IPERFSGSNSGNTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTKLTVL
1062	MPK20299-D1_SCFV	QVQLVESGGGLVKPGGSLRLSCAAS GFTFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGNRIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTKLTVL
1063	MPK20299-C5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYKNRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYEL TQLPSVSVALGQTARITCGHNIGSK GVHWYQQKPGQAPVLVIYRNSNRPS GIPERFSGSNSGNTATLTISRAQAGDE ADYYCQVWDSSTVVFGGGTELTVL
1064	MPK20299-B5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKNRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSVALGQTARITCGHNIGSKGV HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTISRAQAGDEAD YYCQVWDSSTVVFGGGTQLTVL
1065	MPK20299-G9_SCFV	QVQLVESGGDLVQPGRSLRLSCAAS GFTFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPLSVSVALGQTARITCGNNIGSKN VHWYQQKPGQAPVLVIYRNSNRPSG

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		IPERFSGSNSGNTATLTLRSRVQAGDE ADYYCQVWDSSTVVFGGGTKLTVL
1066	MPK20299-G5_SCFV	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSV ALGQTARLTCEGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGNTATLAISRAQAGDES DYYCQVWDSSAVVFGGGTKLTVL
1067	MPK20298-C10_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSV ALGQTARITCGNNIGSKN VHWYQQKPGQAPVLAIRNSNRPSG IPERFTGSNSGNTATLTISGTQAMDE ADYYCQAWDSSTVVFGGGTKLTVL
1068	MPK20298-B5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSV ALGQTARITCGNNIGSQNV HWYQQKPGQAPVLVIYRDSNRPSGIP ERFSGSKSGNTATLAISRAQAGDESD YYCQVWDSSAVVFGGGTQLTVL
1069	MPK20299-F2_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTLSSSGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSV ALGQTARISCGNNIGSKN VHWYQQKPGQAPVLVMYRDSNRPS GIPERFSGSNSGNTATLTISGTQAMDE ADYYCQAWDSGTVVFGGGTKLTVL

SEQ ID NO:	Designation	Sequence
1070	MPK20298-D4_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGSIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGGSGGGSSYELTQ PPSVSVALGQTARITCGGNNIGGKNV HWYQQKPGQAPVLVIYRDSNRPSGIP ERFSGSKSGNTATLTISRAQAGDESD YYCQVWDSSTVVFGGGTQLTVL
1071	MPK20297-F5_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGSIYYKNYYYGMDVWGQGT VTVSSGGGGSGGGGSGGGSSYELT QPLSVSVALGQTARITCGGNNIGSKN VHWYQQKPGQAPVLVIYRNSNRPSG IPERFSGSNSGNTATLTISRAQAGDEA DYCQVWDSSTVVFGGGTKLTVL
1072	MPK20299-D9_SCFV	QVQLVESGGGLVKPGGSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGSIYYKNYYYGMDVWGQGT VTVSSGGGGSGGGGSGGGSSYELT QPPSVSVALGQTARISCGGNNIESKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTQLTVL
1073	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISR DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRT P EVTCTVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAA PIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSFSVMHEAL HNHYTQKSLSLSPGK

SEQ ID NO:	Designation	Sequence
1074	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNRNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSGTDFT LTINSLQAEDVAVYYCQQYYIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDYSLSS TLTLISKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
1075	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYASSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1076	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRAA NRPSGIPERFSGSNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFEGGTQ LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1077	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_ M99E_W109F_S111A)_huIgG1z (mAb)_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYAGSNRYYAASVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH

SEQ ID NO:	Designation	Sequence
		EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1078	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q _M99E_W109F_S111A)_huIgG1z (mAb)_LC	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRQS NRPSGIPERFSGSNSGNTATLTISGTQ AEDEADYYCQAFDAGTVVFGGGTQ LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1079	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G _W109F_S111A)_huIgG1z (mAb)_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYSGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1080	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G _W109F_S111A)_huIgG1z (mAb)_LC	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRQS NRPSGIPERFSGSNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFGGGTQ LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1081	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDISTVVFGGGTEL TVLGQPKAAPSVTLPFPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1082	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_HC	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSNCGMHWVRQAPGKGLEWVA VISYDGGNKYHADS VKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1083	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGKTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTE LTVLGQPKAAPSVTLPFPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1084	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_HC	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSNCGMHWVRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH

SEQ ID NO:	Designation	Sequence
		EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1085	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQKRPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSNTVVFGGGTN LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1086	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYSCAKV YYGSGIYYKNYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1087	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKAGQAPVQVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1088	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFNFNTYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KSTLYLQMNSLRAEDTAVYYCARVY YGSGSYKKNYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1089	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC	SYELTQPLSVSVLALGQTARITCGGNN IGGKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDESDYYCQVWDSSTVVFGGGTLL TVLGQPKAAPSVTLPSPSEELQANK ATLVLCLISDFYPGAVTVAWKADSSP VKAGVETTTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1090	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCAAS GFTLSSYGFHWVRQTPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDN NTLYLQMNSLRGEDTAVYYCARVY YGSGTYKKNRYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK

SEQ ID NO:	Designation	Sequence
1091	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_LC	SYELTQPLSVSEALGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGNTATLTISRAQA GDEADYYCQVWDSSTVVFGGGTKV TVLGQPKAAPSVTLPSPSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTSPKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1092	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCVVS GFNFINNGMHWVRQAPGKGLDWVA VISNDGSNKYYPDSVKGRFTISRDN KNTLYLQMNSLRAEDSAVYYCAKV YYGSGNYYKNYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1093	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_LC	SYELTQPLSVSVALGQTARITCEGNNI GSQNVHWYQQKPGQAPVLVMYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDGSAVVFGGGTT LTVLGQPKAAPSVTLPSPSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTSPKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1094	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_HC	QMQLVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISHDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLGGEDTAVYYCAKV YYGSGIYYKNRYGMDVWGQGT VIVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH

SEQ ID NO:	Designation	Sequence
		EDPEVKFNWYVDGVEVHNAKTKPRE EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1095	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTE LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1096	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSDCGMHWVRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQTDSLRTEDTAVYYCAKVY YSGIYYKNRYYYGMDVWGQGTITV TVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTP PVLDSGDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSP GK
1097	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTGRITCGGNN IGSKNVHWYQQKPGQAPVLVIYRSS NRPSGIPERFSGSNSGNTATLTISRAQ AGDESDYYCQIWDSSSTVVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1098	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISFDGNNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKRNRYYYGMDVWGQGT TTVSTASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1099	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQRPGQAPVLVIYRDS NRPSGIPERLSGSKAGNTATLTISRAH AGDEADYYCQVWDSSTVVFGGGTE LTVQGQPKAAPSVTLPFSSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1100	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAVS GFTFSSNGMHWVRQAPGKGLEWVA VISNDGSNKYYGDSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYRNRYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK

SEQ ID NO:	Designation	Sequence
1101	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTVVFGGGTKLT VLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNNKYAASSYLSLT PEQWKSHRSYSCQVTHEGSTVEKTV APTECS
1102	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFPISRDN KNTLYLQMNSLRGEDITAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VAVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1103	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTVVFGGGTKLT VLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNNKYAASSYLSLT PEQWKSHRSYSCQVTHEGSTVEKTV APTECS
1104	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VAVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH

SEQ ID NO:	Designation	Sequence
		EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1105	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC	SYDLTQPLSVSVVALGQTARITCGGNN IGDKNVHWYQQKPGQAPVLVIYRNN VRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1106	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAAS GLNFSNFGMHWVRQAPGKGLDWVA VISYDGGNKYYADSVKGRFTVSRDN SKNTLFLQMNSLRAEDTALYYCAKV YYGSGSYKKRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1107	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC	SYELTQPLSVSVVALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGAK LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1108	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSSCGMHWVRQAPGKGLEWVA VISYDGTNKYYADSVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKKNYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1109	huCCR8_32360_huIgG1z mAb_HC	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISRD DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSG LYSLSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRT EVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
1110	huCCR8_32360_huIgG1z mAb_LC	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNKNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSGTDFT LTINSLQAEDVAVYYCQYYISIPITFG GGTKEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNFPYPREAKVQWKVD NALQSGNSQESVTEQDSKDYSLSS TLTLKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC

SEQ ID NO:	Designation	Sequence
1111	MPK20298-A4_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGACTGGAGTGGGTGGCA GTTATTTCAAATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAACAGGAACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGACCGATTC TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC AAGCTGACCGTCCTA
1112	MPK20299-D2_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAAGTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
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1113	MPK20299-F11_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCACCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAAAACACGCTGTTTCTGCA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGAGTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCACTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGAAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
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1115	MPK20297-A4_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTCACCATTTCCAGAGACA ATTCCAAGAACACACTGTATCTGCA AATGGACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
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1116	MPK20299-H8_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTCTGTGCGAGA GTTACTATGGTTCGGGGATTATT ATAAAAAGAGATACTACTACGGGA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTGAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGGCAGGCCAGGCCCTGTGCA GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGCGCGATT TCTGGCTCCAACCTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAGGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGTGGGACCA AGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
1117	MPK20300-C11_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAGCTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGGTGTATTACTGTGCGAG AGTTTACTATGGTTCGGGGAGTTAT TATAAAAACCGCTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTCAGTGGC CCCAGGACAGACGGCCAGGATTCC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTACT GGTCATCTATAGGGATATCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAACCTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC GTGGTATTCGGCGGAGGGACCAAG CTGACCGTCCTC
1118	MPK20298-B1_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTCTGTGCGAGA GTTTACTATGGTTCGGGGATTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
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1119	MPK20297-E5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCCTGGTCAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCACTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTCATATCGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACTCTCAGTGTGAGAGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTACT GGTCATCTATAGGGATAGCAACCG GCCCTCAGGGATCCCTGAGCGATTC TCTGGCTCCAACCTCTGGGAACGCGG CCACCCTGACCATCAGTAGGGTCG AAGCCGGGGATGAGGCCGACTATT ACTGTCAGGTGTGGGATAGTAGCA GTGATCATGTGGTATTCTGGCGGAG GCACCCAGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
1120	MPK20299-A3_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTCAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCTGTACT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTCT TCTGGCTCCAACCTCTGGGAACACAG CCACTCTGACCATCAGCGGGACCC AGGCTATGGATGAGGCTGACTATT ACTGTCAGGCGTGGGACAGCAGCA ATGTGGTATTCGGCGGAGGCACCC AGCTGACCGTCCTA
1121	MPK20297-B4_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATAACTACTATTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
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1122	MPK20298-F6_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAACCGCTATTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTGAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAAGTCGGGGACCACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGAGTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC GAGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
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1124	MPK20298-B9_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCGGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGTATTTAT TATAAAAAGAACTACTACTACGGT ATGGACGTCTGGGGCCAAGGGACC ACGGTCACCGTCTCCTCAGGTGGTG GTGGTTCTGGCGGCGGCGGCTCCG

SEQ ID NO:	Designation	Sequence
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1125	MPK20299-E2_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTCATATCGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCACTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGAGGGGAAACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCAATGTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAACGATTC TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGGCCATCAGCAGAGCC CAAGCCGGGGATGAGTCTGACTAT TACTGTCAGGTGTGGGACGGCAGT GCCGTGGTATTCGGCGGAGGGACC AAGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
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1127	MPK20299-A4_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAACTATGG CTTTCAGTGGGTCCGCCAGACTCCA GGCAAGGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA GATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTCCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGCTATATTACTGTGCGAGA GTTTACTATGGTTCGGGGACTTATT ATAAAAACCGCTACTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTTCTGGCGGCGGCGGCTCCGGT

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1128	MPK20300-G5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCACCTTCAGTAACTATGG CTTTCAGTGGGTCCGCCAGACTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA GATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTCCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGCTATATTACTGTGCGAGA GTTTACTATGGTTCGGGGACTTATT ATAAAAACCGCTACTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGCAAACAACATTGGAAG TAAAAATGTTCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCCTGTGCT GGTCATCTATAGAGATTTCAACCGG CCCTCTGGGATCCCTGAGCGATTCT CTGCCTCCAACCTCGGGGAACACGG CCACCCTGACCATCAGCAGAGGCC AAGCCGGGGATGAGGCTGACTATT ACTGTCAGGTGTGGGACAGCAGCA CTGGGAATGTGGTATTCGGCGGAG GGACCAAGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
1129	MPK20299-C3_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTTCATCTTCAGTAACTATGG CTTTCAGTGGGTCCGCCAGACTCCA GGCAAGGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGGTGTATTACTGTGCGAG AGTTTACTATGGTTCGGGGAGTTAT TATAAAAACCGCTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTCAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGACCACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC GAGCTGACCGTCCTA
1130	MPK20299-B7_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTCTGTGCGAGA GTTTACTATGGTTCGGGGATTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
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1131	MPK20299-A5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGGAGCCT CTGGATTCACCTTCAGTGGCTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCAAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGGTGTATTACTGTGCGAG AGTTTATTATGGTTCGGGGATTTAT TATAAAAACCGCTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGGGTCAGTGGC CCTGGGACAGACGGCCAGGATCAC CTGTGGGGGAAACAACCTTGGAAG TAAAAATGTGCACTGGTACCAACA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAACCTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAGGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTATTCGGCGGTGGGACC AAGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
1132	MPK20299-D1_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCCTGGTCAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGGCTGGAGTGGGTGGCA GTCATATCGTATGATGGAAGTAATA AATACTATGCGGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTATTATGGTTCGGGGATTATT ATAAAAACAGGTATTACTACGGGA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCCTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAGAATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGTT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAAGTCGGGGACCACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGAGTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC AAGCTGACCGTCCTA
1133	MPK20299-C5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAAGTATGG CTTTCAGTGGGTCCGCCAGACTCCA GGCAAGGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA GATACTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTCCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGCTATATTACTGTGCGAGA GTTTACTATGGTTCGGGGACTTATT ATAAAAACCGCTACTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTCTGGCGGCGGCGGCTCCGGT

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1134	MPK20299-B5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTATT ATAAAAACCGCTATTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCACTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGACACAACATTGGAAG TAAAGGTGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGTAGT ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA

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1135	MPK20299-G9_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGACTTGGTACAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGT CTGGATTACCTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGACTGGAGTGGGTGGCA GTTATTTCAAATGATGGCAGTAATA AATATTATGCAGATTCCGTGAGGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTATTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAACAGGTACTACTACGGGA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACTCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAACCTCGGGGAACACG GCCACCCTGACTCTTAGCAGAGTCC AAGCCGGGGATGAGGCTGACTATT ACTGTCAGGTGTGGGACAGCAGCA CTGTGGTTTTTCGGCGGAGGGACCA AGCTGACCGTCCTA
1136	MPK20299-G5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGACTGGAGTGGGTGGCA GTTATTTCAAATGATGGCAGTAATA AATATTATGCAGATTCCGTGAGGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACACTGTATCTGCA AATGGACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAACAGGTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
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1137	MPK20298-C10_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAGCTCTGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATAACTACTATTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCACTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGCCATCTATAGGAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT ACTGGCTCCAACCTCGGGGAACACG GCCACCCTGACCATCAGCGGGACC CAGGCTATGGATGAGGCTGACTATT ACTGTCAGGCGTGGGACAGCAGCA CTGTGGTATTCGGCGGAGGGACCA AGCTGACCGTCCTA

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1138	MPK20298-B5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGCTTC TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGGCCATCAGCAGAGCC CAAGCCGGGGATGAGTCTGACTAT TACTGTCAGGTGTGGGACAGCAGT GCCGTGGTATTCGGCGGAGGCACC CAGCTGACCGTCCTA
1139	MPK20299-F2_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCACCCTCAGTAGCTCTGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGGCTGGAGTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCGGACTCCGTGAAG GGCCGGTTCACCATCTCCAGAGAC GATTCCAAGAACACACTGTATCTGC AAATGGACAGCCTGAGAACTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGTATTAT TATAAAAACAGGTACTACTACGGG ATGGACGTCTGGGGCCAAGGGACC ACGGTCACCGTCTCCTCAGGTGGTG GTGGTTCTGGCGGCGGCGGCTCCG

SEQ ID NO:	Designation	Sequence
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1140	MPK20298-D4_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTCACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGAATTAC CTGTGGGGGAAACAACATTGGAGG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGTCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTATTCGGCGGAGGCACC CAGCTGACCGTCCTA

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1141	MPK20297-F5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATAACTACTATTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACTCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAACCTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAGGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGTGGGACCA AGCTGACCGTCCTA
1142	MPK20299-D9_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCTTGGTCAAGCCTGGAGGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATAACTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
		GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTTTC CTGTGGGGGAAACAACATTGAAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGTT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGACCACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGAGTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA
1143	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGAGGTGC AGCTGGTGGAGTCTGGGGGAGGCT TGGTAAAGCCTGGGGGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT TACTTTCAGTAACGCCCCGATGGGC TGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTTGGCCGTATT AAAAGCAAACTGAAGGTGGGACA AGAGACTACGCTGCACCCGTGAAA GGCAGATTCACCATCTCAAGAGAT GATTCAAAAAACACGCTGTATCTGC AAATGAACAGCCTGAAAACCGAGG ACACAGCCGTGTATTATTGTACCTC GTATAGTGGGGTCTGGGGCCAAGG GACAATGGTCACCGTGTCTTCAGCC TCCACCAAGGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGAAC TCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCCTACAGT CCTCAGGACTCTACTCCCTCAGCAG CGTGGTGACCGTGCCCTCCAGCAGC TTGGGCACCCAGACCTACATCTGCA ACGTGAATCACAAGCCCAGCAACA CCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAACCTCACAC ATGCCACCGTGCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTC CTCTTCCCCC AAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGA

SEQ ID NO:	Designation	Sequence
		GGTCACATGCGTGGTGGTGGACGT GAGCCACGAAGACCCTGAGGTCAA GTTCAACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGACAAA GCCGCGGGAGGAGCAGTACAACAG CACGTACCGTGTGGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAC AGGTGTACACCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCG GAGAACAACACTACAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCT TCTTCCTCTATAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTC CGGGCAAATAG
1144	huCCR8_32360_huIgGlz mAb(LC:K38R)_LC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGACATCG TGATGACCCAGTCTCCAGACTCCCT GGCTGTGTCTCTGGGCGAGAGGGC CACCATCAACTGCAAGTCCAGCCA GAGTGTTTTATACAGTTCCAACAAT AGAACTACTTAGCTTGGTACCATC AGAAACCAGGACAGTCTCCTAAGC TGCTCATTTCTGGGCATCTACCCG GGAATCCGGGGTCCCTGACCGATTG AGTGGCAGCGGGTCTGGGACAGAT TTCCTCTCACCATCAACAGCCTGC AGGCTGAAGATGTGGCAGTTTATTA CTGTCAACAATATTATAGTATTCCG ATCACTTTCGGCGGAGGGACCAAG GTGGAGATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGC CATCTGATGAGCAGTTGAAATCTGG AACTGCCTCTGTTGTGTGCTGCTG AATAACTTCTATCCCAGAGAGGCC AAAGTACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCA

SEQ ID NO:	Designation	Sequence
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1145	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z(mAb)_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCCGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAACTATGGCTTTCAC TGGGTCCGCCAGACTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATC TCATATGATGGAAGTAATAGATACT ATGCAAGCTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTCCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GCTATATTACTGTGCGAGAGTTTAC TATGGTTCGGGGACTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTGTCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG

SEQ ID NO:	Designation	Sequence
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1146	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCATATGAGCTGACTCAG CCACCCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTACTGGTCAT CTATAGAGCCGCCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCTGGGAACACAGCCACTCT GACCATCAGCGGGACCCAGGCTGG CGATGAGGCTGACTATTACTGTCAG GCGTTTCGACGCCGGCACTGTGGTAT TCGGCGGAGGCACCCAGCTGACCG TCCTAGGTCAGCCCAAGGCTGCACC CTCGGTCACTCTGTTCCCGCCCTCC TCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATCAGTG ACTTCTACCCGGGAGCCGTGACAGT GGCCTGGAAGGCAGATAGCAGCCC CGTCAAGGCGGGAGTGGAACCAC CACACCCTCCAAACAAAGCAACAA CAAGTACGCGGCCAGCAGCTATCT

SEQ ID NO:	Designation	Sequence
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1147	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q _M99E_W109F_S111A)_huIgG1z (mAb)_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCCGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAACTATGGCTTTCAC TGGGTCCGCCAGACTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATC TCATATGCCGGAAGTAATAGATACT ATGCAGCCTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTCCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GCTATATTACTGTGCGAGAGTTTAC TATGGTTCGGGGACTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTGTCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA

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1148	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q _M99E_W109F_S111A)_huIgG1z (mAb)_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCATATGAGCTGACTCAG CCACCCTCAGTGTGCTGAGGCTG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTACTGGTCAT CTATAGACAGAGCAACCGGCCCTC TGGGATCCCTGAGCGATTCTCTGGC TCCAACCTCTGGGAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTG AAGATGAGGCTGACTATTACTGTCA GGCGTTCGACGCCGGCACTGTGGT ATTCGGCGGAGGCACCCAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1149	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G _W109F_S111A)_huIgG1z (mAb)_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCCGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAACTATGGCTTTCAC TGGGTCCGCCAGACTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATC TCATATAGCGGAAGTAATAGATAC TATGCAGACTCCGTGAAGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTCCAAATGA ACAGCCTGAGAGGTGAGGACACGG CGCTATATTACTGTGCGAGAGTTTA CTATGGTTCGGGGACTTATTATAAA AACCGCTACTACTACGGTATGGAC GTCTGGGGCCAAGGGACCACGGTC ACCGTGTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACC CTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTACGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1150	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G _W109F_S111A)_huIgG1z (mAb)_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCATATGAGCTGACTCAG CCACCCTCAGTGTACGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTACTGGTCAT CTATAGACAGAGCAACCGGCCCTC TGGGATCCCTGAGCGATTCTCTGGC TCCAACCTCTGGGAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTG GCGATGAGGCTGACTATTACTGTCA GGCGTTCGACGCCGGCACTGTGGT ATTCGGCGGAGGCACCCAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1151	Hu anti-huCCR8 LIBC315615-1 Hulg1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAACTGACTCAG CCACTCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACATCAGCACTGTGGTT TTCGGCGGAGGGACCGAGCTGACC GTCCTAGGTCAGCCCAAGGCTGCA CCTCGGTCACCTCTGTTCCCGCCCT CCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGAATTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG

SEQ ID NO:	Designation	Sequence
1152	Hu anti-huCCR8 LIBC315615-1 Hulg1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGCCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CAACTTCAGTAACTGTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAGGTAATAAATATC ATGCGGACTCCGTGAAGGGCCGGT TCACCATCTCCAGAGACGATTCCAA GAACACACTGTATCTGCAAATGGA CAGCCTGAGAACTGAGGACACGGC TGTGTATTACTGTGCGAAAGTTTAC TATGGTTCGGGTATTTATTATAAAA ACAGGTACTACTACGGGATGGACG TCtGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCTGGAAGTCAAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCTCACCCTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAG

SEQ ID NO:	Designation	Sequence
		ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGA CTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1153	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGCTAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAAAACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCGAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCCTCTGTTCCTCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGA CTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1154	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGCCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CAACTTCAGTAACTGTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAGGTAATAAATATT ATGCGGACTCCGTGAAGGGCCGGT TCACCATCTCCAGAGACGATTCCAA GAACACACTGTATCTGCAAATGGA CAGCCTGAGAACTGAGGACACGGC TGTGTATTACTGTGCGAAAGTTTAC TATGGTTCGGGTATTTATTATAAAA ACAGGTATTACTACGGGATGGACG TCTGGGGCCAAGGGACCACGGTCA CCGTCTCCTCAGCCTCCACCAAGGG CCCATCGGTCTTCCCCCTGGCACCC TCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCCTCTTCCCC CCAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTACGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1155	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGCTAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGAAGAGGC CAGGCCAGGCCCCTGTGCTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAACACTGTGGT TTTCGGCGGAGGGACCAACCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTCATAG
1156	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGTAGTCTCTGGATT CAACTTCAGTAACAATGGCATGCA CTGGGTCCGCCAGGCTCCAGGCAA GGGACTGGAGTGGGTGGCAGTTAT TTCAAATGATGGCAGTAATAAATAT TATGCAGATTCCGTGAGGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTCTGTGCGAAAGTTTA CTATGGTTCGGGAATTTATTACAAA AATAACTACTACTACGGTATGGAC GTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACC CTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTACGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1157	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCT _{cct} ATGAGCTGACTCAGC CACTCTCAGTGTCAAGTGGCCCTGGG ACAGACGGCCAGGATTACCTGTGG GGGAAACAACATTGGAAGTAAAAA TGTGCACTGGTACCAGCAGAAGGC AGGCCAGGCCCTGTGCAGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAGGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGTGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTCATAG
1158	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CAACTTCAATACCTATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAAGTAATAAATATT ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAGCACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGC TGTGTATTACTGTGCGAGAGTTTAC TATGGTTTCGGGGAGTTATTATAAAA AGAATTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1159	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAGGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGTCTGACTATTACTGTCA GGTTTGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCACGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTCATAG
1160	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTCAGTAGTTATGGCTTTCAC TGGGTCCGCCAGACTCCAGGCAAG GGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAAGTAATAAAAct ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTCCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GGTGTATTACTGTGCGAGAGTTTAC TATGGTTCGGGGACTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1161	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGAGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTACTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCAAGGTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1162	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGTAGTCTCTGGATT CAACTTCATTAACAATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGACTGGGTGGCAGTTATA TCAAATGATGGAAGTAATAAATAC TATCCAGACTCCGTGAAGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACTCGG CTGTGTATTACTGTGCGAAAGTTTA CTATGGTTCGGGAAATTATTATAAA AACAACTACTACTACGGTATGGAC GTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACC CTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCCCTTCCCC CCAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTACGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1163	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG AGGGAAACAACATTGGAAGTCAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT GTATAGGGATAGCAACCGGCCCTC TGGGATCCCTGAACGATTCTCTGGC TCCAAGTCGGGGAACACGGCCACC CTGGCCATCAGCAGAGCCCAAGCC GGGGATGAGTCTGACTATTACTGTC AGGTGTGGGACGGCAGTGCCGTGG TATTCGGCGGAGGGACCACGCTGA CCGTCCTAGGTACGCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTCATAG
1164	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGATGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAGCTCTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGCCTGGAGTGGGTGGCAGTTATA TCACATGATGGAAGTAATAAATAC TATGCAGACTCCGTGAAGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGA ATAGCCTGGGAGGTGAGGACACGG CGGTGTATTACTGTGCGAAAGTTTA CTATGGTTCGGGGATTTATTATAAA AACCGCTATTACTACGGTATGGACG TCTGGGGCCAAGGGACCACGGTCA TCGTCTCGTCAGCCTCCACCAAGGG CCCATCGGTCTTCCCCCTGGCACCC TCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCCTCTTCCCC CCAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTACGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1165	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCGAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1166	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGctGGTGGAGtctGGGGGAGGCGTG GCCCAGCCTGGGAGGTCCCTGAGA CTCTCCTGTGCAGCCTCTGGATTCA ACTTCAGTGattGTGGCATGCACTGG GTCCGCCaggCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATCATA TGATGGAGGTAATAAATATTATGC GGA CTCCGTGAAGGGCCGGTTCAC CATCTCCAGAGacgATTCCAAGAAC ACACTGTAtcTGCAAcaggacAGCCTG AGAACTGAGGACACGGCTGTGTAT TACTGTGCGAAAGTTTACTATGGTT CGGGTATTTATTATAAAAACAGGTA CTACTACGGGATGGACGTctggggCC AAGGGACCACGGTcaccgTCTCCTCA GCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCCTCCTCCAAGAG CACCTCTGGGGGCACAGCGGCCCT GGGCTGCCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTCTGG AACTCAGGCGCCCTGACCAGCGGC GTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAG CAGCGTGGTGACCGTGCCCTCCAGC AGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTG AGCCCAAATCTTGTGACAAACTC ACACATGCCCACCGTGCCCAGCAC CTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCAAAACCCAA GGACACCCTCATGATCTCCCGGACC CCTGAGGTCACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAG

SEQ ID NO:	Designation	Sequence
		GTCAAGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGCCAAG ACAAAGCCGCGGGAGGAGCAGTAC AACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCCTGCACCAGGACT GGCTGAATGGCAAGGAGTACAAGT GCAAGGTGTCCAACAAAGCCCTCC CAGCCCCCATCGAGAAAACCATCT CCAAAGCCAAAGGGCAGCCCCGAG AACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAA CCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGCGACATCG CCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACACTACAAGACCA CGCCTCCCGTGCTGGACTCCGACGG CTCCTTCTTCTCTATAGCAAGCTC ACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCG TGATGCATGAGGCTCTGCACAACC ACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGCAAATAG
1167	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGCTGAGCCCTGG GACAGACGGGCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGGAGTAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGTCTGACTATTACTGTCA AATATGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGAATTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTCATAG
1168	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAGCTATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAATAATAAATACT ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTATATCTGCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GGTGTATTACTGTGCGAGAGTTTAT TATGGTTTCGGGGAGTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCACAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1169	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAACTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTACACTGGTACCAGCAGAGGC CAGGCCAGGCCCTGTGTTGGTCAT CTACAGGGATAGCAACCGGCCCTC TGGGATCCCTGAGCGATTATCTGGC TCCAAAGCGGGGAACACGGCCACC CTGACCATCAGCAGAGCCCACGCC GGGGATGAGGCTGACTATTACTGTC AGGTGTGGGACAGCAGCACTGTGG TTTTTCGGCGGAGGGACCGAGCTGA CCGTCCAAGGTCAGCCCAAGGCTG CACCCTCGGTCACTCTGTTCCCGCC CTCCTCTGAGGAGCTTCAAGCCAAC AAGGCCACACTGGTGTGTCTCATCA GTGACTTCTACCCGGGAGCCGTGAC AGTGGCCTGGAAGGCAGATAGCAG CCCCGTCAAGGCGGGAGTGGAAC CACCACACCCTCCAAACAAAGCAA CAACAAGTACGCGGCCAGCAGCTA

SEQ ID NO:	Designation	Sequence
		TCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTG CCAGGTCACGCATGAAGGGAGCAC CGTGGAGAAGACAGTGGCCCCTAC AGAATGTTCATAG
1170	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AATTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCTCTGAG ACTCTCCTGTGCAGTCTCTGGATTG ACGTTTCAGTAGCAATGGCATGCACT GGGTCCGCCAGGCTCCAGGCAAGG GGCTGGAGTGGGTGGCAGTTATAT CAAATGATGGAAGTAATAAATATT ATGGAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGC TGTGTATTACTGTGCGAAAGTTTAC TATGGTTCGGGAATTTATTACAGAA ACAACTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTGAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1171	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTATACTGGTCAT CTATAGGAATACCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGTCG GGGATGAGTCTGACTATTTCTGTCA GGTGTGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1172	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGtctGGGGGAGGCGT GGTCCAGccTGGGAGGTTCcCTGAGA CTCTCCTGTGGAGCCTCTGGATTCA CcttCAGtggcTATGGCATgcACTGGGT CcgCAGgcTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGA TGGAAGTAATAAATACTATGCAGA CTCCGTgAAGGGCCGATTCCCCATC TCAAGAgAaCAATTCCAAGAACACGC TGTATCTGCAAATGAACAGcCTGAG AGGTGAGGACACGGCGGTGTATTA CTGTgcGAGAGTTTATTATGGTTTCGG GGATTTATTATAAAAACCGCTacTaC TACGGTAtgGACGtctGGGGCCAAGG GACCACGGTgcCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAAct CAGGCGCCCTGACCAGCGGCGTGC ACACCTTCCCGGCTGTCTACAGTC CTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCT TGGGCACCCAGACCTACATCTGCA ACGTGAATCACAAGCCCAGCAACA CCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAActCACAC ATGCCCACCGTGCCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTC CTCTTCCCCC AAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGT GAGCCACGAAGACCCTGAGGTCAA

SEQ ID NO:	Designation	Sequence
		GTTCAACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGACAAA GCCGCGGGAGGAGCAGTACAACAG CACGTACCGTGTGGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAC AGGTGTACACCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCG GAGAACAACACTACAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCT TCTTCCTCTATAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTC CGGGCAAATAG
1173	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTATACTGGTCAT CTATAGGAATACCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGTCG GGGATGAGTCTGACTATTTCTGTCA GGTGTGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGAATTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTCATAG
1174	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGGAGCCTCTGGATT CACCTTCAGTGGCTATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCAAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GGTGTATTACTGTGCGAGAGTTTAT TATGGTTCGGGGATTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTTCGC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1175	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGACCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAGATAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGGAATAACGTCCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1176	Hu anti-huCCR8 LIBC322176-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAATCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGGCT CAACTTCAGTAACTTTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGACTGGGTGGCAGTTATA TCATATGATGGAGGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGAT TCACCGTCTCCAGAGACAATTCCAA GAACACGCTCTTTCTGCAAATGAAC AGCCTGAGAGCTGAGGACACGGCT CTGTATTACTGTGCGAAAGTTTACT ATGGCTCGGGCAGTTATTATAAAA AGAGGTACTACTACGGTATGGACG TCTGGGGCCAGGGGACCACGGTCA CCGTCTCCTCAGCCTCCACCAAGGG CCCATCGGTCTTCCCCCTGGCACCC TCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCCTCTTCCCC CCAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTACGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1177	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGGCCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACA GAATGTTTCATAG
1178	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CAACTTCAGTAGCTGTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAATAATAAATACT ATGCGGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGC TGTGTATTACTGTGCGAAAGTTTAC TATGGTTTCGGGTATTTATTATAAAA AGAACTACTACTACGGTATGGACG TCTGGGGCCAAGGGACCACGGTCA CCGTCTCCTCAGCCTCCACCAAGGG CCCATCGGTCTTCCCCCTGGCACCC TCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1179	huCCR8_32360_huIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGAGGTGC AGCTGGTGGAGTCTGGGGGAGGCT TGGTAAAGCCTGGGGGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT TACTTTCAGTAACGCCCGGATGGGC TGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTTGGCCGTATT AAAAGCAAACTGAAGGTGGGACA AGAGACTACGCTGCACCCGTGAAA GGCAGATTACCATCTCAAGAGAT GATTCAAAAAACACGCTGTATCTGC AAATGAACAGCCTGAAAACCGAGG ACACAGCCGTGTATTATTGTACCTC GTATAGTGGGGTCTGGGGCCAAGG GACAATGGTCACCGTCTCTTCAGCC TCCACCAAGGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAAC TCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCTTACAGT

SEQ ID NO:	Designation	Sequence
		CCTCAGGACTCTACTCCCTCAGCAG CGTGGTGACCGTGCCCTCCAGCAGC TTGGGCACCCAGACCTACATCTGCA ACGTGAATCACAAGCCCAGCAACA CCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAACCTCACAC ATGCCCACCGTGCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTC CTCTTCCCCC AAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGT GAGCCACGAAGACCCCTGAGGTCAA GTTCAACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGACAAA GCCGCGGGAGGAGCAGTACAACAG CACGTACCGTGTGGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAC AGGTGTACACCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCG GAGAACAAC TACAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCT TCTTCCTCTATAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTC CGGGCAAATAG
1180	huCCR8_32360_huIgG1z mAb_LC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGACATCG TGATGACCCAGTCTCCAGACTCCCT GGCTGTGTCTCTGGGCGAGAGGGC CACCATCAACTGCAAGTCCAGCCA GAGTGTTTTATACAGTTCCAACAAT AAGAACTACTTAGCTTGGTACCATC AGAAACCAGGACAGTCTCCTAAGC TGCTCATTTTCTGGGCATCTACCCG GGAATCCGGGGTCCCTGACCGATTG AGTGGCAGCGGGTCTGGGACAGAT TTCAC TCTCACCATCAACAGCCTGC AGGCTGAAGATGTGGCAGTTTATTA

SEQ ID NO:	Designation	Sequence
		CTGTCAACAATATTATAGTATTCCG ATCACTTTCGGCGGAGGGACCAAG GTGGAGATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGC CATCTGATGAGCAGTTGAAATCTGG AACTGCCTCTGTTGTGTGCCTGCTG AATAACTTCTATCCCAGAGAGGCC AAAGTACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCA AGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTT CAACAGGGGAGAGTGTTAG
1181	HCDR1 Consensus	X ₁ X ₂ GX ₄ H X ₁ = N, S, D, G, T, or R, X ₂ = C, N, Y, S, or F, X ₄ = M or F
1182	LCDR2 Consensus	RX ₂ X ₃ X ₄ RPS X ₂ = A, N, D, S, or Q, X ₃ = S, T, N, I, F, or A, and X ₄ = N or V

CLAIMS

We claim:

1. A T cell engager (TCE) molecule comprising (i) an scFab that binds to a tumor antigen, wherein the scFab comprises a first heavy chain variable region (scFab VH), a CH1 domain, a first light chain variable region (scFab VL), and a Cκ or Cλ domain, and (ii) an scFv that binds CD3, comprising a second VL and a second VH, and wherein the TCE molecule is a single chain.
2. The TCE molecule of Claim 1, wherein the scFab comprises a C-terminus portion that is connected by a linker to an N-terminal portion of the scFv.
3. The TCE molecule of Claim 1 or 2, wherein the TCE molecule further comprises an scFc.
4. The TCE molecule of Claim 3, wherein the scFc comprises an N-terminus portion that is connected by a linker to a C-terminal portion of the scFv.
5. The TCE molecule of any one of Claims 1-4, wherein the scFv binds human CD3.
6. The TCE molecule of any one of Claims 1-5, wherein the scFab has an orientation in the following order, from N-terminus to C-terminus, VH, CH1, VL, and either Cκ or Cλ .
7. The TCE molecule of any one of Claims 1-5, wherein the scFab has an orientation in the following order, from N-terminus to C-terminus, VL, either Cκ or Cλ, VH, and CH1.
8. The TCE molecule of any one of Claims 1-6, wherein the scFab comprises a linker that connects the CH1 and scFab VL, wherein the linker is (G4S)6, (G4S)7, (G4S)8, (G4Q)6, (G4Q)7, or (G4Q)8.
9. The TCE molecule of any one of Claims 1-5 and 7, wherein the TCE molecule comprises a linker that connects the scFab Cκ or Cλ and the scFab VH, wherein the linker is (G4S)6, (G4S)7, (G4S)8, (G4Q)6, (G4Q)7, or (G4Q)8.
10. The TCE molecule of any one of Claims 1-9, wherein CH1, Cκ and/or Cλ domains are IgG, IgM, IgA, IgD, or IgE.
11. The TCE molecule of Claim 10, wherein the domains are IgG.
12. The TCE molecule of Claim 10 or 11, wherein the domains are IgG1.
13. The TCE molecule of any one of Claims 1-12, wherein the scFab contains a cysteine clamp between CH1 and either Cκ or Cλ .

14. The TCE molecule of any one of Claims 1-13, wherein the orientation of the TCE molecule from N-terminus to C-terminus is: VH-CH1-Linker-VL-Ck or Cλ-Linker-VH-Linker-VL-Linker- Fc1 (CH2-CH3) -Linker-Fc2 (CH2-CH3).
15. The TCE molecule of any one of Claims 1-13, wherein the orientation of the TCE molecule from N-terminus to C-terminus is: VL-CH1-Linker-VH-Ck or Cλ-Linker-VH-Linker-VL-Linker- Fc1 (CH2-CH3) -Linker-Fc2 (CH2-CH3).
16. The TCE molecule of any one of Claims 1-15, wherein the tumor antigen is CCR8.
17. The TCE molecule of any one of Claims 1-16, wherein the scFv that binds CD3 is I2E.
18. The TCE molecule of any one of Claims 1-16, wherein the scFv that binds CD3 is I2C.
19. A TCE molecule comprising (i) a first scFv that binds CCR8, wherein the first scFv comprises a first VH region (CCR8 scFv VH) and a first VL region (CCR8 scFv VL), and (ii) a second scFv that binds CD3, wherein the second scFv comprises a second VH region and a second VL region, and wherein the TCE molecule is a single chain.
20. The TCE molecule of any one of Claims 1-19, wherein the first VH comprises HCDR1, HCDR2, HCDR3, and the first VL comprises LCDR1, LCDR2, and LCDR3, and wherein:
 - a. HCDR1 comprises an amino acid sequence given by SEQ ID NO: 1, SEQ ID NO: 17, SEQ ID NO: 33, SEQ ID NO: 49, SEQ ID NO: 65, SEQ ID NO: 81, SEQ ID NO: 97, or SEQ ID NO: 113;
 - b. HCDR2 comprises an amino acid sequence given by SEQ ID NO: 2, SEQ ID NO: 18, SEQ ID NO: 34, SEQ ID NO: 50, SEQ ID NO: 66, or SEQ ID NO: 82;
 - c. HCDR3 comprises an amino acid sequence given by SEQ ID NO: 3, SEQ ID NO: 19, SEQ ID NO: 35, SEQ ID NO: 51, SEQ ID NO: 67, or SEQ ID NO: 83;
 - d. LCDR1 comprises an amino acid sequence given by SEQ ID NO: 4, SEQ ID NO: 20, SEQ ID NO: 36, SEQ ID NO: 52, SEQ ID NO: 68, or SEQ ID NO: 84;

- e. LCDR2 comprises an amino acid sequence given by SEQ ID NO: 5, SEQ ID NO: 21, SEQ ID NO: 37, SEQ ID NO: 53, SEQ ID NO: 69, or SEQ ID NO: 85, and
 - f. LCDR3 comprises an amino acid sequence given by SEQ ID NO: 6, SEQ ID NO: 22, SEQ ID NO: 38, SEQ ID NO: 54, SEQ ID NO: 70, or SEQ ID NO: 86.
- 21. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 1, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 2, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 3, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 4, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 5, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 6.
 - 22. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 17, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 18, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 19, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 20, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 21, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 22.
 - 23. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 33, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 34, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 35, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 36, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 37, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 38.
 - 24. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 49, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 50, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 51, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 52, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 53, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 54.
 - 25. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 65, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 66, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 67, LCDR1 comprises an amino acid sequence given by SEQ ID

- NO: 68, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 69, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 70.
26. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 81, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 82, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 83, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 84, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 85, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 86.
27. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 97, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 98, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 99, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 100, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 101, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 102.
28. The TCE molecule of Claim 20, wherein HCDR1 comprises an amino acid sequence given by SEQ ID NO: 113, HCDR2 comprises an amino acid sequence given by SEQ ID NO: 114, HCDR3 comprises an amino acid sequence given by SEQ ID NO: 115, LCDR1 comprises an amino acid sequence given by SEQ ID NO: 116, LCDR2 comprises an amino acid sequence given by SEQ ID NO: 117, and LCDR3 comprises an amino acid sequence given by SEQ ID NO: 118.
29. The TCE molecule of any one of Claims 19-28, wherein the first VH comprises an amino acid sequence given by SEQ ID NO: 7, SEQ ID NO: 23, SEQ ID NO: 39, SEQ ID NO: 55, SEQ ID NO: 71, SEQ ID NO: 87, SEQ ID NO: 103, or SEQ ID NO: 119, and wherein the first VL comprises an amino acid sequence given by SEQ ID NO: 8, SEQ ID NO: 24, SEQ ID NO: 40, SEQ ID NO: 56, SEQ ID NO: 72, SEQ ID NO: 88, SEQ ID NO: 104, or SEQ ID NO: 120.
30. The TCE molecule of any one of Claims 19-29, wherein the first scFv comprises an amino acid sequence given by SEQ ID NO: 9, 25, 41, 57, 73, 89, 105, or 121.
31. The TCE molecule of any one of Claims 19-30, comprising an amino acid sequence given by SEQ ID NO: 10, SEQ ID NO: 26, SEQ ID NO: 42, SEQ ID NO: 58, SEQ ID NO: 74, SEQ ID NO: 90, SEQ ID NO: 106, or SEQ ID NO: 122.
32. The TCE molecule of any one of Claims 19-31, further comprising an scFc, wherein the TCE molecule comprises an amino acid sequence given by SEQ ID

- NO: 11, SEQ ID NO: 27, SEQ ID NO: 59, SEQ ID NO: 75, SEQ ID NO: 91, SEQ ID NO: 107, or SEQ ID NO: 123.
33. The TCE molecule of any one of Claims 1-18 and 20-28, wherein the first VH and CH1 comprise an amino acid sequence given by SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 44, SEQ ID NO: 60, SEQ ID NO: 76, SEQ ID NO: 92, SEQ ID NO: 108, or SEQ ID NO: 124.
34. The TCE molecule of any one of Claims 1-18, 20-28, and 33, comprising a C κ , wherein the first VL and C κ comprise an amino acid sequence given by SEQ ID NO: 13, SEQ ID NO: 29, SEQ ID NO: 45, SEQ ID NO: 61, SEQ ID NO: 77, SEQ ID NO: 93, SEQ ID NO: 109, or SEQ ID NO: 125.
35. The TCE molecule of any one of Claims 1-18, 20-28, 33, and 34, comprising an amino acid sequence given by SEQ ID NO: 14, SEQ ID NO: 30, SEQ ID NO: 46, SEQ ID NO: 62, SEQ ID NO: 78, SEQ ID NO: 94, SEQ ID NO: 110, or SEQ ID NO: 126.
36. The TCE molecule of any one of Claims 1-18, 20-28, and 33-35, comprising an amino acid sequence given by SEQ ID NO: 15, SEQ ID NO: 31, SEQ ID NO: 47, SEQ ID NO: 63, SEQ ID NO: 79, SEQ ID NO: 95, SEQ ID NO: 111, or SEQ ID NO: 127.
37. The TCE molecule of any one of Claims 3-18, 20-28, 33-36, wherein the TCE molecule comprises an amino acid sequence given by SEQ ID NO: 16, SEQ ID NO: 32, SEQ ID NO: 48, SEQ ID NO: 64, SEQ ID NO: 80, SEQ ID NO: 96, SEQ ID NO: 112, or SEQ ID NO: 128.
38. A method of treating cancer in a patient comprising administering an effective amount of the TCE molecule of any one of Claims 1-37 to the patient.
39. The method of Claim 38, wherein the cancer is a solid tumor.
40. The method of Claim 38 or 39, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer.
41. The method of any one of Claims 38-40, wherein the method further comprises administering to the patient a PD-1 antagonist antibody or PD-L1 antagonist antibody.

42. The method of Claim 41, wherein the PD-1 antagonist antibody or PD-L1 antagonist antibody is administered prior to, concurrently with, and/or after administration of the TCE molecule.
43. The method of Claim 41 or 42, wherein the PD-1 antagonist antibody is pembrolizumab, nivolumab, cemiplimab, or antibody 20C1.009.
44. The method of Claim 41 or 42, wherein the PD-L1 antagonist antibody is atezolizumab, avelumab, or durvalumab.
45. The TCE molecule of any one of Claims 1-37 for use in therapy.
46. The TCE molecule of any one of Claims 1-37 for use in treating cancer.
47. The TCE molecule of Claim 46 for use in treating cancer, wherein the cancer is a solid tumor.
48. The TCE molecule of Claim 46 or 47 for use in treating cancer, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer.
49. The TCE molecule of any one of Claims 46-48 for use in treating cancer, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, or triple-negative breast cancer.
50. The TCE molecule of any one of Claims 46-49 for use in treating cancer, wherein the use further comprises administering to the patient a PD-1 antagonist antibody or PD-L1 antagonist antibody.
51. The TCE molecule of Claim 50 for use in treating cancer, wherein the PD-1 antagonist antibody or PD-L1 antagonist antibody is administered prior to, concurrently with, and/or after administration of the TCE molecule.
52. The TCE molecule of Claim 50 or 51 for use in treating cancer, wherein the PD-1 antagonist antibody is pembrolizumab, nivolumab, cemiplimab, or antibody 20C1.009.
53. The TCE molecule of Claim 50 or 51 for use in treating cancer, wherein the PD-L1 antagonist antibody is atezolizumab, avelumab, or durvalumab.
54. The use of the TCE molecule of any one of Claims 1-37 for the manufacture of a medicament for the treatment of cancer.
55. The use of Claim 54, wherein the cancer is a solid tumor.
56. The use of Claim 54 or 55, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma,

- triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer.
57. The use of any one of Claims 54-56, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, or triple-negative breast cancer.
58. A pharmaceutical composition comprising the TCE molecule of any one of Claims 1-37 and one or more pharmaceutically acceptable carriers, diluents, or excipients.
59. A TCE molecule comprising an scFv that comprises HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, each comprising an amino acid sequence given by SEQ ID NO: 217, 218, 219, 220, 221, and 220, respectively.
60. The TCE molecule of Claim 59, comprising a VH and VL comprising an amino acid sequence given by SEQ ID NO: 223 and SEQ ID NO: 224, respectively.
61. The TCE molecule of Claim 59 or Claim 60, wherein the TCE molecule comprises an scFv comprising an amino acid sequence given by SEQ ID NO: 225.
62. The TCE molecule of any one of Claims 59-61, comprising an amino acid sequence given by SEQ ID NO: 226.
63. The TCE molecule of Claim 62, comprising an amino acid sequence given by SEQ ID NO: 227.
64. A TCE molecule comprising an scFv that comprises HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, each comprising an amino acid sequence given by SEQ ID NO: 228, 229, 230, 231, 232, and 233, respectively.
65. The TCE molecule of Claim 64, comprising a VH and VL comprising an amino acid sequence given by SEQ ID NO: 234 and SEQ ID NO: 235, respectively.
66. The TCE molecule of Claim 64 or Claim 65, wherein the TCE molecule comprises an scFv comprising an amino acid sequence given by SEQ ID NO: 236.
67. The TCE molecule of any one of Claims 64-66, comprising an amino acid sequence given by SEQ ID NO: 237.
68. The TCE molecule of Claim 67, comprising an amino acid sequence given by SEQ ID NO: 238.
69. A TCE molecule comprising an scFab that comprises HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, each comprising an amino acid sequence given by SEQ ID NO: 239, 240, 241, 242, 243, and 244, respectively.

70. The TCE molecule of Claim 69, comprising a VH-CH1 comprising an amino acid sequence given by SEQ ID NO: 245.
71. The TCE molecule of Claim 69 or Claim 70, wherein the TCE molecule comprises a VL-C κ comprising an amino acid sequence given by SEQ ID NO: 246.
72. The TCE molecule of any one of Claims 69-71, wherein the scFab comprises an amino acid sequence given by SEQ ID NO: 247.
73. The TCE molecule of any one of Claims 69-72, comprising an amino acid sequence given by SEQ ID NO: 248.
74. The TCE molecule of Claim 73, comprising an amino acid sequence given by SEQ ID NO: 249.
75. A TCE molecule comprising an scFab that comprises HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, each comprising an amino acid sequence given by SEQ ID NO: 250, 251, 252, 253, 254, and 255, respectively.
76. The TCE molecule of Claim 75, comprising a VH-CH1 comprising an amino acid sequence given by SEQ ID NO: 256.
77. The TCE molecule of Claim 75 or Claim 76, wherein the TCE molecule comprises a VL-C κ comprising an amino acid sequence given by SEQ ID NO: 257.
78. The TCE molecule of any one of Claims 75-77, wherein the scFab comprises an amino acid sequence given by SEQ ID NO: 258.
79. The TCE molecule of any one of Claims 75-78, comprising an amino acid sequence given by SEQ ID NO: 259.
80. The TCE molecule of Claim 79, comprising an amino acid sequence given by SEQ ID NO: 260.
81. A method of treating cancer in a patient comprising administering an effective amount of the TCE molecule of any one of Claims 59-80 to the patient.
82. The method of Claim 81, wherein the cancer is a solid tumor.
83. The method of Claim 81 or 82, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer.

84. The method of any one of Claims 81-83, wherein the method further comprises administering to the patient a PD-1 antagonist antibody or PD-L1 antagonist antibody.
85. The method of Claim 84, wherein the PD-1 antagonist antibody or PD-L1 antagonist antibody is administered prior to, concurrently with, and/or after administration of the TCE molecule.
86. The method of Claim 84 or 85, wherein the PD-1 antagonist antibody is pembrolizumab, nivolumab, cemiplimab, or antibody 20C1.009.
87. The method of Claim 84 or 85, wherein the PD-L1 antagonist antibody is atezolizumab, avelumab, or durvalumab.
88. The TCE molecule of any one of Claims 59-80 for use in therapy.
89. The TCE molecule of any one of Claims 59-80 for use in treating cancer.
90. The TCE molecule of any one of Claims 59-80 for use in treating cancer, wherein the cancer is a solid tumor.
91. The TCE molecule of any one of Claims 59-80 for use in treating cancer, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, triple-negative breast cancer, colorectal cancer, pancreatic cancer, or metastatic castrate-resistant prostate cancer.
92. The TCE molecule of any one of Claims 59-80 for use in treating cancer, wherein the cancer is non-small cell lung cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular carcinoma, or triple-negative breast cancer.
93. The TCE molecule of any one of Claims 59-80 for use in treating cancer, wherein the use further comprises administering to the patient a PD-1 antagonist antibody or PD-L1 antagonist antibody.
94. The TCE molecule of Claim 93 for use in treating cancer, wherein the PD-1 antagonist antibody is pembrolizumab, nivolumab, cemiplimab, or antibody 20C1.009.
95. The TCE molecule of Claim 93 or 94 for use in treating cancer, wherein the PD-L1 antagonist antibody is atezolizumab, avelumab, or durvalumab.
96. The use of the TCE molecule of any one of Claims 59-80 for the manufacture of a medicament for the treatment of cancer.
97. The use of Claim 96, wherein the cancer is a solid tumor.

98. A pharmaceutical composition comprising the TCE molecule of any one of Claims 59-80 and one or more pharmaceutically acceptable carriers, diluents, or excipients.
99. A method of treating cancer in a patient comprising administering to the patient an effective amount of a CCR8 TCE molecule that binds human CCR8 at an epitope wherein the epitope comprises at least one residue of SEQ ID NO: 134.
100. The method of Claim 99, wherein the epitope comprises at least two residues of SEQ ID NO: 134.
101. The method of Claim 99 or Claim 100, wherein the epitope comprises at least three residues of SEQ ID NO: 134.
102. The method of any one of Claims 99-101, wherein the epitope comprises at least four residues of SEQ ID NO: 134.
103. The method of any one of Claims 99-102, wherein the epitope comprises at least five residues of SEQ ID NO: 134.
104. The method of any one of Claims 99-102, wherein the epitope comprises a threonine residue at position 4 of SEQ ID NO: 134.
105. A TCE molecule that binds to human CCR8, which comprises an HCDR1 amino acid sequence of SEQ ID NO: 787; an HCDR2 amino acid sequence of SEQ ID NO: 788; an HCDR3 amino acid sequence of SEQ ID NO: 789; an LCDR1 amino acid sequence of SEQ ID NO: 336, wherein X₁ is K or R; an LCDR2 amino acid sequence of SEQ ID NO: 791; and an LCDR3 amino acid sequence of SEQ ID NO: 792.
106. The TCE molecule of Claim 105, wherein the TCE molecule comprises a VH amino acid sequence of SEQ ID NO: 965 and a VL amino acid sequence of SEQ ID NO: 342, wherein X₁ is K or R, X₂ is H or Q, and/or X₃ is S or P.
107. A TCE molecule that binds to human CCR8, which comprises: (a) an HCDR1 amino acid sequence of X₁X₂GX₄H, (SEQ ID NO: 1181), wherein (i) X₁ is N, S, D, G, T, or R, (ii) X₂ is C, N, Y, S, or F, and (iii) X₄ is M or F; (b) an HCDR2 amino acid sequence of SEQ ID NOs: 596, 602, 608, 614, 620, 626, 632, 638, 644, 650, 656, 662, 668, 674, 680, 686, 692, 698, 704, 710, 716, 722, 728, 734, 740, 746, 752, 758, 764, 770, 776, 782, 788, 794, 800, 806, 815, 821, 827, 833, 839, 845, 851, 857, 863, 869, 875, 881, 887, or 893; (c) an HCDR3 amino acid sequence of SEQ ID NOs: 597, 603, 609, 615, 621, 627, 633, 639, 645, 651, 657, 663, 669, 675, 681, 687, 693, 699, 705, 711, 717, 723, 729, 735, 741, 747, 753,

- 759, 765, 771, 777, 783, 795, 801, 807, 816, 822, 828, 834, 840, 846, 852, 858, 864, 870, 876, 882, 888, or 894; (d) an LCDR1 amino acid sequence of any one of SEQ ID NOs: 598, 604, 610, 616, 622, 628, 634, 640, 646, 652, 658, 664, 670, 676, 682, 688, 694, 700, 706, 712, 718, 724, 730, 736, 742, 748, 754, 760, 766, 772, 778, 784, 796, 802, 808, 811, 817, 823, 829, 835, 841, 847, 853, 859, 865, 871, 877, 883, or 889; (e) an LCDR2 amino acid sequence of RX₂X₃X₄RPS (SEQ ID NO: 1182), wherein (i) X₂ is A, N, D, S, or Q, (ii) X₃ is S, T, N, I, F, or A, and (iii) X₄ is N or V; and (f) an LCDR3 amino acid sequence of SEQ ID NOs: 600, 606, 612, 618, 624, 630, 636, 642, 648, 654, 660, 666, 672, 678, 684, 690, 696, 702, 708, 714, 720, 726, 732, 738, 744, 750, 756, 762, 768, 774, 780, 786, 798, 804, 810, 813, 819, 825, 831, 837, 843, 849, 855, 861, 867, 873, 879, 885, 891.
108. The TCE molecule of Claim 107, wherein HCDR1 comprises an amino acid sequence of SEQ ID NOs: 595, 601, 607, 613, 619, 625, 631, 637, 643, 649, 655, 661, 667, 673, 679, 685, 691, 697, 703, 709, 715, 721, 727, 733, 739, 745, 751, 757, 763, 769, 775, 781, 793, 799, 805, 814, 820, 826, 832, 838, 844, 850, 856, 862, 868, 874, 880, 886, or 892.
109. The TCE molecule of Claim 107 or Claim 108, wherein the LCDR2 comprises an amino acid sequence of SEQ ID NOs: 599, 605, 611, 617, 623, 629, 635, 641, 647, 653, 659, 665, 671, 677, 683, 689, 695, 701, 707, 713, 719, 725, 731, 737, 743, 749, 755, 761, 767, 773, 779, 785, 797, 803, 809, 812, 818, 824, 830, 836, 842, 848, 854, 860, 866, 872, 878, 884, or 890.
110. The TCE molecule of Claims 107 to 109, wherein the VH comprises an amino acid sequence of SEQ ID NOs: 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 967, 969, 971, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, or 1000.
111. The TCE molecule of Claims 107 to 110, the VL comprises an amino acid sequence of SEQ ID NOs: 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, or 999.
112. A TCE molecule that binds to human CCR8, comprising: (a) a VH comprising an amino acid sequence of SEQ ID NO: 967 and a VL comprising an amino acid sequence of SEQ ID NO: 968; (b) a VH comprising an amino acid sequence of

SEQ ID NO: 969 and a VL comprising an amino acid sequence of SEQ ID NO: 970; (c) a VH comprising an amino acid sequence of SEQ ID NO: 971 and a VL comprising an amino acid sequence of SEQ ID NO: 972; (d) a VH comprising an amino acid sequence of SEQ ID NO: 974 and a VL comprising an amino acid sequence of SEQ ID NO: 973; (e) a VH comprising an amino acid sequence of SEQ ID NO: 976 and a VL comprising an amino acid sequence of SEQ ID NO: 975; (f) a VH comprising an amino acid sequence of SEQ ID NO: 978 and a VL comprising an amino acid sequence of SEQ ID NO: 977; (g) a VH comprising an amino acid sequence of SEQ ID NO: 980 and a VL comprising an amino acid sequence of SEQ ID NO: 979; (h) a VH comprising an amino acid sequence of SEQ ID NO: 982 and a VL comprising an amino acid sequence of SEQ ID NO: 981; (i) a VH comprising an amino acid sequence of SEQ ID NO: 984 and a VL comprising an amino acid sequence of SEQ ID NO: 983; (j) a VH comprising an amino acid sequence of SEQ ID NO: 986 and a VL comprising an amino acid sequence of SEQ ID NO: 985; (k) a VH comprising an amino acid sequence of SEQ ID NO: 988 and a VL comprising an amino acid sequence of SEQ ID NO: 987; (l) a VH comprising an amino acid sequence of SEQ ID NO: 990 and a VL comprising an amino acid sequence of SEQ ID NO: 989; (m) a VH comprising an amino acid sequence of SEQ ID NO: 992 and a VL comprising an amino acid sequence of SEQ ID NO: 991; (n) a VH comprising an amino acid sequence of SEQ ID NO: 994 and a VL comprising an amino acid sequence of SEQ ID NO: 993; (o) a VH comprising an amino acid sequence of SEQ ID NO: 996 and a VL comprising an amino acid sequence of SEQ ID NO: 995; (p) a VH comprising an amino acid sequence of SEQ ID NO: 998 and a VL comprising an amino acid sequence of SEQ ID NO: 997; or (q) a VH comprising an amino acid sequence of SEQ ID NO: 1000 and a VL comprising an amino acid sequence of SEQ ID NO: 999.

FIG. 1

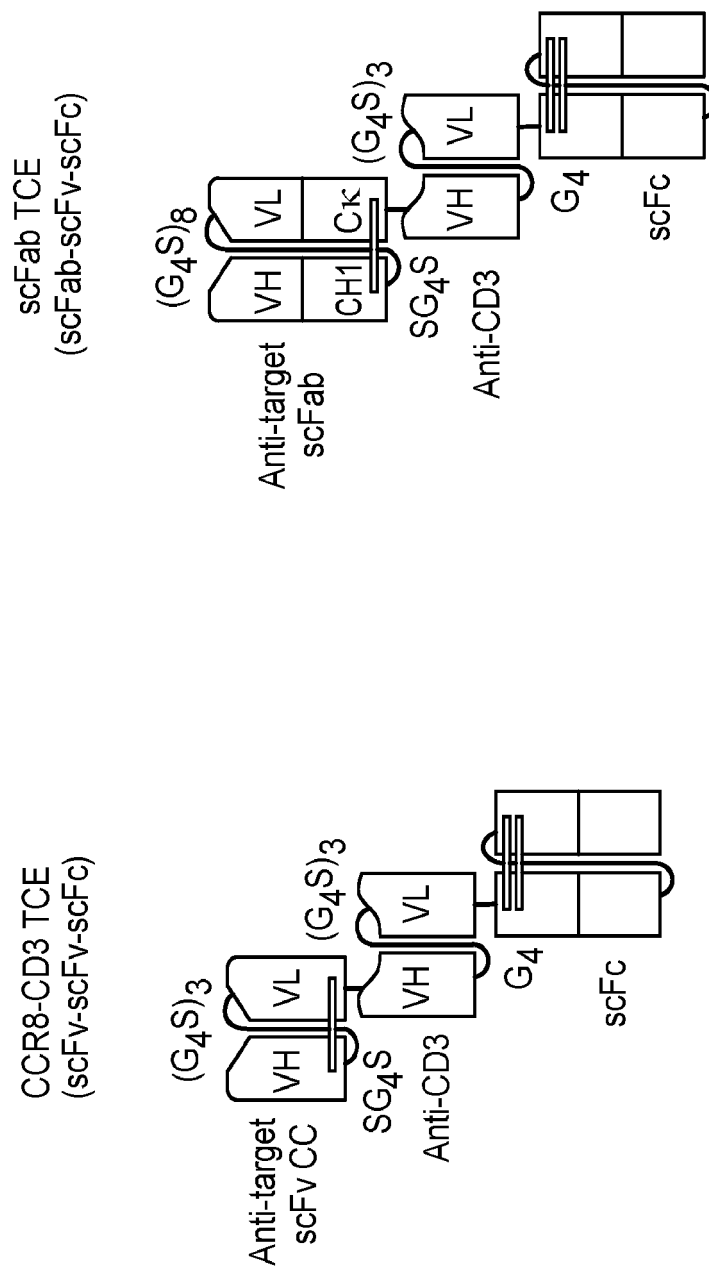


FIG. 2

