

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 Cκ or Cλ), 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 Cκ or Cλ), 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 Cκ or Cλ, 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 Cκ or Cλ, 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-scFv-scFc format. In some embodiments, the TCE molecule comprises the following orientation: VH-CH1-Linker-VL-Cκ/Cλ-Linker-VH-Linker-VL-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises the following orientation: VL-Cκ/Cλ-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-Cκ/Cλ-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-Cκ/Cλ-Linker-VL-Linker-VH-Linker-VH-Linker-VL-Linker-Fc1-Linker-Fc2. In some embodiments, the TCE molecule comprises Cκ. In some embodiments, the TCE molecule comprises Cλ.

[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
STRESGVPDRFSGSGSGTDFLTINSQAEDVAVYYCQQYYIPITFGGGTKVEIKR (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., MAb 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 zeluvlimab. 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: GGGGQGGGQGGGQGGGQ (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 Cλ, 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 (MDMRVPAQLL GLLLLWLRGA RC) which is encoded by SEQ ID NO: 214 (atggacatga gagtcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 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 ctgggcc). The leader polynucleotide sequence may comprise a polynucleotide sequence given by SEQ ID NO: 594

(ATGGACATGAGAGTGCCTGCACAGCTGCTGGGCCTGCTGCTGCTGTGGCTGAGA GGCGCCAGATG)

[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-acetylgalactosamine, 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 K_d values and standard deviations are calculated with Microsoft Excel. Mean K_d 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 K _d [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 $\pm$ 7	27174.0 $\pm$ 376.7 0 $\pm$ 2	1.00
TCE8 scFab x I2E x scFc	8799.00 $\pm$ 197.8 9	18919.6 $\pm$ 250.3 7 $\pm$ 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 (Kd) values are calculated with the one site specific binding evaluation tool of the GraphPad Prism software. Mean Kd values and affinity gaps are calculated with Microsoft Excel. Mean Kd

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 NH₄Cl, 10 mM KHCO₃, 100 μ M 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% CO₂ 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 μ L/ 10⁷ 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 μ L/10⁷ cells) are added and incubated for 15 minutes at 4 to 8° C. The cells are washed with MACS isolation buffer (1 - 2 mL/10⁷ cells). After centrifugation (see above), supernatant is discarded, and cells are resuspended in MACS isolation buffer (500 μ L/10⁸ cells). CD14/CD56 negative cells are isolated using LS Columns (Miltenyi Biotec, #130-042-401). PBMC without CD14⁺/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 10⁶ cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μ L/10⁶ 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 x 10⁵ 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 μ L of this suspension is transferred to each well of a 96-well plate. 20 μ L 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 +) 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 P_1-35 (SEQ ID NO: 133)) is divided into three consecutive segments (designated P_1-12 (SEQ ID NO: 134), P_13-24 (SEQ ID NO: 135), P_25-35 (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 P₁₃₋₂₄. However, TCE1 bound to the truncated N-terminal peptide P₁₋₁₂.

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 P_1-35. All molecules except TCE1 bound to the truncated N-terminal CCR8 peptide P_13-24. Interestingly, TCE1 binds to the truncated N-terminal CCR8 peptide P_1-12, 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)QVQLVESGGGVVQPGRSLRLSCEASGFTFSSYVMHWVRQAPGKCLEWVSVISYDGSSQ
YYTDSVKGRFTISRDN SKNTLNLQMNSLRAEDTAVYYCVRGRLATAILFDYWGGQTLV
TVSS**TCE3 CCR8 scFv VL (SEQ ID NO: 8)**EILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFWYLQRP GQPQLLIYEVS NRFS
GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQSIKLPLTFGCGTKVEIK**TCE3 CCR8 scFv (SEQ ID NO: 9)**QVQLVESGGGVVQPGRSLRLSCEASGFTFSSYVMHWVRQAPGKCLEWVSVISYDGSSQ
YYTDSVKGRFTISRDN SKNTLNLQMNSLRAEDTAVYYCVRGRLATAILFDYWGGQTLV
TVSSGGGGQGGGGQGGGGQEILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFW
YLQRP GQPQLLIYEVS NRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQSIKLPL
TFGCGTKVEIK**TCE3 scFv (CCR8) x scFv (CD3) TCE (SEQ ID NO: 10)**QVQLVESGGGVVQPGRSLRLSCEASGFTFSSYVMHWVRQAPGKCLEWVSVISYDGSSQ
YYTDSVKGRFTISRDN SKNTLNLQMNSLRAEDTAVYYCVRGRLATAILFDYWGGQTLV
TVSSGGGGQGGGGQGGGGQEILMTQTPLSLSVTPGQPASISCKSSQSLLYSDGKTYLFW

QVQLVESGGGVVQGRSLRLSCEASGFTSSYVMHWVRQAPGKGLEWVSVISYDGSSQ
YYTDSVKGRFTISRDNKNTLNLQMNSLRAEDTAVYYCVRGRLATAILFDYWGQGTLV
TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGG
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
YSDGKTYLFWYLQRPQPPQLLIYEVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDVGI
YYCMOSIKLPLTFGGGTKEIKRTVAAPSVEFIPPSDEOLKSGTASVVCLLNNFYPREAK

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 SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGTL
VTVSS**TCE4 CCR8 scFv VL (CCR8) (SEQ ID NO: 24)**DTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRLPLTFGCGTKVEIK**TCE4 CCR8 scFv (SEQ ID NO: 25)**QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGTL
VTVSSGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLF
WYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRL
PLTFGCGTKVEIK**TCE4 scFv (CCR8) x scFv (CD3) TCE (SEQ ID NO: 26)**QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGTL
VTVSSGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLF
WYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRL
PLTFGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQA
PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY
CARAGNFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSP
GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL**TCE4 CCR8 scFv (CCR8) x scFv (CD3) TCE x scFc (SEQ ID NO: 27)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LVTSSGGGGGGGGGGGGGGGGGGQDVTMTQTPLSLSVTPGQPASISCKSSQSLHSDGKTYLF
 WYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRL
 PLTFGGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTVYLQMN NLKTEDTAVYY
 CARAGNFSSYISYWAYWGQGT LVTSSGGGGGGGGGGGGGGGGGGQQT VVTQEP SLTVSP
 GGTVTITCGSSSTGAVTSGNYPNWVQKKPGQAPRGLIGG TKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFP
 PKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
 NVFSCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 QCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEV
 HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
 GSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGK

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

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

DTVMTQTPLSLSVTPGQPASISCKSSQSLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFS
 GVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQSLRLPLTFGGG TKVEIKRTVAAPSVFI
 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL
 STLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

TCE4 CCR8 scFab (SEQ ID NO: 30)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGGGGGGGGG
 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 LLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDV
 GFYYCMQSLRLPLTFGGG TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGEC

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWGQGT
 LVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGGGGGGGGG

GGGQGGGGQGGGGQGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQS
 LLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDV
 GFYYCMQSLRLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGECSSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY
 CARAGNFGSSYISYWAYWGQGTLLVTVSSGGGGQGGGGQGGGGQQTIVVTQEPSTLVSP
 GGTVTITCGSSGTAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK
 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRYFDWFLFDYWQGTLL
 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGG
 GGGQGGGGQGGGGQGGGGQGGGGQGGGGQDTVMTQTPLSLSVTPGQPASISCKSSQS
 LLHSDGKTYLFWYLQKPGQPPQLLISEVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDV
 GFYYCMQSLRLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGECSSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA
 PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY
 CARAGNFGSSYISYWAYWGQGTLLVTVSSGGGGQGGGGQGGGGQQTIVVTQEPSTLVSP
 GGTVTITCGSSGTAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFP
 PKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG
 NVFSCSVSMHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGG
 QCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEV
 HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
 GSFFLYSKLTVDKSRWQQGNVFSCSVSMHEALHNHYTQKSLSLSPGK

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)

VTLVRGVIFDY

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

RVSQSVSSQLA

GASSRAT

OOYGNSRT

EVQLVESGGGLVKPGGSLRLAC AASGFIFSNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LVTVSS

EIVLTQFPGTSLSPGESATLSCRVSQSVSSSQLAWYQQKPGQAPRLLIYGASSRATGIPD
RESGSGSGTDFTLIIIRLEPEDEAVYYCOOYGNSRTEGCGTKVEIK

EVQLVESGGGLVKPGGSLRLACAASGFI¹SN²AWMSWVRQAPGKCLEWVGRIK³RTDGG
T⁴TDYAAPVKGRFTISR⁵DDSKNTLYLLMNSLKIEDTAVYYCTV⁶VL⁷VRGVIFDYWGQGT⁸L
VT⁹VSSGGGGQGGGGQGGGQ¹⁰Q¹¹Q¹²Q¹³Q¹⁴Q¹⁵Q¹⁶Q¹⁷Q¹⁸Q¹⁹Q²⁰Q²¹Q²²Q²³Q²⁴Q²⁵Q²⁶Q²⁷Q²⁸Q²⁹Q³⁰Q³¹Q³²Q³³Q³⁴Q³⁵Q³⁶Q³⁷Q³⁸Q³⁹Q⁴⁰Q⁴¹Q⁴²Q⁴³Q⁴⁴Q⁴⁵Q⁴⁶Q⁴⁷Q⁴⁸Q⁴⁹Q⁵⁰Q⁵¹Q⁵²Q⁵³Q⁵⁴Q⁵⁵Q⁵⁶Q⁵⁷Q⁵⁸Q⁵⁹Q⁶⁰Q⁶¹Q⁶²Q⁶³Q⁶⁴Q⁶⁵Q⁶⁶Q⁶⁷Q⁶⁸Q⁶⁹Q⁷⁰Q⁷¹Q⁷²Q⁷³Q⁷⁴Q⁷⁵Q⁷⁶Q⁷⁷Q⁷⁸Q⁷⁹Q⁸⁰Q⁸¹Q⁸²Q⁸³Q⁸⁴Q⁸⁵Q⁸⁶Q⁸⁷Q⁸⁸Q⁸⁹Q⁹⁰Q⁹¹Q⁹²Q⁹³Q⁹⁴Q⁹⁵Q⁹⁶Q⁹⁷Q⁹⁸Q⁹⁹Q¹⁰⁰Q¹⁰¹Q¹⁰²Q¹⁰³Q¹⁰⁴Q¹⁰⁵Q¹⁰⁶Q¹⁰⁷Q¹⁰⁸Q¹⁰⁹Q¹¹⁰Q¹¹¹Q¹¹²Q¹¹³Q¹¹⁴Q¹¹⁵Q¹¹⁶Q¹¹⁷Q¹¹⁸Q¹¹⁹Q¹²⁰Q¹²¹Q¹²²Q¹²³Q¹²⁴Q¹²⁵Q¹²⁶Q¹²⁷Q¹²⁸Q¹²⁹Q¹³⁰Q¹³¹Q¹³²Q¹³³Q¹³⁴Q¹³⁵Q¹³⁶Q¹³⁷Q¹³⁸Q¹³⁹Q¹⁴⁰Q¹⁴¹Q¹⁴²Q¹⁴³Q¹⁴⁴Q¹⁴⁵Q¹⁴⁶Q¹⁴⁷Q¹⁴⁸Q¹⁴⁹Q¹⁵⁰Q¹⁵¹Q¹⁵²Q¹⁵³Q¹⁵⁴Q¹⁵⁵Q¹⁵⁶Q¹⁵⁷Q¹⁵⁸Q¹⁵⁹Q¹⁶⁰Q¹⁶¹Q¹⁶²Q¹⁶³Q¹⁶⁴Q¹⁶⁵Q¹⁶⁶Q¹⁶⁷Q¹⁶⁸Q¹⁶⁹Q¹⁷⁰Q¹⁷¹Q¹⁷²Q¹⁷³Q¹⁷⁴Q¹⁷⁵Q¹⁷⁶Q¹⁷⁷Q¹⁷⁸Q¹⁷⁹Q¹⁸⁰Q¹⁸¹Q¹⁸²Q¹⁸³Q¹⁸⁴Q¹⁸⁵Q¹⁸⁶Q¹⁸⁷Q¹⁸⁸Q¹⁸⁹Q¹⁹⁰Q¹⁹¹Q¹⁹²Q¹⁹³Q¹⁹⁴Q¹⁹⁵Q¹⁹⁶Q¹⁹⁷Q¹⁹⁸Q¹⁹⁹Q²⁰⁰Q²⁰¹Q²⁰²Q²⁰³Q²⁰⁴Q²⁰⁵Q²⁰⁶Q²⁰⁷Q²⁰⁸Q²⁰⁹Q²¹⁰Q²¹¹Q²¹²Q²¹³Q²¹⁴Q²¹⁵Q²¹⁶Q²¹⁷Q²¹⁸Q²¹⁹Q²²⁰Q²²¹Q²²²Q²²³Q²²⁴Q²²⁵Q²²⁶Q²²⁷Q²²⁸Q²²⁹Q²³⁰Q²³¹Q²³²Q²³³Q²³⁴Q²³⁵Q²³⁶Q²³⁷Q²³⁸Q²³⁹Q²⁴⁰Q²⁴¹Q²⁴²Q²⁴³Q²⁴⁴Q²⁴⁵Q²⁴⁶Q²⁴⁷Q²⁴⁸Q²⁴⁹Q²⁵⁰Q²⁵¹Q²⁵²Q²⁵³Q²⁵⁴Q²⁵⁵Q²⁵⁶Q²⁵⁷Q²⁵⁸Q²⁵⁹Q²⁶⁰Q²⁶¹Q²⁶²Q²⁶³Q²⁶⁴Q²⁶⁵Q²⁶⁶Q²⁶⁷Q²⁶⁸Q²⁶⁹Q²⁷⁰Q²⁷¹Q²⁷²Q²⁷³Q²⁷⁴Q²⁷⁵Q²⁷⁶Q²⁷⁷Q²⁷⁸Q²⁷⁹Q²⁸⁰Q²⁸¹Q²⁸²Q²⁸³Q²⁸⁴Q²⁸⁵Q²⁸⁶Q²⁸⁷Q²⁸⁸Q²⁸⁹Q²⁹⁰Q²⁹¹Q²⁹²Q²⁹³Q²⁹⁴Q²⁹⁵Q²⁹⁶Q²⁹⁷Q²⁹⁸Q²⁹⁹Q³⁰⁰Q³⁰¹Q³⁰²Q³⁰³Q³⁰⁴Q³⁰⁵Q³⁰⁶Q³⁰⁷Q³⁰⁸Q³⁰⁹Q³¹⁰Q³¹¹Q³¹²Q³¹³Q³¹⁴Q³¹⁵Q³¹⁶Q³¹⁷Q³¹⁸Q³¹⁹Q³²⁰Q³²¹Q³²²Q³²³Q³²⁴Q³²⁵Q³²⁶Q³²⁷Q³²⁸Q³²⁹Q³³⁰Q³³¹Q³³²Q³³³Q³³⁴Q³³⁵Q³³⁶Q³³⁷Q³³⁸Q³³⁹Q³⁴⁰Q³⁴¹Q³⁴²Q³⁴³Q³⁴⁴Q³⁴⁵Q³⁴⁶Q³⁴⁷Q³⁴⁸Q³⁴⁹Q³⁵⁰Q³⁵¹Q³⁵²Q³⁵³Q³⁵⁴Q³⁵⁵Q³⁵⁶Q³⁵⁷Q³⁵⁸Q³⁵⁹Q³⁶⁰Q³⁶¹Q³⁶²Q³⁶³Q³⁶⁴Q³⁶⁵Q³⁶⁶Q³⁶⁷Q³⁶⁸Q³⁶⁹Q³⁷⁰Q³⁷¹Q³⁷²Q³⁷³Q³⁷⁴Q³⁷⁵Q³⁷⁶Q³⁷⁷Q³⁷⁸Q³⁷⁹Q³⁸⁰Q³⁸¹Q³⁸²Q³⁸³Q³⁸⁴Q³⁸⁵Q³⁸⁶Q³⁸⁷Q³⁸⁸Q³⁸⁹Q³⁹⁰Q³⁹¹Q³⁹²Q³⁹³Q³⁹⁴Q³⁹⁵Q³⁹⁶Q³⁹⁷Q³⁹⁸Q³⁹⁹Q⁴⁰⁰Q⁴⁰¹Q⁴⁰²Q⁴⁰³Q⁴⁰⁴Q⁴⁰⁵Q⁴⁰⁶Q⁴⁰⁷Q⁴⁰⁸Q⁴⁰⁹Q⁴¹⁰Q⁴¹¹Q⁴¹²Q⁴¹³Q⁴¹

EVQLVESGGGLVKPGGSLRLACAASGFIISNAWMSWVRQAPGKCLEWVGRIKRTDGG
TDDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGVIFDYWGQGT
LTVTVSSGGGGQGGGGQGGGGQGEIVLTQFPGTSLSPGESATLSRVSSQSVSSSQLAWYQQ
KPGQAPRLLLIYGASSRATGIPDRFSGSGSGTDFTLISRLEPEDFAVYYCQQYGNRSTFGC
GTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSACAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGT LTVTVSSGGGGQGGGGQGGGGQQT VTVTQEPSLTVSPGGTVTI
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLTG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

EVQLVESGGGLVKPGGSLRLACAASGFIISNAWMSWVRQAPGKCLEWVGRIKRTDGG
TDDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVTLVRGVIFDYWGQGT
LTVTVSSGGGGQGGGGQGGGGQGEIVLTQFPGTSLSPGESATLSRVSSQSVSSSLAWYQQ
KPGQAPRLLLIYGASSRATGIPDRFSGSGSGTDFTLISRLEPEDFAVYYCQQYGNRSTFGC
GTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPGGTIVT
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLTG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV

LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPDSIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKG GGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEEPVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT TLV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPDSIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVPGGSLRLAC AASGFIFSNAWMSWVRQAPGKGLEWVGRIKRKTDG
GTTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLRGVIFDYWGQGT
LTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLOSSGLYSLSSVTVTPSSSLGTOTYICNVNHHKPSNTKVDKKVEPKSC

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

EIVLTQFPGLTSLSPGESATLSCRVSQSVSSSQLAWYQQKPGQAPRLLIYGASSRATGIPD
 RFSGSGSGTDFTLIISRLEPEDFAVYYCQQYGNSRFTGQGTKVEIKRTVAAPSVFIFPPSDE
 QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLS
 KADYEKHKVYACEVTHOGLSSPVTKSFNRGEC

TCE5 CCR8 scFab (SEQ ID NO: 46)

EVQLVESGGGLVKPGGSLRLAC AASGFIFSNAWMSWVRQAPGKGLEWVGRIKRKTDG
GTTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLRGVIFDYWGQGT
LTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ
GGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGEIVLTQFPGTSLSPGESATLSCRVSQS
VSSSQLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLISRLEPEDFAVYYC
QQYGNSRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

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

EVQLVESGGGLVPGGSLRLAC AASGFIFSNAWMSWVRQAPGKGLEWVGRIKRTDGT
GTTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGVIFDYWGQGT
LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQ
GGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
VSSSQLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTIISRLEPEDFAVYYC
QQYGNSTRTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKIDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGECSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLVTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
TCGSSTGAVTSGNYPNWVQKKPGQAPRLIGGTFKFLAPGTPARFSGSLSGGKAALTLTG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGLVT
VSS

TCE2 CCR8 scFv VL (SEQ ID NO: 56)

DFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFWYLQKPGQPPHLLIYEVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLPITFGCGTKVEIN

TCE2 CCR8 scFv (SEQ ID NO: 57)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGLVT
VSSGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFW
YLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP
ITFGCGTKVEIN

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGLVT
VSSGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFW
YLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP
ITFGCGTKVEINSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAP
GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYC
ARAGNFGSSYISYWAYWGQGLVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPG
GTVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKCLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKKTLYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGLVT
VSSGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFW
YLQKPGQPPHLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLP
ITFGCGTKVEINSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAP
GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYC
ARAGNFGSSYISYWAYWGQGLVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPG
GTVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVH
NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF
FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

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

DFVMTQTPLSLSVTPGQPASISCKYSQSLLHSDGKTYLFWYLQKPGQPPHLLIYEVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQTLKLPLTFGGGTKEINRTVAAPSVF
IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

TCE2 CCR8 scFab (SEQ ID NO: 62)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGG
GQGGGGQGGGGQGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLL
HSDGKTYLFWYLQKPGQPPHLLIYEVSNRFSGVDRFSGSGSGTDFTLKISRVEAEDVGL
YYCMQTLKLPLTFGGGTKEINRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGG
GQGGGGQGGGGQGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLL
HSDGKTYLFWYLQKPGQPPHLLIYEVSNRFSGVDRFSGSGSGTDFTLKISRVEAEDVGL
YYCMQTLKLPLTFGGGTKEINRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGECGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP
GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYC
ARAGNFGSSYISYWAYWGQGTLLVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLTVSPG
GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA
LTLGVPEDAEYYCVLWYSNRWVFGSGTKLTVL

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSN
KFYADSVKGRFTISRDNSSKTLTYLQMSSLRVEDTAVYYCARAGGIGRFDYWGQGTLLV
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGG
GQGGGGQGGGGQGGGGQGGGGQGGGGQDFVMTQTPLSLSVTPGQPASISCKYSQSLL
HSDGKTYLFWYLQKPGQPPHLLIYEVSNRFSGVDRFSGSGSGTDFTLKISRVEAEDVGL
YYCMQTLKLPLTFGGGTKEINRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS

PVTKSFNRGECSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP
GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYC
ARAGNFGSSYISYWAYWGQGLVTVSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPG
GTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVH
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)
VTLVRGIIFY

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
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVT LVRGIIFYWGQGL
VTVSS

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

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

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

EVQLVESGGGLVPGGSLRLSCAASGFISSNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGIFDYWGQGT
LTVTSSGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGESATLSCRVSQSVSSSQLAWYQQ
KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSTRFGC
GTKVEIKSGGGGQGEVQLVESGGGLVPGGSLKLSAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGT LTVTSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGTVTI
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLG
VOPEDAEYYCVLWYSNRWVFGSGTKLTVL

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

EVQLVESGGGLVPGGSLRLSCAASGFFSNAWMSWRVQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGIIFDYWGQGT
LTVTSSGGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGESATLSCRVSQSVSSSQLAWYQ
KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSTRFCG
GTKVEIKSGGGGQEVQLVESGGGLVPGGSLKLSAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGT LTVTSSGGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGTVTI
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLG
VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPPKPKDT
LMISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
LVKGFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC
VMHEALHNHYTQKSLSLSPGKGGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQ
CPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAK
TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLLVKGFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLY
SKLTVDKSRWQQGNVFC

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

EVQLVESGGGLVPGGSLRLSCAASGFFSNAWMSWVRQAPGKGLEWVGRIRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGIIFDYWGQGT
LTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLOSSGLYSLSSVTVPPSSSLGTOTYICNVNHKPSNTKVDKKVEPKSC

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

EIVLTQSPGTLSPGESATLSCRVVSQVSSSQLAWYQQKPGQAPRLLIYGASSRATGIPD
 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSRTFGQGTKVEIKRTVAAPSVFIFPPSD
 EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
 LSKADYEKHKVYACEVTHOGLSPPVTKSFNRGEC

TCE6 CCR8 scFab (SEO ID NO: 78)

EVQLVESGGGLVLPKPGASLRLSCTAASGFIFSNAWMSWVRQAPGKGLEWVGRIKRKTDDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVTVLVRGIIDFYWGQGTL
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPFEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVTPVSSSLGTQTQYICNVNHKPSNTKVDDKKVEPKSCGGGGQGGGGQG
GGGQGGGGQGGGGQGGGGQGGGGQGGGGQEIVLTQSPGTLSPGESATLSRVTSQSV
SSSQLAWYQQKPGQAPRLLIYGASSRATGIPDRFGSGSGSDFTLTISRLEPEDFAVYYCQ
QYGNRSRTFGOGTKVEIKRTVAAPSVPFIPPSDEOLKSGTASVVCLLNFPYPREAKVOWK

RASOSVSSOLA

GASSRAT

OOYGNSTR

EVQLVESGGDLVKPGGSLRLSCAASGFFISNAWMSWVRQAPGKCLEWVGRIKRTDGG
TVDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLEVRGVIFDYWGQGT
LTVSS

EIVLTQSPGDTLSLSPGESATLSLSCRASQSVSSSQLAWYQQKPGQTPRLLIYGASSRATGIPD
RFSGSGSGTDFTLTISRLEPEDFAVYYCOOYGNSRTEGCGTKVEIK

EVQLVESGGDLVKPGGSLRLSCAASGFISSNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTSSGGGGGGGGGGGGGGQEIIVLTQSPGTLSPGESATLSCRASQSVSSSQLAWYQQ
KPGQTPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGNSTRFC
GTKVEIK

EVQLVESGGDLVKPGGSLRLSCAASGFFISNAWMSWVRQAPGKCLEWVGRIKRKTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTSSGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGESATLSCRASQSVSSSQLAWYQQ
KPGQTPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSTRFGC
GTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGTLTVTSSGGGGQGGGGQGGGGQQT VVTQEPSLTVSPGGTVTI
TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLG
VPEDEAEYYCVLWYSNRWVFGSGTKLTVL

[illegible]

EVQLVESGGDLVKPGGSLRLSCAASGFFISNAWMSWVRQAPGKGLEWVGRIRKRTDGG
TTDYAAPVKGRFTISRDDSKNTLYLLMNSLKIEDTAVYYCTVVTLVRGVIFDYWGQGT
LTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQG
GGGQGGGGQGGGGQGGGGQGGGGQGGGGQEIVLTQSPGTLSPGESATLSCRASQSV
SSSLAWYOOKPGOTPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCO

QYGNRSRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGECSSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLF
WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGN
FGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQTQVVTQEPSLTVSPGGTVTIT
CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGV
QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPPKPKDTL
MISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSV
MHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCP
PELLGGPSVFLFPPKPKDTLTMISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAKTK
PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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)
VTMVRGV IADY

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)
 00YGSSRT

TCE8 CCR8 scFv VH (SEQ ID NO: 103)
 EVQLVESGGGLVPGGSLRLSCAASGFI¹FSNAWMSWVRQAPGKCLEWVARIKRRTDGG
 TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVTMVRGVIADYWGQGT
 LTVSS

TCE8 CCR8 scFv VL (SEQ ID NO: 104)
EIVLTQSPGTL^{SL}SPGERATL^{SCR}ASQSVSSGSLAWYQQKLGQAPRLLIYGASSRATGIPD
RFSGSGSGTDF^{FTL}TISSLEPEDFAVYYCOOYGSSRTFGCGTKVELK

TCE8 CCR8 scFv (SEQ ID NO: 105)
 EVQLVESGGGLVPGGSLRLSCAASGFIFSNAWMSWVRQAPGKCLEWVARIKRRTDGG
 TTDYAAPVKDRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTVTMVRGVIADYWQGQT
 LTVTSSGGGGQGGGGQGGGGQGEIVLTQSPGTLSPGERATLSCRASQSVSSGSLAWYQ
 QKLGPAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSRTFG
 CGTKVELK

TCE1 CCR8 scFv and scFab LCDR1 (SEQ ID NO: 116)

KSSQSVLYSSNNKNYLA

TCE1 CCR8 scFv and scFab LCDR2 (SEQ ID NO: 117)

WASTRES

TCE1 CCR8 scFv and scFab LCDR3 (SEQ ID NO: 118)

QQYYSIPIT

TCE1 CCR8 scFv VH (SEQ ID NO: 119)EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSS**TCE1 CCR8 scFv VL (SEQ ID NO: 120)**EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTR
ESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFGCGTKVEIK**TCE1 CCR8 scFv (SEQ ID NO: 121)**EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSG
GGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQ
KPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFG
CGTKVEIK**TCE1 scFv (CCR8) x scFv (CD3) (SEQ ID NO: 122)**EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSG
GGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQ
KPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFG
CGTKVEIKSGGGGQEIVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCARA
GNFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQTQVVTQEPSTVSPGGTV
TITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLS
GVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL**TCE1 scFv (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 123)**EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSG
GGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQ
KPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFG
CGTKVEIKSGGGGQEIVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCARA
GNFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQQTQVVTQEPSTVSPGGTV
TITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLS
GVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPPCPAPELLGGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC
SVMHEALHNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCPPC

PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEEPEVKFNWYVDGVEVHNAK
TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY
SKLTVDKSRWOOGNVFCFSVMHEALHNHYTOKLSLSLSPGK

TCE1 CCR8 scFab VH and CH1 (SEO ID NO: 124)

EVQLVESGGGLVPGGSLRLSCAASGFTFSNARMGWVRQAPGKGLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDAVYYCTSYSGVWGQGTMTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

TCE1 CCR8 scFab VL and Ck (SEO ID NO: 125)

EIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTR
 ESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYsipITFGGgTKVEIKRTVAAPSV
 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
 LSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC

TCE1 CCR8 scFab (SEQ ID NO: 126)

EVQLVESGGGLVPGGSLRLSCAASGFTFSNARMGWVRQAPGKGLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGGGQG
GGGQGGGGQGGGGQGGGGQGGGGQGEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSN
NKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSQAEDVAVYY
CQQYYSIPITFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

TCE1 scFab (CCR8) x scFv (CD3) (SEQ ID NO: 127)

EVQLVESGGGLVPGGSLRLSCAASGFTFSNARMGWVRQAPGKGLEWVGRIKSKTEGG
TRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGMVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHFTPAVLQSSG
LYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGGGQ
GGGQGGGGQGGGGQGGGGQGGGGQGEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSN
NKNYLAWYHQKPGQSPKLLISWASTRESGPVDRFSGSGSGTDFTLTINSIQAEDVAVYY
CQQYYSIPITFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKIDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGECSGGGGQEVQLVESGGGLVPGGSLRLSCAASGFTFNKYAINWVRQAPGKGL
EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAG
NFGSSYISYWAYWGQGLTVTVSSGGGGQGGGGQGGGGQGGGGQQTAVTQEPSTVSPGGT
TCGSDTGAVTSGNYPNWVQKPKGAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSS
VQPEDAEAYYCVLWYSNRWVFGSGTKLTVL

TCE1 scFab (CCR8) x scFv (CD3) x scFc (SEQ ID NO: 128)

EVQLVDSGGGLVKPGRSLRLSCAASGFTFSNARMGWVYRQAPGKGLEWVGRIKSKTEGG
TRDYAAPVKGKFTISRDDSKNTLYLQMNLSLKTEDTAVVYCTSYSGVWGQGTMTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGQGGGGQGGGGQG
GGGQGGGGQGGGGQGGGGQGGGGQGEIVMTQSPDSLAVSLGERATINCKSSQSVLYSSN
NKNYLAWYHOKPGOSPCLLISWASTRESGVPDRFSGSGSGTDFTLTINSLOAEDVAVVY

CQQYYSIPITFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTLLTVTSSGGGGGQGGGGQGGGGQQTTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHLVQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK

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

MDYTLDPSTMTMDYYPDSLSSPCDGLIQRNDKLLAVFYCLLFVFSLLGNSLVILVL
VVCKKLRNITDIYLLNLALSDLLFVFSFPQTYQLDQWVFGTVMCKVVS GFYYIGFYSS
MFFITLMSVDRYLAVVHAVYAIKVRTIRMGTTLSLVVWLTAIMATIPLLVFYQVASEDG
VLQCYSFYNQQTWKWKIFTNFEMNILGLLIPFTIFMFCYIKILHQLKRCQNHNTKTAIRLV
LIVVIASLLFWVPFNVVLFSLHSMHILDGCSISQQLNYATHVTEISFTHCCVNPVIYAF
VGEKFKKHLSEIFOKSCSHIFIYLGROMPRESCEKSSSSCOOHSFRSSSIDYIL

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

MDYRLDPSMTTMTDYYPDSLSSPCDGLIQRNDKLLAVFYCLLFVFSLLGNSLVILVL
VVCKKLRNITDIYLLNLALSDLLFVFSFPQTYQYQLDQWVFGTVMCKVVS GFYYIGFYSS
MFFITLMSVD RYLAVVHAVYAIKVRTIRMGTTLSLVVWLTAIMATIPLLVFYQVASEDG
VLQCYSFYNQQTLKWIKFTNFEMNILGLLIPFTIFMFCYIKILHQLKRCQNHNKTKAIRLV
LIVVIASLLFWVPFNVVLF L TSLHSMHILDGCSISQQLNYATHVTEIISFTHCCVNPVIYAF
VGEKFKKHLSEIFOKSCSHIFIYLGROMPRESCEKSSSCOOHSFRSSSIDYIL

Human CCR8 (SEQ ID NO: 131)

MDYTLDSLVTVDYYPIDFSSPCDAELIQTNGLLLAVFYCLLFVFSLLGNSLVILVLV
VCKKLRSITDVYLLNLALSDLLFVFSFPQTYLLDQWVFGTVMCKVVS GFYYIGFYSS
MFFITLMSVDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLL VFYQVASEDG
VLQCYSFYNQQLKWKIFTNFKMNILGLIPFTIFMFCYIKILHQLKRCQNHNKTKAIRLV
LIVVIASLLFWVPFNVVLF L TSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAF
VGEKFKKHLSEIFOKSCSQIFNYLGRMPRESCEKSSSCQOHSRSSSVDYIL

Human A27G CCR8 (SEQ ID NO: 132)

MDYTLDSLVTVDYYPIDIFSSPCDGLIQTNGKLLAVFYCLLFVFSLLGNSLVILVLV
VCKKLRSITDVYLLNLALSDLLFVFSFPQTYLLDQWVFGTVMCKVVS GFYYIGFYSS
MFFITLMSVDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLL VFYQVASEDG
VLQCYSFYNQQTWKIFTNFKMNLGLLIPFTIFMFCYIKILHQLKRCQNHNTKKAIRLV
LIVVIASLLFWVPFNVVLFSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAF
VGEKFKKHLSEIFOKSCSOIFNYLGROMPRESCEKSSSCOHHSSRSSSVDYIL

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

MDYTLDSVTTVTDYYYPDIFSSPCDAELIOTNGK

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

MDYTLDLSVTTV

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

TDYYYPDIFSSP

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

CDAELIQTNKG

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)DIQMTQSPSSVSASVGDRVITTCRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFGSGSGTDFTLTISLQPEDFATYYCQQAESFPHTFGGGTKVEIK**Antibody 20C1.009 VH (SEQ ID NO: 146)**EVQLLESQGGGLVQPGGSLRLSCAASGFTFSYDMSWVRQAPGKGLEWVSLISGGGSQTY
YAESVKGRFTISRDNKNTLYQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITV
VSS**Antibody 20C1.009 LC (SEQ ID NO: 147)**DIQMTQSPSSVSASVGDRVITTCRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFGSGSGTDFTLTISLQPEDFATYYCQQAESFPHTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLT
LTKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

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

EVQLLESQGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSQTY
YAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITV
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK

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)

QAFESSTEY

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)

DPSSLTGSTGYGMDV

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

SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGIPER
FSGNSGNTATLTISGTQAMDEADYYCQAFESSTEYFGGGTKLTVL

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVALIWYDASK
KYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCARDPSSLTGSTGYGMDVW
GQGTTVTVSS

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

SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGIPER
FSGNSGNTATLTISGTQAMDEADYYCQAFESSTEYFGGGTKLTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAASSYLS
LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

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

QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVALIWYDASK
KYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCARDPSSLTGSTGYGMDVW
GQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE

PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

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
FSGSSSGTMTLTISGAQVEDEADYYCYSTDASGNHRVFGGGTKLTVL

Antibody 20D4.6 VH (SEQ ID NO: 166)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNGGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFDPWGQGT
LTVTVSS

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

Antibody 20D4.6 HC (SEQ ID NO: 168)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNGGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFDPWGQGT
LTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK
PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

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
FSGSSSGTMTLTISGAQVEDEADYYCYSTDASGNHRVFGGGTKLTVL

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

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

Antibody 20D4.17 HC (SEQ ID NO: 178)
EVQLVESGGSVVRPGGSLRLSCAASGFTVDDYSMSWVRQVPGKGLEWVSGINWNAGR
TRYADAVKGRFTISRDSAKNSLYLQMNSLRAEDTALYYCAREFNNFESNWFD PWGQGT
LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

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)

DIQMTQSPSSVSASVGDRVITTCRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFSGSGSGTDFTLTISLQPEDFATYYCQQAESFPHTFGGGTKVEIK

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

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSNTY
YAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGT TTVT
VSS

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

DIQMTQSPSSVSASVGDRVITTCRASQGISNWLAWYQQKPGKAPKLLIFAASSLQSGVPS
RFSGSGSGTDFTLTISLQPEDFATYYCQQAESFPHTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT
SKADYEEKHKVYACEVTHQGLSPVTKSFNRGEC

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

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSNTY
YAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGT TTVT
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVL
QSSGLYSLSSTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
LGGPSTVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
EQYGSTYRCVSVLT VLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGK

G4S linker (SEQ ID NO: 189)

GGGS

(G4S)4 linker (SEQ ID NO: 190)

GGGSGGGSGGGSGGGGS

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
TPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

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
PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

G4Q Linker (SEQ ID NO: 207)

GGGGQ

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

GGGGQGGGGQGGGGQGGGGQ

mCCR8 (SEQ ID NO: 209)

MDYTMENVTMTDYYPDFFTAPCDAEFLLRGSMYLAIFYCVLFVLGLLGNSLVILVLV
 GCKKLRSITDIYLLNLAASDLLFVLSIPFQTHNLLDQWVFGTAMCKVVSGLYYIGFFSSM
 FFITLMSVDRYLAIVHAVYAIKVRTASVGTALSLTVWLA AVTATIPLMVFYQVASEDGM
 LQCFQFYEEQSLRWKLFTHFEINALGLLLPFAILLFCYVRILQQLRGCLNHNRTAIKLV
 TVVIVSLLFWVPFNVALFLTSLHDLHLDGCATRQRLALAIHVTEVISFTHCCVNPVIYAFI
 GEKFKKHLMDVDFQKSCSHIFLYLGRQMPVGALERQLSSNQSSHSSTLDDIL

Rat CCR8 (SEQ ID NO: 210)

MDYTLNVTMTDYYPDFFTPCDTELLLRGGTLYLAVLYCILFVLGLLGNSLVILVLVA
 CKKLRSITDVYLLNLAASDLLFVLSIPFQTHNLLDQWVFGTVMCKVVSGLYYIGFFSSML
 FITLMSVDRYLAIVHPVHAIVKVRTARVGTALSLAVWLA AIAATVPLMVFYQVSSDGM
 LQCFQLYDEQSLRWKLFTHFEVNALGLLLPFAILLFCYVRILQQLRGCLNHNRTAIKLV
 LTIVVVSLLFWVPFNVLFLTSLHDMHILEGCATRQRLALATHVTEVISFMHCCVNPVIY
 AFIGEKFKKHLVDVDFQKSCSHIFLYVGRQMPVGALERQLSSNQSSHSSTLDYIL

hCCR4 (SEQ ID NO: 211)

MNPTDIADTTLDESIYSNYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVL
 VLFKYKRLRSMTDVYLLNLAISDLLFVFSLPFWGYYAADQWVFGGLCKMISWMYLVG
 FYSGIFVVMLMSIDRYLAIVHAVFSRLARTLTYGVTSLATWSVAVFASLPGLFSTCYTE
 RNHTYCKTKYSLNSTTWKVLSSLEINILGLVIPLGIMLFCYSMIIRTLQHCKNEKKNKAV
 KMIFAVVVFLFGFWTPYNIVLFLETLEVEVLQDCTFERYLDAIATETLAFVHCCLNPI
 IYFFLGEKFRKYILQLFKTCRGLFVLCQYCGLLQIYSADTPSSSYTQSTMDHDLHDAL

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

EVQLLESGLLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSLISGGGSQTY
 YAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITV
 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
 LGGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPCPE
 EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
 PSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Leader sequence (SEQ ID NO: 213)

MDMRVPAQLL GLLLLWLRGA RC

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

atggacatga gagtgctgc acagctgctg ggctgctgc tgcgtggct gagaggcgcc agatgc.

Leader sequence (SEQ ID NO: 215)

MAWALLLLTL LTQGTGSA

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

atggcctggg ctctgctgc cctcacctc ctactcagg gcacagggtc ctgggcc

Table 24. TCE molecule sequences.

SEQ ID NO:	Designation	Sequence
CCR8 TCE 1.1 (CC EI GQ x I2E GQ x scFmod delGK)		
217	HCDR1	NARMG
218	HCDR2	RIKSKTEGGTRDYAAPVKG
219	HCDR3	YSGV
220	LCDR1	KSSQSVLYSSNNKNYLA
221	LCDR2	WASTRES
222	LCDR3	QQYYSSIPIT
223	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSS
224	VL	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAW YHQKPGQSPKLLISWASTRESGVPDRFSGSGGTDFLTINS LQAEDVAVYYCQQYYSSIPITFGCGTKVEIK
225	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGGQ GGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGS GSGTDFLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIK
226	TCE 1.1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGGQ GGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGS GSGTDFLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIK SGGGGQEVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYISYW AYWGQGTMTVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLT VSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLSGGKAALTLGVQPEDEAEYYCVL WYSNRWVFGSGTKLTVL
227	TCE 1.1 HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGGQ GGGGQGGGGQEIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLAWYHQKPGQSPKLLISWASTRESGVPDRFSGS GSGTDFLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIK SGGGGQEVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYISYW AYWGQGTMTVTVSSGGGGQGGGGQGGGGQQTIVTQEPSLT VSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLSGGKAALTLGVQPEDEAEYYCVL WYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSHPEEVKFNWYVDGVEVH

		NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQCPPEPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEEPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
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	QQYYSSIPIT
234	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSS
235	VL	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWEYHQPQGSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIK
236	SCFV	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGQGGGGQGGGGQEIIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWEYHQPQGSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIK
237	TCE 1.2	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGQGGGGQGGGGQEIIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWEYHQPQGSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIKSGGGGQEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLYQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGGGTLTVTVSSGGGGQGGGGQGGGGQQTTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWWVQKKPGQAPRGLIGGTKFLAPGTTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
238	TCE 1.2 HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQAPGKCLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSGGGGQGGGGQGGGGQEIIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWEYHQPQGSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSSIPITFGCGTKVEIK

		SGGGGQEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTVYLQMNLLKTEDTAVYYCARAGNFGSSYISYW AYWGQGTLLTVSSGGGGQGGGGQGGGGQQTVVVTQEPSLT VSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGG TKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGSGTKLTVLGGGGCPCPAPELLGGPSVFLFPP KPKDTLYITREPEVTCVVVDVSHEEPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGG GGQGGGGQGGGGQGGGGQGGGGQGGGGQCPPCPAPELL GGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEEPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK
CCR8 TCE 1.3 (EI scFab x I2E GQ x scFmod delGK_YTE)		
239	HCDR1	NARMG
240	HCDR2	RIKSKTEGGTRDYAAPVKG
241	HCDR3	YSGV
242	LCDR1	KSSQSVLYSSNNKNYLA
243	LCDR2	WASTRES
244	LCDR3	QQYYSSIPIT
245	VH-CH1	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSC
246	VL-Ck	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAW YHQKPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSSIPITFGGGTKVEIKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
247	SCFAB	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSSIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP

		REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
248	TCE 1.3	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQPQSPKLLISWASTRESG VPDRFSGSGSTDFTLTINSLQAEDVAVYYCQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSSGGGGQE VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNSLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT VTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVF GSGTKLTVL
249	TCE 1.3 HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQPQSPKLLISWASTRESG VPDRFSGSGSTDFTLTINSLQAEDVAVYYCQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSSGGGGQE VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNSLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT VTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVF GSGTKLTVLGGGGCPPCPAPPELLGGPSVFLFPPKPKDTLYIT REPEVTCVVDVSHREEPKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCVMHEALHNHYTQKSLSLSPGGGGQGGGG QGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGG PKPKDTLYITREPEVTCVVDVSHREEPKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL

		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 YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSC
257	VL-Ck	EIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAW YHQKPGQSPKLLISWASTRESGVPDRFSGSGSGTDFTLTINS LQAEDVAVYYCQQYYSIPITFGGGTKVEIKRTVAAPSVFIFP PSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
258	SCFAB	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGGG GQGGGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINC KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
259	TCE 1.4	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGGG GQGGGGQGGGGQGGGGQEIVMTQSPDSLAVSLGERATINC KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGGGQE VQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT LTVSSGGGGQGGGGQGGGGQGTQVVTQEPSTVSPGGTVTI

		TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGT PARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GSGTKLTVL
260	TCE 1.4 HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNARMGWVRQA PGKGLEWVGRIKSKTEGGTRDYAAPVKGRFTISRDDSKNTL YLMNSLKTEDTAVYYCTSYSGVWGQGTMTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCGGGGQGGGGQGGGGQGGGGQGGG GQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG KSSQSVLYSSNNKNYLAWYHQKPGQSPKLLISWASTRESG VPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSSGGGGQ VQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLMNNSLKTEDTAVYYCARAGNFGSSYISYWAYWGQGT VTVSSGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGG TCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGT PARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GSGTKLTVLGGGGCPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVDSHEEPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGQGGGG QGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGGQGGGG PKPKDTLMISRTPEVTCVVDVDSHEEPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 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	TISGSGGGTYAASVKG
263	HCDR3	GKGVHLGFDY
264	LCDR1	GGNNIGSKSVH
265	LCDR2	DDNDRPS
266	LCDR3	QVWDYRTLTDWV

267	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSS
268	VL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADY YCQVWDYRTL DWVF GCGTKLTVL
269	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIISR VEAGDEADYYCQVWDYRTL DWVF GCGTKLTVL
270	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIISR VEAGDEADYYCQVWDYRTL DWVF GCGTKLTVLSSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
271	BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSTISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIISR VEAGDEADYYCQVWDYRTL DWVF GCGTKLTVLSSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
MA 03-D8 AS scFab x I2C x scFc		

272	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
273	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADY YCQVWDYRTLDWVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTAWKADSSPVKAGVETTPSKQ SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
274	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS RVEAGDEADYYCQVWDYRTLDWVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSSPVK AGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECS
275	scFab- BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS RVEAGDEADYYCQVWDYRTLDWVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSSPVK AGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGQTVV TQEPSLTVSPGGTVLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
276	scFab-BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSTISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS

		RVEAGDEADYYCQVWDYRTLDDWVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTVV TQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWVQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKG GGSGGGGGSGGGSGGGSGGGSGGGSGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYCKVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGK
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	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSS
284	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVMVVDNDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYSPLRHVFVCGGCKLTVL
285	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVVDNDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSPLRHVFVCGGCKLTVL
286	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVVDNDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSPLRHVFVCGGCKLTVLSSGGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ

		MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
287	BiTE HLE	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSPLRHVFGCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCVMHEALHNHYTQKSLSLSPGK
MA 98-C7 scFab x I2C x scFc		
288	VH-CH1	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
289	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYSPLRHVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
290	scFab	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSSISGSGGGTYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVLGQPKAAP

		SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECS
291	scFab- BISPECIFIC MOL.	EVQLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KLEWVSSISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGQTVV TQEPSLTVSPGGTVLTCGSSTGAVTSGNYPNWVQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
292	scFab-BiTE HLE	EVQLES GGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KLEWVSSISGSGGGTYYAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGQTVV TQEPSLTVSPGGTVLTCGSSTGAVTSGNYPNWVQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGKG GGSGGGSGGGSGGGSGGGSGGGSGGGSGDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYCKVSNKALPAIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD

		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	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQSYSSPFTFGCGTKVEIK
301	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSYSSPFTFGCGTKVEIK
302	BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSYSSPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTV SSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGVQPEDEAEYYCVLWYSNRWVFVGGGKLTIVL
303	BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSYSSPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTV SSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLGVQPEDEAEYYCVLWYSNRWVFVGGGKLTIVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP

		REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGG GGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTRYCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK
MA 09-E2 scFab x I2C x scFc		
304	VH-CH1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC
305	VL-CL	DIQMTQSPSSLSASVGDRTITCRISQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQSYSSPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY SLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
306	scFab	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGSGGGSGGGSGG GGGSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISLQPEDFATYYCQQSYSSPFTFGPGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
307	scFab- BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGSGGGSGGGSGG GGGSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISLQPEDFATYYCQQSYSSPFTFGPGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGGG LKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGG QTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP

		GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
308	scFab-BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITC RTSQSISSYLNWYQQKPKRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPFTFGPGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGGG LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTLLTVSSGGGSGGGGSGGGGSG QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK
MA 03-E11 AS CC scFv x I2C x scFc		
309	HCDR1	SHAMS
310	HCDR2	AISSGGGTYNAASVKG
311	HCDR3	GKGVHLGFDY
312	LCDR1	GGNNIGSKSVH
313	LCDR2	DDNDRPS
314	LCDR3	QVWDYYSNRAV
315	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDNKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGTLLTVSS
316	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYYSNRAVFGCGTKLTVL
317	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDNKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGTLLTVSSGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH

		WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYYSNRAVFGCGTKLTVL
318	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYYSNRAVFGCGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
319	BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYYSNRAVFGCGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSG GGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSV MHEALHNHYTQKSLSLSPGK
MA 03-E11 AS scFab x I2C x scFc		
320	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
321	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYYSNRAVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ

		SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
322	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECS
323	scFab- BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
324	scFab-BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAAYYCVTGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVLGGGGDKHTCPCPAPELLG

		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK GGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKHTCPPCA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL GKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS SLSPGK
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 GKCLEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATYYCAYRRYNWNYENWFDWPWGQGLTVTVSS
332	VL	DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATY YCQQSYYYPTLFGCGTKVEIK
333	SCFV	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSGG GGSGGGSGGGSGDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGCGTKVEIK
334	BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSGG GGSGGGSGGGSGDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGCGTKVEIKSGGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGSGQTVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
335	BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSGG GGSGGGSGGGSGDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGCGTKVEIKSGGGGSEV

		QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLKTLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGSEFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRWQQGN 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 GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSC
338	VL-CL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATY YCQQSYYYPTLFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
339	scFab	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGGGGGGGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFT LTISLQPEDFATYYCQQSYYYPTLFGPGTKVEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
340	scFab- BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAS

		TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATYYCQQSYYYPTLFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
341	scFab-BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVLTMTNMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATYYCQQSYYYPTLFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
CCR8 TCE		
342	VL consensus	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNX₁NYLAWYX₂QKPGQX₃PKLLISWASTRESGVPRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYISIPITFGGGTKVEIKR, wherein X₁ is K or R, X₂ is H or Q, and/or X₃ is S or P

MA 09-G10 CC scFv x I2C x scFc		
343	HCDR1	THKMGVD
344	HCDR2	GIHIYDDKRYSPSLQS
345	HCDR3	RRYNWNYENWFD
346	LCDR1	QASQDISNYFN
347	LCDR2	AASSLQS
348	LCDR3	QQSYITPFT
349	VH	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSS
350	VL	DIQMTQSPSSLSASVGDRTITCQASQDISNYFNWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFLTITSSLPEDFATYYC QQSYITPFTFGCGTKVEIK
351	SCFV	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISN YFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFLT ISSLPEDFATYYCQQSYITPFTFGCGTKVEIK
352	BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISN YFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFLT ISSLPEDFATYYCQQSYITPFTFGCGTKVEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGG GSGGGGSGGGGSGTVVTQEPSTVSPGGTVLTCGSSTGAVT SGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
353	BiTE HLE	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISN YFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFLT ISSLPEDFATYYCQQSYITPFTFGCGTKVEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGG GSGGGGSGGGGSGTVVTQEPSTVSPGGTVLTCGSSTGAVT SGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEA LHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGG

		GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFV MHEALHNHYTQKSLSLSPGK
MA 09-G10 scFab x I2C x scFc		
354	VH-CH1	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
355	VL-CL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYFNWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQSYITPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
356	scFab	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSGDIQMTQSPSSLSASVGDRVTITCQASQDIS NYFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQQSYITPFTFGPGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
357	scFab- BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSGDIQMTQSPSSLSASVGDRVTITCQASQDIS NYFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQQSYITPFTFGPGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLVTVSSGGGGSGGGSGGGGSQTVVT QEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTFKFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
358	scFab-BiTE HLE	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KALEWLAGIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTN

		MDPVDATATYYCAYRRYNWNYENWFDWPWGQGLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYFNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYITPFTFGPGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGGSGTQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLS SLSPGK
MA 09-H7 CC scFv x I2C x scFc		
359	HCDR1	THKMGVD
360	HCDR2	LIYWNDKRYSPSLQS
361	HCDR3	RRYNWNYENWFDP
362	LCDR1	QASQDISNYLN
363	LCDR2	AASSLQS
364	LCDR3	QQSYFPVVE
365	VH	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLVTVSS
366	VL	DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYY CQQSYFPVVEFGCGTKVEIK
367	SCFV	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLVTVSSGG GGSGGGGSGGGSDIQMTQSPSSLSASVGDRVITTCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGCGTKVEIK
368	BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVVLMT

		NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDIS NYLWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKG LEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGSGGGGSGTQVVTQEPSTLVSPGGTVTLTCSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
369	BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKCLEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDIS NYLWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKG LEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGSGGGGSGTQVVTQEPSTLVSPGGTVTLTCSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC VMHEALHNHYTQKSLSLSPGK
MA 09-H7 scFab x I2C x scFc		
370	VH-CH1	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSC
371	VL-CL	DIQMTQSPSSLSASVGDRVITITCQASQDISNYLWYQQKPGK APKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYY CQQSYFPVVEFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
372	scFab	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA

		LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGSGGGGSDIQTQSPSSLSASVGDRVITITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNREGC
373	scFab- BISPECIFIC MOL.	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGSGGGGSDIQTQSPSSLSASVGDRVITITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNREGCSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
374	scFab-BiTE HLE	QITLKESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPP GKALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMT NMDPVDATATYYCAYRRYNWNYENWFDWPWGQGLTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGSGGGGSDIQTQSPSSLSASVGDRVITITCQASQDIS NYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQSYFPVVEFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNREGCSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSQSVSMHEALHNHYTQKSLSLSPGKG GGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPAP

		ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSL SLSPGK
MA 09-H10 CC scFv x I2C x scFc		
375	HCDR1	THKMGVD
376	HCDR2	LIYWNDKRYSPSLQS
377	HCDR3	RRYNWNYENWFD
378	LCDR1	QASQDISNYLN
379	LCDR2	AASSLQS
380	LCDR3	QQSYTPPTT
381	VH	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSS
382	VL	DIQMTQSPSSLSASVGDRVITITCQASQDISNYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISLQPEDFATY YCQQSYTPPTTFGCGTKVEIK
383	SCFV	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLT ISLQPEDFATYYCQQSYTPPTTFGCGTKVEIK
384	BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLT ISLQPEDFATYYCQQSYTPPTTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGG GGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
385	BiTE HLE	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KCLEWLALIIYWNDDKRYSPSLQSRLTITKDTSKNQVLTMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQASQDISN YLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLT ISLQPEDFATYYCQQSYTPPTTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGG GGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGG

		GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
MA 09-H10 scFab x I2C x scFc		
386	VH-CH1	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWDDKRYSPSLQSRLTITKDTSKNQVLTMTNMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
387	VL-CL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYTCQQSYTPPTTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC
388	scFab	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWDDKRYSPSLQSRLTITKDTSKNQVLTMTNMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGGGSGGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYTCQQSYTPPTTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
389	scFab-BISPECIFIC MOL.	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLALIYWDDKRYSPSLQSRLTITKDTSKNQVLTMTNMDPVDATATYYCAYRRYNWNYENWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGGGSGGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYTCQQSYTPPTTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYASDVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF

		GNSYISYWAYWGQGLVTVSSGGGSGGGGSGGGGSGQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
390	scFab-BiTE HLE	QITLKESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPG KALEWLALIYWNDKRYSPSLQSRLTITKDTSKNQVVLMTN MDPVDATATYYCAYRRYNWNYENWFDPWGQGLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGG GGSGGGGSGGGSDIQMTQSPSSLSASVGDRVTTITCQASQDIS NYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGRSGTDFT LTISSLQPEDFATYYCQQSYTPPTTFGPGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLVTVSSGGGSGGGGSGGGGSGQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
MA 10-D3 CC scFv x I2C x scFc		
391	HCDR1	NAWMS
392	HCDR2	RITSSRYGGTTDYAAPVKG
393	HCDR3	PSYSGSYNYFSVMDV
394	LCDR1	RTSQSISSYLN
395	LCDR2	AASSLQG
396	LCDR3	QQTYSMPFT
397	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SS
398	VL	DIQMTQSPSSLSASVGDRVTTITCRTSQSISSYLNWYQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTITSSLQPEDFATYYC QQTYSMPFTFGCGTKVDIK

399	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRTS QSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVDIK
400	BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRTS QSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQA PGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITV VSSGGGSGGGGSGGGGSGTQVTVTQEPSTVSPGGTVTLTCS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVPQPEDEAEYYCVLWYSNRWVFGGKTLT VL
401	BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQ MNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTV SSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRTS QSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQA PGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITV VSSGGGSGGGGSGGGGSGTQVTVTQEPSTVSPGGTVTLTCS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVPQPEDEAEYYCVLWYSNRWVFGGKTLT VLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK
MA 10-D3 scFab x I2C x scFc		
402	VH-CH1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKLEWVGRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQIYIC NVNHKPSNTKVDKKVEPKSC

403	VL-CL	DIQMTQSPSSLSASVGDRVITITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQTYSMPTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
404	scFab	EVQLVESGGGLVQPGGSLRLSAAAGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTDDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC
405	scFab- BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSAAAGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTDDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGG SLKLSAAAGFTFNKYAMNWVRQAPGKLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG GSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGKLTVL
406	scFab-BiTE HLE	EVQLVESGGGLVQPGGSLRLSAAAGFTFSNAWMSWVRQAP GKGLEWVGRITSSRYGGTDDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGECGGGGSEVQLVESGGGLVQPGG SLKLSAAAGFTFNKYAMNWVRQAPGKLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG

		GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNL GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNL GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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 QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTVSS
414	VL	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQTYSMPFTFGCGTKVDIK
415	SCFV	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTVSS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVDIK
416	BISPECIFIC MOL.	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTVSS GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSS GGGGSGGGGSGGGGSGQTVVTQEPSLTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

417	BiTE HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIQTQSPSSLSASVGDRVITICRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGGT DFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVDIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTITLTCSG STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK
MA 10-D6 scFab x I2C x scFc		
418	VH-CH1	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC
419	VL-CL	DIQTQSPSSLSASVGDRVITICRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQTYSMPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
420	scFab	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQTQSPSSLSASVGDRVITIC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPFTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC

421	scFab-BISPECIFIC MOL.	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSSITLTLKADYEKHKVYAC EVTHQGLSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTIVTVSSGGGSGGGGSGGG GSQTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGKFLAPGTPARFSGSLLGGKAALTLGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
422	scFab-BiTE HLE	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSLSSITLTLKADYEKHKVYAC EVTHQGLSPVTKSFNRGECSSGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTIVTVSSGGGSGGGGSGGG GSQTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGKFLAPGTPARFSGSLLGGKAALTLGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWKVDGVEVHNAKTKPCEEQYGSTYRCVSVLTIVLHGDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTIVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDS DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK
MA 10-G10 AS CC scFv x I2C x scFc		
423	HCDRI	SHAMS

424	HCDR2	AI SGSGGGTYNAASVKG
425	HCDR3	GKGVHLGFDY
426	LCDR1	GGNNIGSKSVH
427	LCDR2	DDNDRPS
428	LCDR3	QVWDYVAPRHV
429	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSS
430	VL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYVAPRHVFGCGTKLTVL
431	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYVAPRHVFGCGTKLTVL
432	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYVAPRHVFGCGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFSGGTKLTVL
433	BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KCLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYVAPRHVFGCGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFSGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV MHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSG GGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ

		YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
MA 10-G10 AS scFab x I2C x scFc		
434	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSC
435	VL-CL	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQA PVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYVAPRHVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ SNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPT ECS
436	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLT ISRVEAGDEADYCYQVWDYVAPRHVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECS
437	scFab- BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGSGGGSGGGSGGGSGGGSGGGG SGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLT ISRVEAGDEADYCYQVWDYVAPRHVFGGGTKLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
438	scFab-BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPG KGLEWVSAISGSGGGTYNAASVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP

		SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGSGGGGSSYVLTPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVVDNDNRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYVAPRHVFGGGKTLTVLGQPKAA PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNNKYAASSYLSLTPEQWKSYSYSCQVTH EGSTVEKTVAPTECSSGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHG NFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLS LSLSPGK
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	QKYNAPFT
445	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSS
446	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKV PKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYY CQKYNAPFTFGCGTKVEIK
447	SCFV	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSGGGGSGGG GSGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWY QQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQ EDVATYYCQKYNAPFTFGCGTKVEIK
448	BISPECIFIC MOL.	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSGGGGSGGG

		GSGGGGSDIQMTQSPSSLSASVGDRVITICRASQGISNYLAWY QQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQ EDVATYYCQKYNAPFTFGCGTKVEIKSGGGGSEVQLVESGG GLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVA RIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSG GGSGGGGSGTQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
449	BiTE HLE	QVQLVESGGGVVQPGRLRLSCAASGFTFSTYGMHWVRQAP GKCLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSGGGSGGG GSGGGGSDIQMTQSPSSLSASVGDRVITICRASQGISNYLAWY QQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQ EDVATYYCQKYNAPFTFGCGTKVEIKSGGGGSEVQLVESGG GLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVA RIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSG GGSGGGGSGTQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHN HYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHE ALHNHYTQKSLSLSPGK
MA 86-A4-N-F5 scFab x I2C x scFc		
450	VH-CH1	QVQLVESGGGVVQPGRLRLSCAASGFTFSTYGMHWVRQAP GKGLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSC
451	VL-CL	DIQMTQSPSSLSASVGDRVITICRASQGISNYLAWYQQKPGKV PKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDVATYY CQKYNAPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
452	scFab	QVQLVESGGGVVQPGRLRLSCAASGFTFSTYGMHWVRQAP GKGLEWVAVISYDAETVKYAESVKGRFTISRDNKNTLYLQM NSLRAEDTAVYYCARGQLLTGYWGQGLTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV

[illegible]

		GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
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 KCLEWVS YISKSSYTVTYADAVKGRFTISRDN AKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLVTVSS
462	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVLVYDDADRP SGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDASAGYGVVFGCGTKLTVL
463	SCFV	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVS YISKSSYTVTYADAVKGRFTISRDN AKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLVTVSSGGGSGG GGSGGGSSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHW YQQKPGQAPVLVYDDADRP SGIPERFSGSNSGNTATLTISR V EAGDEADYYCQVWDASAGYGVVFGCGTKLTVL
464	BISPECIFIC MOL.	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVS YISKSSYTVTYADAVKGRFTISRDN AKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLVTVSSGGGSGG GGSGGGSSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHW YQQKPGQAPVLVYDDADRP SGIPERFSGSNSGNTATLTISR V EAGDEADYYCQVWDASAGYGVVFGCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVS SGGGSGGGSGGGGSQT VVTQEP SLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
465	BiTE HLE	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KCLEWVS YISKSSYTVTYADAVKGRFTISRDN AKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLVTVSSGGGSGG GGSGGGSSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHW YQQKPGQAPVLVYDDADRP SGIPERFSGSNSGNTATLTISR V EAGDEADYYCQVWDASAGYGVVFGCGTKLTVLSGGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVS SGGGSGGGSGGGGSQT VVTQEP SLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR

		CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK MA 88-B3-F9 scFab x I2C x scFc
466	VH-CH1	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYSISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
467	VL-CL	SYVLTQPPSVSVAPGQATARITCGGNIGSKSVHWYQQKPGQAPVLVYDDADRP SGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSSPVKAGVETTTPSKQSN NKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
468	scFab	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYSISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQATARITCGGNIGSKSVHWYQQKPGQAPVLVYDDADRP SGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSSPVKAGVETTTPSKQSN NKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
469	scFab-BISPECIFIC MOL.	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYSISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQATARITCGGNIGSKSVHWYQQKPGQAPVLVYDDADRP SGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSSPVKAGVETTTPSKQSN NKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSGOTVY

		TQEPLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
470	scFab-BiTE HLE	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPG KGLEWVSYISKSSYTVTYADAVKGRFTISRDNKNSLYLQMN SLRAEDTAVYYCATYNYGHFDYWGQGLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVH WYQQKPGQAPVLVYDDADRPSGIPERFSGNSGNTATLTISR VEAGDEADYYCQVWDASAGYGVVFGGGTKLTVLGQPKAAP SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHE GSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLVTVSSGGGSGGGGSGGGGSGQTVV TQEPLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLGGGGDKHTCPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKHTCPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
MA SG-F28 CC scFv x I2C x scFc		
471	HCDR1	SNPYYWS
472	HCDR2	YISYSGITNYPNPSLKS
473	HCDR3	EKMWFGVLNYYYGMDV
474	LCDR1	RSSQSLLHRSGYNYLD
475	LCDR2	LGSNRAS
476	LCDR3	MQALQTPWT
477	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTITVTS S
478	VL	DIVMTQTPLSLPVTGPGEPAISCRSSQSLLHRSGYNYLDWYLQ KPGQSPQLLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAGD VGYYCMQALQTPWTFGCGTKVEIK
479	SCFV	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTMSVDTSKNQFSLKLTS

		LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SGGGSGGGSGGGSDIVMTQTPLSLPVTGPASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGCGTKVEIK
480	BISPECIFIC MOL.	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SGGGSGGGSGGGSDIVMTQTPLSLPVTGPASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGCGTKVEIK SGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGGTV TLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGT PARFSGSLGGAALTLGVQPEDEAEYYCVLWYSNRWVFG GGTKLTVL
481	BiTE HLE	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SGGGSGGGSGGGSDIVMTQTPLSLPVTGPASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGCGTKVEIK SGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDD SKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGGTV TLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGT PARFSGSLGGAALTLGVQPEDEAEYYCVLWYSNRWVFG GGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGSGGG GSGGGSGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
MA SG-F28 scFab x I2C x scFc		
482	VH-CH1	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKCLEWIGYISYSGITNYPNPSLKSRTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGVLNYYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSC
483	VL-CL	DIVMTQTPLSLPVTGPASISCRSSQSLLHRSGYNYLDWYLQ KPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAGD

		VGYYCMQALQTPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC
484	scFab	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKGLEWIGYISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGLNYYYGMDVWGQGTITVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWN SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC
485	scFab- BISPECIFIC MOL.	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKGLEWIGYISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGLNYYYGMDVWGQGTITVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWN SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQ PGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFNGSYISYWAYWGQGTITVTVSSGGGSGGGGSG GGGSGTQVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWV QQKPGQAPRGLIGGKFLAPGTPARFSGSLLGKAAALTLGSGVQ PEDEAEYYCVLWYSNRWVFGGGTKLTVL
486	scFab-BiTE HLE	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHP GKGLEWIGYISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTS LTAADTAVYYCAREKMWFGLNYYYGMDVWGQGTITVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWN SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSDIVMTQTPLSLPVTGPGEASISCRSSQS LLHRSGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS GSGTDFTLKISRVEAGDVGYYCMQALQTPWTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGECSSGGGSEVQLVESGGGLVQ PGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFNGSYISYWAYWGQGTITVTVSSGGGSGGGGSG GGGSGTQVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWV

		QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKHTCPCPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQK SLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKT HTCPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSTREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN 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 KCLEWVSAISGSGGGTYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSS
494	VL	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQA PVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY YCQVWDYSGQRQVFGCGTKLTVL
495	SCFV	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSGQRQVFGCGTKLTVL
496	BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH WYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTIS RVEAGDEADYYCQVWDYSGQRQVFGCGTKLTVLSSGGGGSE VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
497	BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPG KCLEWVSAISGSGGGTYAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSG GGGSGGGGSSYVLTQPPSVSVAPGQTARITCGNNIGSKSVH

		WYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGKLTTLVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKLTTLVGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
MA 03-G10 AS scFab x I2C x scFc		
498	VH-CH1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTYAAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
499	VL	SYVLTQPPSVSVAPGQTARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGKLTTLV
500	scFab	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTYAAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGKLTTLV
501	scFab-BISPECIFIC MOL.	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTYAAASVKGRFTISRDN SKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGGGSSYVLTQPPSVSVAPGQTARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGKLTTLVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ

		MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSTLVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
502	scFab-BiTE HLE	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPG KGLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMS SLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS VHTFPAVLQSSGLYSLSSVTVPSSTLTQTYICNVNHPKPSNT KVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSV HWYQQKPGQAPVMVVDNDNRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVLSGGGGSE VQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWSVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGGSGGGGSGGGGSGTQVVTQEPSTLVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSGFFLYSKLTVDKSRWQQGN 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 GKCLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSS
510	VL	DIQMTQSPSSLSASVGDRTITCRISQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQTYSMPFTFGCGTKVEIK
511	SCFV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTITV VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRT

		SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVEIK
512	BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTIVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VL
513	BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKCLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSGGGSGGGGSGGGGSDIQTQSPSSLSASVGDRVTITCRT SQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQTYSMPFTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTIVT VSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSG SLLGGKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLT VLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK
MA 10-B5 scFab x I2C x scFc		
514	VH-CH1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC
515	VL-CL	DIQTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGRA PKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQTYSMPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV

		VCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY SLSSLTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
516	scFab	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSLTLTLKADYEKHKVYAC EVTHQGLSSPVTKSFNREGC
517	scFab- BISPECIFIC MOL.	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSLTLTLKADYEKHKVYAC EVTHQGLSSPVTKSFNREGCSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
518	scFab-BiTE HLE	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAP GKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFL QMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITC RTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSMPTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSLTLTLKADYEKHKVYAC EVTHQGLSSPVTKSFNREGCSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA

		PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK
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	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSS
526	VL	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQQYGSSPITFGCGTKLEIK
527	SCFV	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSGGGGSGGGSGGG GSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGCGTKLEIK
528	BISPECIFIC MOL.	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSGGGGSGGGSGGG GSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGG GSQTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
529	BiTE HLE	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK CLEWIGRISSSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSGGGGSGGGSGGG GSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPG

		GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGG GSQTVVTQEPLSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK
CD20 29-F5 CC scFv x I2C x scFc		
530	HCDR1	GYWWS
531	HCDR2	EINHRGSTNYPNPSLKS
532	HCDR3	GYSSSWYTGYYVFDY
533	LCDR1	TGTSSDVFGYDYVS
534	LCDR2	DVSNRPS
535	LCDR3	SSYKSSSTVV
536	VH	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYYVFDYWGQGLTVTVSS
537	VL	QSALTQPASVSGSPGQSITISCTGTSSDVFGYDYVSWYQQHPG KAPKLMYDVSNRPSGVSNRFSGSKSGNAASLTISGLQAEDEA DYCYSSYKSSSTVVFGCGTKLTVL
538	SCFV	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYYVFDYWGQGLTVTVSSGGG GSGGGSGGGGQSALTQPASVSGSPGQSITISCTGTSSDVFGY DYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNAAS LTISGLQAEDEADYCYSSYKSSSTVVFGCGTKLTVL
539	BISPECIFIC MOL.	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKSRTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTGYYVFDYWGQGLTVTVSSGGG GSGGGSGGGGQSALTQPASVSGSPGQSITISCTGTSSDVFGY DYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNAAS LTISGLQAEDEADYCYSSYKSSSTVVFGCGTKLTVLSSGGGG EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTV SSGGGGSGGGSGGGGSQTVVTQEPLSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

540	BiTE HLE	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP GKCLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSGGG GSGGGGSGGGGQSALTQPASVSGSPGQSITISCTGTSSDVFGY DYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNAA SLTISGLQAEDEADYYCSSYKSSSTVVFSGCTKLTVLSSGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTV SSGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCSST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN 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 KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQTVVTQEPSTLVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
551	BiTE HLE	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAP GQCLEWMGWISAYSIGNAIYAQKLQGRVTMTRDTSTSTAYME LRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGLTVTVSSG GGSGGGSGGGSGGGSEIVLTQSPATLSVSPGERATLSCRASQSV SSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFT LTISSLQSEDFAVYYCQQYHSWPLLTFGCGTKVEIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGSGGGGSQTVVTQEPSTLVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGSGGGSGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
CD20 99-E5 CC scFv x 12C x scFc		
552	HCDR1	SYWMH
553	HCDR2	YITPSTGYTEYNQKFKG
554	HCDR3	VHDYDRAEMEY
555	LCDR1	KASQDINKYIA
556	LCDR2	YTSTLQP
557	LCDR3	LQYASYPFT
558	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAEMEYWGQGTITVTVSS
559	VL	DIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPGKG PKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDATYYC LQYASYPFTFGCGTRLEIK
560	SCFV	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAEMEYWGQGTITVTVSSGGGG SGGGSGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDATYYCLQYASYPFTFGCGTRLEIK

561	BISPECIFIC MOL.	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED AVYYCARVHDYDRAMEYWGQGTITVTVSSGGGG SGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVE SGGGLVQP GGS LKLSAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGG GSGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTLTCGSSTGAVT SGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
562	BiTE HLE	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED AVYYCARVHDYDRAMEYWGQGTITVTVSSGGGG SGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVE SGGGLVQP GGS LKLSAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGG GSGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTLTCGSSTGAVT SGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSGSEFLYSLKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGSEFLYSLKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
CD20 99-E5 scFab x I2C x scFc		
563	VH-CH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED AVYYCARVHDYDRAMEYWGQGTITVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
564	VL-CL	DIQMTQSPSSLSASVGDRVITITCKASQDINKYIAWYQQKPGKG PKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISLQPEDIAATYYC LQYASYPFTFGQGRLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKSTY SLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
565	scFab	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME

		LSSLTSED TAVYYC ARVHDY DRAMEYWGQGT TVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDATYYCLQYASYPFTFGQGRLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
566	scFab- BISPECIFIC MOL.	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYC ARVHDY DRAMEYWGQGT TVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDATYYCLQYASYPFTFGQGRLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVT QEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
567	scFab-BiTE HLE	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYC ARVHDY DRAMEYWGQGT TVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISSLQPEDATYYCLQYASYPFTFGQGRLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSEVQLVESGGGLVQPGGSLKLSCA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVT QEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPR GLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY

		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKG GGSGGGSGGGSGGGSGGGSGGGSGGGSDKTHTCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK
CD20 29-F5 scFab x I2C x scFc		
568	VH-CH1	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSC
569	VL-CL	QSALTQPASVSGSPGQSITISCTGTSSDVFGYDYVSWYQQHPG KAPKLMYDVSNRPSGVSNRFGSGKSGNAASLTISGLQAEDEA DYCYSSYKSSSTVVFSGGTCLTVLGQPKAAPSVTLFPPSSEEL QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS
570	scFab	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSGSALTQPASVSGSPGQSITISCTGTSSDVFG YDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSGKSGNA ASLTISGLQAEDEADYCYSSYKSSSTVVFSGGTCLTVLGQPKA APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP VKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
571	scFab- BISPECIFIC MOL.	QVQLQQWGAGLLKPSETLSLTC AVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYPNPSLKSRVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSGGGSGGGSGSALTQPASVSGSPGQSITISCTGTSSDVFG YDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSGKSGNA ASLTISGLQAEDEADYCYSSYKSSSTVVFSGGTCLTVLGQPKA APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP VKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGQT VVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQ

		APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
572	scFab-BiTE HLE	QVQLQQWGAGLLKPSETLSLTCVYGGSFSGYYWSWIRQPP GKGLEWIGEINHRGSTNYNPSLKSRVTISGDTSKNQFSLKLSSV NAADTAVYYCARGYSSSWYTG YVFDYWGQGLTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGQSALTQPASVSGSPGQSITISCTGTSSDVFG YDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSKSGNA ASLTISGLQAEDEADYYCSSYKSSSTVVFGGGKTLTVLGQPKA APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVT HEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGT VVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG KGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
CD22 11-C3 scFab x 12C x scFc		
573	VH-CH1	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSC
574	VL-CL	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY CQYQGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
575	scFab	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSGDVDYNPSLKSRVTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG

		GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
576	scFab- BISPECIFIC MOL.	QVQLQESGPGLVKPSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVVDYNPSLKSRTISVDTSKNQFSLKSSVTA ADTAVYYCAREGGFYWGQGTLLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW GQGTLLTVSSGGGSGGGGSGGGGSGTQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVL
577	scFab-BiTE HLE	QVQLQESGPGLVKPSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVVDYNPSLKSRTISVDTSKNQFSLKSSVTA ADTAVYYCAREGGFYWGQGTLLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW GQGTLLTVSSGGGSGGGGSGGGGSGTQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPG TPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGG GGSGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA

		LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVD KSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
578	CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAMEYWGQGT VTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSGVQLVQ SGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEW MGWISAYSIGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSD DTAVYYCARDPDYYGSGSYSDYWGQGT LTVTVSSGGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQS EDFAVYYCQYHSWPLLTFGCGTKVEIK
579	CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv x I2C	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAMEYWGQGT VTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSGVQLVQ SGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEW MGWISAYSIGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSD DTAVYYCARDPDYYGSGSYSDYWGQGT LTVTVSSGGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQS EDFAVYYCQYHSWPLLTFGCGTKVEIKSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWV ARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSSGGGGSG GGSGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
580	CD20 99-E5 CC scFv x CD22 28-B7 N655 CC scFv x I2C x scFc	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQCLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAMEYWGQGT VTVSSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCKASQDINKY IAWYQQKPGKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTTIS SLQPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSGVQLVQ SGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEW MGWISAYSIGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSD DTAVYYCARDPDYYGSGSYSDYWGQGT LTVTVSSGGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQS EDFAVYYCQYHSWPLLTFGCGTKVEIKSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWV ARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSSGGGGSG GGSGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL

		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 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 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 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 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 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 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 G 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 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 SSSWYTGYVFDYWGQGLTVTVSSGGGSGGGGSGGGGSQSA LTQPASVSGSPGQSITISCTGTSSDVFYDYVSWYQQHPGKAP KLMIYDVSNRPSGVSNRFSGSKSGNAASLTISGLQAEDEADYY CSSYKSSSTVVFSGCTKLTVLSSGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNVWQQ KPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLGSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSL SLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH YTQKSLSLSPGK
584	CD20 99-E5 scFab x CD22 28-B7 N655 CC scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAMEYWGQGTITVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISLQPEDIAITYYCLQYASYPFTFGQGRLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGECSGGGGSQVQLVQSGAEVKKPGASVKVSCK ASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNAIYAQKL QGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGS GSYSDYWGQGLTVTVSSGGGSGGGGSGGGGSEIVLTQSPAT LSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASS RATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQYHSPWLL TFGCGTKVEIK
585	CD20 99-E5 scFab x CD22 28-B7 N655 CC scFv x 12C	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSED TAVYYCARVHDYDRAMEYWGQGTITVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISLQPEDIAITYYCLQYASYPFTFGQGRLEIKRTVAAPSVFIF

		PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLKADYEKHKVYACEVTHQGL SSPVTKSFNREGCSGGGGSQVQLVQSGAEVKKPGASVKVSCK ASGYTFTSYGISWVRQAPGQCLEWMGWISAYSGNAIYAQKL QGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGS GSYSDYWGGQTLVTVSSGGGSGGGGSGGGGSEIVLTQSPAT LSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASS RATGIPARFSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLL TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQTLVTVSSGGGSGGGGSGGGGSGTQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
586	CD20 99-E5 scFab x CD22 28-B7 N655 CC scFv x I2C x scFc	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQA PGQGLEWIGYITPSTGYTEYNQKFKGRVTMTRDKSTSTVYME LSSLTSEDYAVYYCARVHDYDRAMEYWGQTTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGSGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDIN KYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTF TISLQPEDATYYCLQYASYPFTFGQGRLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSSSTLTLKADYEKHKVYACEVTHQGL SSPVTKSFNREGCSGGGGSQVQLVQSGAEVKKPGASVKVSCK ASGYTFTSYGISWVRQAPGQCLEWMGWISAYSGNAIYAQKL QGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGS GSYSDYWGGQTLVTVSSGGGSGGGGSGGGGSEIVLTQSPAT LSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASS RATGIPARFSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLL TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQTLVTVSSGGGSGGGGSGGGGSGTQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGG GSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF

		LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
587	CD22 11-C3 scFab x CD20 29-F5 scFab	QVQLQESGPGLVKPSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECGGGSGSQVQLQWAGLLKPSETLSLTCAVYGGSFSGYY WSWIRQPPGKLEWIGEINHRGSTNYPNPSLKSRTISGDTSKN QFSLKLSSVNAADTAVYYCARGYSSSWYTG YVFDYWGQGLT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSGGGGSGSALTQPASVSGSPGQSITISC TGTSSDVFGYDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRF SGSKSGNAASLTISGLQAEDEADYYCSSYKSSSTTVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVAPTECS
588	CD22 11-C3 scFab x CD20 29-F5 scFab x I2C	QVQLQESGPGLVKPSETLSLTCTVSGGSISSFYWSWIRQPPGK GLEWIGRISSSGDVDYNPSLKSRTISVDTSKNQFSLKLSSVTA ADTAVYYCAREGGFYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECGGGSGSQVQLQWAGLLKPSETLSLTCAVYGGSFSGYY WSWIRQPPGKLEWIGEINHRGSTNYPNPSLKSRTISGDTSKN QFSLKLSSVNAADTAVYYCARGYSSSWYTG YVFDYWGQGLT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGGGSGGGGSGSALTQPASVSGSPGQSITISC TGTSSDVFGYDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRF SGSKSGNAASLTISGLQAEDEADYYCSSYKSSSTTVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVAPTECS SSGGGGSEVQLVESGGGLV QPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRS KYNKYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA

		VYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGSGGGGS GGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVL
589	CD22 11-C3 scFab x CD20 29-F5 scFab x I2C x scFc	QVQLQESGPGLVKPSSETLSLTCTVSGGSISFYWSWIRQPPGK GLEWIGRISSGDVDYNPSLKSRTVISVDTSKNQFSLKSSVTA ADTAVYYCAREGGFYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGG GGSEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSDTFTLTISRLEPEDFA VYYCQQYGSSPITFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG ECSGGGGSQVQLQWAGLLKPSETLSLTCAVYGGSFSGYY WSWIRQPPGKLEWIGGINHRGSTNYPNPSLKSRTVISGDTSKN QFSLKSSVNAADTAVYYCARGYSSSWYTG YVFDYWGQGLV TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCGGGSGGGSGGGSGGGSGGG SGGGSGGGSGGGSGGGSGGGSGSALTQPAVSFSGSPGQSITISC TGTSSDVFGYDYVSWYQQHPGKAPKLMYDVSNRPSGVSNRF SGSKSGNAASLTISGLQAEDEADYYCSSYKSSSTVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVAPTECSSGGGGSEVQLVESGGGLV QPGGSLKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRS KYNKYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGSGGGGS GGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGSDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK

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

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BLANK UPON FILING

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

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

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ACTACACCCAGAAGTCCCTGTCTCTGTCCCCTGGAGGCGGAGGACAAGGCGGAGGT
GGTCAAGGTGGTGGTGGCCAAGGCGGAGGCGGACAAGGCGGCGGAGGACAAGGTG
GCGGTGGACAGTGTCTCCATGTCCAGCACCTGAGCTTCTCGGAGGCCCTTCTGTGTT
TCTGTTCCACCTAAGCCAAAGGATACACTCATGATCAGCCGCACACCTGAAGTCAC
ATGTGTGCTGCTGGATGTCTCTCATGAAGAACCAGAAGTCAAGTTTAATTGGTATGT
CGATGGCGTCGAGGTCCACAATGCTAAGACCAAGCCTTGTGAAGAACAATATGGCA
GCACCTATCGCTGTGTGTCTGTCTGACCGTCTGCATCAAGACTGGCTCAATGGGA
AAGAATACAAATGCAAAGTCTCTAACAAGCTCTGCCCGCACCAATCGAGAAAACC
ATCAGCAAGGCTAAAGGACAGCCTCGCGAGCCTCAAGTGTATACCCTGCCACCTTCT
CGCGAGGAAATGACAAAAAATCAAGTCTCCCTCACCTGTCTCGTGAAGGGATTCTAT
CCCAGCGACATTGCCGTCGAGTGGGAGTCTAATGGCCAGCCTGAAAACAATTATAA
GACAACCCACCTGTCTGGACAGCGACGGCTCATTTTTTCTCTACTCTAAACTCACC
GTGGATAAGAGCCGGTGGCAACAGGGAAATGTGTTTCAGCTGTAGCGTGATGCATGA
AGCTCTCCACAACCATTATACACAGAAGAGTCTGAGCCTGTCTCTGGCAAATGA

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

GAGGTGCAGCTGGTGAATCTGGCGGAGGACTTGTGAAGCCTGGCGGCTCTCTGAG
ACTGTCTTGTGCCGCTTCTGGCTTCACCTTCAGCAACGCCAGAATGGGCTGGGTCCG
ACAGGCTCCTGGAAAAGGACTGGAATGGGTGGACGGATCAAGTCCAAGACCGAAG
GCGGCACCAGAGACTACGCCGCTCCTGTGAAGGGCAGATTACCATCTCTCGGGACG
ACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGAAAACCGAGGACACCGCC
GTGTACTACTGCACCTCTTACTCTGGCGTGTGGGGCCAGGGCACAATGGTCACAGTT
TCTTCCGCTCCACCAAGGGACCCAGCGTTTTCCCTCTGGCTCCATCCTCCAAGTCTA
CCTCTGGCGGAACAGCTGCTCTGGGCTGCCTGGTCAAGGACTACTTTCCTGAGCCTG
TGACCGTGTCTCGAACTCTGGCGCTCTGACATCTGGCGTGCACACCTTTCAGCTGT
GCTGCAGTCTCCGCGCTGTACTCTGTCTGTCTGTCTGTCGTGACCGTGCCTTCCAGCTCT
CTGGGAACCCAGACCTACATCTGCAATGTGAACCAAGCCTTCCAACCAAGGTG
GACAAGAAGGTGGAACCCAAGTCTTGTGGCGGAGGCGGACAAGGTGGTGGTGGTCA
AGGTGGCGGAGGACAAGGCGGTGGCGGCCAAGGCGGAGGTGGACAAGGCGGCGGA
GGCCAAGGTGGCGGCGGTCAAGGCGGCGGTGGTCAAGAAATTGTGATGACCCAGTC
TCCTGACAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCATCAACTGCAAGTCCAG
CCAGTCCGTGCTGTACTCCTCCAACAACAAGAACTACCTGGCCTGGTATCACCAGAA
GCCAGGCCAGTCTCCAAAGCTGCTGATCTCCTGGGCCTCTACCAGAGAATCCGGCGT
GCCCGACAGATTTTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCAATTCC
CTGCAGGCCGAGGATGTGGCTGTGTACTATTGCCAGCAGTACTACAGCATCCCCATC
ACCTTCGGAGGTGGCACCAAGGTCGAGATCAAGAGAACCGTGGCCGCTCCTTCCGTG
TTCATCTTCCCACCTTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCTGTCTGTGTC
TGCTGAACAACCTTCTACCCTCGGGAAGCCAAGGTGCAGTGGAAAGTGGATAACGCC
CTGCAGTCCGGCAACTCCCAAGAGTCTGTGACCGAGCAGGACTCCAAGGACAGCAC
CTACAGCCTGTCTCCACACTGACCCTGTCCAAGGCCGACTACGAGAAGCACAAAGGT
GTACCGCTGCGAAGTGACCCATCAGGGCCTGTCTAGCCCTGTGACCAAGTCTTCAA
CCGGGGCGAGTGTTCGGGAGGTGGAGGGCAGGAAGTGCAGCTGGTTGAATCTGGCG
GCGGATTGGTTCAGCCTGGCGGATCTCTGAAGCTGTCTTGTGCCGCTCTGGCTTCAC
CTTCAACAAATACGCCATCAACTGGGTCCGACAGGCCCTGGCAAAGGACTGGAAT
GGGTGCCCCGGATCAGATCCAAGTACAACAACACTACGCTACCTACTACGCCGACGCCG

TGAAGGACCGGTTACCATCTCCAGAGATGACTCCAAGAACACCGTGTACCTGCAGA
TGAACAACCTCAAGACCGAGGACACCGCCGTGTACTACTGTGCCAGAGCCGGCAAC
TTCGGCTCCTCCTACATCAGCTACTGGGCCTATTGGGGCCAGGGCACACTGGTCACA
GTTAGTTCAGGTGGCGGTGGACAGGGCGGCGAGGTCAGGGTGGCGGAGGCCAGCA
AACAGTGGTCACCCAAGAGCCTAGCCTGACCGTTTCTCCTGGCGGCACCGTGACCAT
CACCTGTGGATCTTCTACCGGCGCTGTGACCTCCGGCAACTACCCTAATTGGGTGCA
GAAGAAGCCCCGGCCAGGCTCCTAGAGGACTGATCGGAGGCACCAAGTTTCTGGCTC
CCGGCACTCCTGCCAGATTCTCCGGTTCTCTGTCTGGCGGAAAGGCCGCTCTGACATT
GTCTGGCGTGCAGCCTGAGGATGAGGCTGAGTACTATTGCGTGCTGTGGTACTCCAA
CAGATGGGTGTTCCGGCTCCGGCACCAAGCTGACAGTTCTCGGCGGAGGTGGATGCC
TCCTTGCTCCTGCTCCTGAATTGCTCGGCGGACCCTCCGTGTTCTGTTTCTCCAAAG
CCTAAGGACACCCTGTACATCACCCGCGAGCCTGAAGTGACCTGCGTGGTGGTGGAT
GTGTCCCACGAGGAACCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGT
GCACAACGCCAAGACAAAAGCCCTGCGAGGAACAGTACGGCTCCACCTACAGATGCG
TGTCCGTGCTGACAGTGTGACACAGGATTGGCTGAACGGCAAAGAGTACAAGTGC
AAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAAAAGACCATCTCCAAGGCCAAG
GGCCAGCCTAGAGAGCCCCAGGTTTACACCCTGCCTCCAAGCAGAGAAGAGATGAC
CAAGAACCAGGTGTCCCTGACCTGCCTGGTCAAGGGCTTCTACCCTTCCGATATCGC
CGTGGAATGGGAGAGCAATGGACAGCCCGAGAACAATAAGACCACACCTCCTG
TGCTGGACTCCGACGGCTCATTCTTCTGTACTCCAAGCTGACCGTGGACAAGTCCA
GATGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGAGGCCCTGCACAATC
ACTACACCCAGAAGTCCCTGTCTCTGTCCCCTGGAGGCGGAGGACAAGGCGGAGGT
GGTCAAGGTGGTGGTGGCCAAGGCGGAGGCGGACAAGGCGGCGGAGGACAAGGTG
GCGGTGGACAGTGTCTCCATGTCCAGCACCTGAGCTTCTCGGAGGCCCTTCTGTGTT
TCTGTTCCCACCTAAGCCAAAGGATACACTCTACATCACCCGCGAGCCTGAAGTCAC
ATGTGTCGTCGTGGATGTCTCTCATGAAGAACCAGAAGTCAAGTTTAATTGGTATGT
CGATGGCGTCGAGGTCCACAATGCTAAGACCAAGCCTTGTGAAGAACAATATGGCA
GCACCTATCGTGTGTGTCTGTCTGACCGTCTGCATCAAGACTGGCTCAATGGGA
AAGAATACAAATGCAAAGTCTTAACAAAGCTCTGCCCCGACCAATCGAGAAAACC
ATCAGCAAGGCTAAAGGACAGCCTCGCGAGCCTCAAGTGTATACCCTGCCACCTTCT
CGCGAGGAAATGACAAAAAATCAAGTCTCCCTCACCTGTCTCGTGAAGGGATTCTAT
CCCAGCGACATTGCCGTCGAGTGGGAGTCTAATGGCCAGCCTGAAAACAAATTATAA
GACAACCCACCTGTCTGACAGCGACGGCTCATTTTTTCTCTACTCTAAACTCACC
GTGGATAAGAGCCGGTGGCAACAGGGAAATGTGTTTCAAGCTGTAGCGTGATGCATGA
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	QVWDSSSDHV
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	QAWDSSNVV
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	VYYGSGIYYKNNYYYGMDV
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	VYYGSGSYKKNRYYYGMDV
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
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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	VYYGSGIYYKNRYYYGMDV
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	VYYGSGIYYKNNYYYGMDV
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	VYYGSGIYYKNNYYYGMDV
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 HulgG1z mAb LC huCCR8 LV lv_cdr1	GGHNIGSKGVH
812	Hu anti-huCCR8 LIBC315615-1 HulgG1z mAb LC huCCR8 LV lv_cdr2	RNSNRPS
813	Hu anti-huCCR8 LIBC315615-1 HulgG1z mAb LC huCCR8 LV lv_cdr3	QVWDISTVV
814	Hu anti-huCCR8 LIBC315615-1 HulgG1z mAb HC huCCR8 HV hv_cdr1	NCGMH
815	Hu anti-huCCR8 LIBC315615-1 HulgG1z mAb HC huCCR8 HV hv_cdr2	VISYDGGNKYHADSVKG
816	Hu anti-huCCR8 LIBC315615-1 HulgG1z mAb HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
817	Hu anti-huCCR8 LIBC317152-1 HulgG1z mAb LC huCCR8 LV lv_cdr1	GGHNIGSKGVH
818	Hu anti-huCCR8 LIBC317152-1 HulgG1z mAb LC huCCR8 LV lv_cdr2	RNSNRPS
819	Hu anti-huCCR8 LIBC317152-1 HulgG1z mAb LC huCCR8 LV lv_cdr3	QVWDSSTVV
820	Hu anti-huCCR8 LIBC317152-1 HulgG1z mAb HC huCCR8 HV hv_cdr1	NCGMH
821	Hu anti-huCCR8 LIBC317152-1 HulgG1z mAb HC huCCR8 HV hv_cdr2	VISYDGGNKYYADSVKG
822	Hu anti-huCCR8 LIBC317152-1 HulgG1z mAb HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
823	Hu anti-huCCR8 LIBC317471-1 HulgG1z mAb LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
824	Hu anti-huCCR8 LIBC317471-1 HulgG1z mAb LC huCCR8 LV lv_cdr2	RDSNRPS
825	Hu anti-huCCR8 LIBC317471-1 HulgG1z mAb LC huCCR8 LV lv_cdr3	QVWDSNTVV
826	Hu anti-huCCR8 LIBC317471-1 HulgG1z mAb HC huCCR8 HV hv_cdr1	NNGMH
827	Hu anti-huCCR8 LIBC317471-1 HulgG1z mAb HC huCCR8 HV hv_cdr2	VISNDGSNKYYADSVRG
828	Hu anti-huCCR8 LIBC317471-1 HulgG1z mAb HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
829	Hu anti-huCCR8 LIBC317977-1 HulgG1z mAb LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
830	Hu anti-huCCR8 LIBC317977-1 HulgG1z mAb LC huCCR8 LV lv_cdr2	RNSNRPS
831	Hu anti-huCCR8 LIBC317977-1 HulgG1z mAb LC huCCR8 LV lv_cdr3	QVWDSSTVV
832	Hu anti-huCCR8 LIBC317977-1 HulgG1z mAb HC huCCR8 HV hv_cdr1	TYGMH
833	Hu anti-huCCR8 LIBC317977-1 HulgG1z 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	VYYGSGNYYKNNNYYYGMDV
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 Hulg1z mAb HC huCCR8 HV hv cdr2	VISYDGGNKYYADSVKG
858	Hu anti-huCCR8 LIBC320384-1 Hulg1z mAb HC huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
859	Hu anti-huCCR8 LIBC320689-1 Hulg1z mAb LC huCCR8 LV lv cdr1	GGNNIGSKNVH
860	Hu anti-huCCR8 LIBC320689-1 Hulg1z mAb LC huCCR8 LV lv cdr2	RSSNRPS
861	Hu anti-huCCR8 LIBC320689-1 Hulg1z mAb LC huCCR8 LV lv cdr3	QIWDSSTVV
862	Hu anti-huCCR8 LIBC320689-1 Hulg1z mAb HC huCCR8 HV hv cdr1	SYGMH
863	Hu anti-huCCR8 LIBC320689-1 Hulg1z mAb HC huCCR8 HV hv cdr2	VISFDGNNKYYADSVKG
864	Hu anti-huCCR8 LIBC320689-1 Hulg1z mAb HC huCCR8 HV hv cdr3	VYYGSGSYYKNRYYYGMDV
865	Hu anti-huCCR8 LIBC321408-1 Hulg1z mAb LC huCCR8 LV lv cdr1	GGNNIGSKNVH
866	Hu anti-huCCR8 LIBC321408-1 Hulg1z mAb LC huCCR8 LV lv cdr2	RDSNRPS
867	Hu anti-huCCR8 LIBC321408-1 Hulg1z mAb LC huCCR8 LV lv cdr3	QVWDSSTVV
868	Hu anti-huCCR8 LIBC321408-1 Hulg1z mAb HC huCCR8 HV hv cdr1	SNGMH
869	Hu anti-huCCR8 LIBC321408-1 Hulg1z mAb HC huCCR8 HV hv cdr2	VISNDGSNKYYGDSVKG
870	Hu anti-huCCR8 LIBC321408-1 Hulg1z mAb HC huCCR8 HV hv cdr3	VYYGSGIYYRNNRYYYGMDV
871	Hu anti-huCCR8 LIBC321824-1 Hulg1z mAb LC huCCR8 LV lv cdr1	GGNNIGSKNVH
872	Hu anti-huCCR8 LIBC321824-1 Hulg1z mAb LC huCCR8 LV lv cdr2	RNTNRPS
873	Hu anti-huCCR8 LIBC321824-1 Hulg1z mAb LC huCCR8 LV lv cdr3	QVWDSSTVV
874	Hu anti-huCCR8 LIBC321824-1 Hulg1z mAb HC huCCR8 HV hv cdr1	GYGMH
875	Hu anti-huCCR8 LIBC321824-1 Hulg1z mAb HC huCCR8 HV hv cdr2	VISYDGSNKYYADSVKG
876	Hu anti-huCCR8 LIBC321824-1 Hulg1z mAb HC huCCR8 HV hv cdr3	VYYGSGIYYKNRYYYGMDV
877	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb LC huCCR8 LV lv cdr1	GGNNIGSKNVH
878	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb LC huCCR8 LV lv cdr2	RNTNRPS
879	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb LC huCCR8 LV lv cdr3	QVWDSSTVV

SEQ ID NO:	Designation	Sequence
880	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb_HC huCCR8 HV hv_cdr1	GYGMH
881	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb_HC huCCR8 HV hv_cdr2	VISYDGSNKYYADSVKG
882	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKNRYYYGMDV
883	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGDKNVH
884	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_LC huCCR8 LV lv_cdr2	RNNVRPS
885	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
886	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_HC huCCR8 HV hv_cdr1	NFGMH
887	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_HC huCCR8 HV hv_cdr2	VISYDGGNKYYADSVKG
888	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGSYKKRYYYGMDV
889	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_LC huCCR8 LV lv_cdr1	GGNNIGSKNVH
890	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_LC huCCR8 LV lv_cdr2	RDSNRPS
891	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_LC huCCR8 LV lv_cdr3	QVWDSSTVV
892	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_HC huCCR8 HV hv_cdr1	SCGMH
893	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_HC huCCR8 HV hv_cdr2	VISYDGTNKYYADSVKG
894	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_HC huCCR8 HV hv_cdr3	VYYGSGIYYKKNRYYYGMDV
895	huCCR8_32360_hulg1z mAb_HC huCCR8 HV hv_cdr1	NARMG
896	huCCR8_32360_hulg1z mAb_HC huCCR8 HV hv_cdr2	RIKSKTEGGTRDYAAPVKG
897	huCCR8_32360_hulg1z mAb_HC huCCR8 HV hv_cdr3	YSGV
898	huCCR8_32360_hulg1z mAb_LC huCCR8 LV lv_cdr1	KSSQSVLYSSNNKNYLA
899	huCCR8_32360_hulg1z mAb_LC huCCR8 LV lv_cdr2	WASTRES
900	huCCR8_32360_hulg1z mAb_LC huCCR8 LV lv_cdr3	QQYYSIPIT
901	MPK20298-A4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKLEWVA VISNDGSNKYYADSVKGRFTISRDNS KNTLYLQMNSLRTEDTAVYYCAKV

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

SEQ ID NO:	Designation	Sequence
910	MPK20297-A4_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARITCGGHN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTQ LTVL
911	MPK20299-H8_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGSIYYKKRYYYGMDVWGQGT TVSS
912	MPK20299-H8_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKAGQAPVQVIYRNS NRPSGIPARFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTTVFGGGTK LTVL
913	MPK20300-C11_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKKNRYYYGMDVWGQGT TVTVSS
914	MPK20300-C11_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARIPCGGNNI GSKNVHWYQQKPGQAPVLVIYRDIN RPSGIPERFSGSNSGNTATLTISRAQA GDEADYYCQVWDSSTTVFGGGTKLT VL
915	MPK20298-B1_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGSIYYKKRYYYGMDVWGQGT TVSS
916	MPK20298-B1_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARLTCEGNN IGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRQ AGDEADYYCQAWDSSTTVFGGGTQ LTVL
917	MPK20297-E5_SCFV HV huCCR8	QVQLVESGGGLVKPGGSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT TVSS
918	MPK20297-E5_SCFV LV huCCR8	SYELTQPLSVSEALGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSNSGNAATLTISRVEA

SEQ ID NO:	Designation	Sequence
		GDEADYYCQVWDSSSDHVVFGGGTQLTVL
919	MPK20299-A3_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSS
920	MPK20299-A3_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRNSN RPSGIPERFSGSNSGNTATLTISGTQA MDEADYYCQAWDSSNVVFGGGTQLTVL
921	MPK20297-B4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGGIYYKNYYYGMDVWGQGT TVSS
922	MPK20297-B4_SCFV LV huCCR8	SYELTQPLSVSVALGQTARITCGGNN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPDRFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTQLTVL
923	MPK20298-F6_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGGIYYKNRYYYGMDVWGQGT TVSS
924	MPK20298-F6_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAQA GDEAEYYCQVWDSSTVVFGGGTELT VL
925	MPK20299-H3_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSS
926	MPK20299-H3_SCFV LV huCCR8	SYELTQPLSVSVALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLAIYRNS NRPSGIPERFTGSNSGNTATLTISRAQ AGDESDYYCQIWDSSTVVFGGGTKL TVL

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

SEQ ID NO:	Designation	Sequence
		YYGSGTYYYKNRYYYGMDVWGQGT TVTVSS
936	MPK20300-G5_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARITCGANN IGSKNVHWYQQKPGQPPVLVIYRDF NRPSGIPERFSASNSGNTATLTISRQ AGDEADYYCQVWDSSTGNVVFSGG TKLTVL
937	MPK20299-C3_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFIFSNYGFHWVRQTPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDNK NTLYLQMNSLRGEDITAVYYCARVY YGSGSYYYKNRYYYGMDVWGQGT TVTVSS
938	MPK20299-C3_SCFV LV huCCR8	SYELTQPPSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRQA GDEADYYCQVWDSSTVVFGGGTELT VL
939	MPK20299-B7_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNK KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSS
940	MPK20299-B7_SCFV LV huCCR8	SYELTQSSSVSVAPGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRVEA GDEADYYCQVWDSSTVAHVIFGGG TKLTVL
941	MPK20299-A5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNK KNTLYLQMNSLRGEDITAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
942	MPK20299-A5_SCFV LV huCCR8	SYELTQPPSGSV ALGQTARITCGGNN LGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRQ AGDEADYYCQVWDSSTVVFGGGTK LTVL
943	MPK20299-D1_SCFV HV huCCR8	QVQLVESGGGLVKPGGSLRLSCAAS GFTFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNK KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS

SEQ ID NO:	Designation	Sequence
944	MPK20299-D1_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARITCGGNRI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRQA GDEAEYYCQVWDSSTVVFGGGTKLT VL
945	MPK20299-C5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYKKNRYYYGMDVWGQGT TVTVSS
946	MPK20299-C5_SCFV LV huCCR8	SYELTQLPSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRQA AGDEADYYCQVWDSSTVVFGGGTE LTVL
947	MPK20299-B5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKNRYYYGMDVWGQGT TVSS
948	MPK20299-B5_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRQA AGDEADYYCQVWDSSTVVFGGGTQ LTVL
949	MPK20299-G9_SCFV HV huCCR8	QVQLVESGGDLVQPGRSLRLSCAAS GFTFSNNGMHWRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
950	MPK20299-G9_SCFV LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTLSRVQ AGDEADYYCQVWDSSTVVFGGGTK LTVL
951	MPK20299-G5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNNGMHWRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
952	MPK20299-G5_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARLTCEGNN IGSKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLAISRQA

SEQ ID NO:	Designation	Sequence
		AGDESDYYCQVWDSSAVVFGGGTK LTVL
953	MPK20298-C10_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHVVRQAPGKGLEWVA 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 YGSIGIYYKKRYYYGMDVWGQGT TVSS
956	MPK20298-B5_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGSQNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDSSAVVFGGGTQ LTVL
957	MPK20299-F2_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTLSSSGMHVVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVSS
958	MPK20299-F2_SCFV LV huCCR8	SYELTQPPSVSVALGQTARISCGGNNI GSKNVHWYQQKPGQAPVLVMIYRDS NRPSGIPERFSGSNSGNTATLTISGTQ AMDEADYYCQAWDSGTVVFGGGTK LTVL
959	MPK20298-D4_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSIGIYYKKRYYYGMDVWGQGT TVSS
960	MPK20298-D4_SCFV LV huCCR8	SYELTQPPSVSVALGQTARITCGGNN IGGKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDESDYYCQVWDSSSTVVFGGGTQ LTVL

SEQ ID NO:	Designation	Sequence
961	MPK20297-F5_SCFV HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNYYYYGMDVWGQGT TVTVSS
962	MPK20297-F5_SCFV LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVL
963	MPK20299-D9_SCFV HV huCCR8	QVQLVESGGGLVKPGGSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNYYYYGMDVWGQGT TVTVSS
964	MPK20299-D9_SCFV LV huCCR8	SYELTQPPSVSV ALGQTARISCGGNNI ESKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGTTATLTISRAQA GDEAEYYCQVWDSSTVVFGGGTQLT VL
965	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC HV huCCR8	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISR DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVTVSS
966	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC LV huCCR8	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNRNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSGTDF LTINSLQAEDVAVYYCQYYISIPITFG GGTKVEIKR
967	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYAASSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSS
968	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC LV huCCR8	SYELTQPPSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRAA NRPSGIPERFSGSNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFGGGTQ LTVLG
969	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_ M99E_W109F_S111A)_huIgG1z (mAb)_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYAGSNRYAASSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV

SEQ ID NO:	Designation	Sequence
		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 AGDEADYYCQVWDISTVVFGGGTEL TVLG
974	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSGMHWRQAPGKGLEWVA VISYDGGNKYHADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
975	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGKTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTE LTVLG
976	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSGMHWRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
977	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQKRPQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSNTVVFGGGTN LTVLG

SEQ ID NO:	Designation	Sequence
978	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYSCAKV YYGSGIYYKNYYYYGMDVWGQGT VTVSS
979	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKAGQAPVQVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLG
980	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAAS GFNFNTYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KSTLYLQMNSLRAEDTAVYYCARVY YGSGSYKKNYYYYGMDVWGQGT VTVSS
981	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGGKNVHWYQQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDESDYYCQVWDSSTVVFGGGTTL TVLG
982	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_HC HV huCCR8	QVQVVESGGGVVQPGRSLRLSCAAS GFTLSSYGFWVRQTPGKGLEWYAV ISYDGSNKYYADSVKGRFTISRDN NTLYLQMNSLRGEDTAVYYCARVY YSGGTYYKNRYYYGMDVWGQGT VTVSS
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 YYGSGNYYKNYYYYGMDVWGQGT TVTVSS
985	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCEGNNI GSQNVHWYQQKPGQAPVLV MYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDGSAVVFGGGTT LTVLG
986	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_HC HV huCCR8	QMQVVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWVRQAPGKGLEWVA VISHDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLGGEDTAVYYCAKV

SEQ ID NO:	Designation	Sequence
		YYGSGIYYKNRYYYGMDVWGQGT VIVSS
987	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTE LTVLG
988	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSDCGMHWRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQTDSLRTEDTAVYYCAKVY YSGIYYKNRYYYGMDVWGQGTIV TVSS
989	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTGRITCGGNN IGSKNVHWYQQKPGQAPVLVIYRSS NRPSGIPERFSGSNSGNTATLTISRAQ AGDESDYYCQIWDSSTVVFGGGTKL TVLG
990	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC HV huCCR8	QVQVVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISFDGNNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKNRYYYGMDVWGQGT TVTVST
991	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQRPGQAPVLVIYRDS NRPSGIPERLSSGSKAGNTATLTISRAH AGDEADYYCQVWDSSTVVFGGGTE LTVQG
992	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC HV huCCR8	QVQLVESGGGVVQPGRSLRLSCAVS GFTFSSNGMHWRQAPGKGLEWVA VISNDGSNKYYGDSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYRNRYYYGMDVWGQGT VTVSS
993	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC LV huCCR8	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTVVFGGGTKLT 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 KNTLYLQMNSLRGEDITAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT TAVSS
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 YYGSGIYYKNRYYYGMDVWGQGT TVTVSS
1001	huCCR8_32360_huIgG1z mAb_HC HV huCCR8	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISR DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVTVSS
1002	huCCR8_32360_huIgG1z mAb_LC LV huCCR8	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNKNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSGTDFT LTINSLQAEDVAVYYCQYYISIPITFG GGTKVEIKR

SEQ ID NO:	Designation	Sequence
1003	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1004	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC Constant	TVAAPSVFIFPPSDEQLKSGTASVVC LNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSSTYSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFN RGE
1005	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
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 KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV

SEQ ID NO:	Designation	Sequence
		DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPGK
1008	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_M99E_W109F_S111A)_huIgG1z (mAb)_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ 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 YPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPGK
1010	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G_W109F_S111A)_huIgG1z (mAb)_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1011	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1012	Hu anti-huCCR8 LIBC315615-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPGK

SEQ ID NO:	Designation	Sequence
1013	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1014	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1015	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1016	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1017	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1018	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN

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

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1024	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1025	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1026	Hu anti-huCCR8 LIBC320384-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1027	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1028	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK

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		DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1029	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1030	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1031	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1032	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1033	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS

SEQ ID NO:	Designation	Sequence
1034	Hu anti-huCCR8 LIBC321845-1 Hulg1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
1035	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1036	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
1037	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_LC Constant	QPKAAPSVTLFPPSSEELQANKATLV CLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPT ECS
1038	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV L

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		DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1039	huCCR8_32360_huIgG1z mAb_HC Constant	ASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPV DSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
1040	huCCR8_32360_huIgG1z mAb_LC Constant	TVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDYSLSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFN RGE
1041	MPK20298-A4_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKRNYYGMDVWGQGT VTVSSGGGGSGGGSGGGGSSYELT QPPSVSVALGQTARITCGGNNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPDRFSGSKSGNTATLTISRAGDEA DYCQVWDSSTVVFGGKLTVL
1042	MPK20299-D2_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGGSSYELTQ PPSVSVALGQTARITCGGHNIGSKGV HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTITRAQAGDEAD YYCQVWDSSTVVFGGKLTVL

SEQ ID NO:	Designation	Sequence
1043	MPK20299-F11_SCFV	QVQLVESGGGVVQPGRSLRLSCAPS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLFLQMNSLRAEDTAVYFCARVY YGSGSYKKRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGGNNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGNTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTQLTVL
1044	MPK20298-H6_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSGMHWVRQAPGKGLEWVA VISYDGTNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGGHNIGSKG VHWYQQKPGQAPVLVIYRNSNRPSG IPERFSGSNSGNTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTQLTVL
1045	MPK20297-A4_SCFV	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNYGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGGHNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGNTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTQLTVL
1046	MPK20299-H8_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSVAPGQTARITCGGNNIGSKNV HWYQQKAGQAPVQVIYRNSNRPSGI PARFSGSNSGNTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTKLTVL
1047	MPK20300-C11_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITAVYYCARV YYGSGSYKKRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYEL TQPPSVSVAPGQTARIPCGGNNIGSK NVHWYQQKPGQAPVLVIYRDINRPS

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		GIPERFSGSNSGNTATLTISRAGDE ADYYCQVWDSSVVFGGGTKLTVL
1048	MPK20298-B1_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSSGGGSGGGSGGGSSYELTQ PPSVSV ALGQTARLTCEGNNIGSKNV HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTISRVAQDEAD YYCQAWDSSTVVFGGGTQLTVL
1049	MPK20297-E5_SCFV	QVQLVESGGGLVKPGGSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYSGGIYYKKRYYYGMDVWGQGT VTVSSGGGSGGGSGGGSSYELT QPLSVSEALGQTARITCGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSNSGNAATLTISRVEAGDEA DYYCQVWDSSSDHVVFGGGTQLTV L
1050	MPK20299-A3_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSSGGGSGGGSGGGSSYELTQ PPSVSVAPGQTARITCGNNIGSKNV HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTISGTQAMDEAD YYCQAWDSSNVVFGGGTQLTVL
1051	MPK20297-B4_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGGIYYKNYYYYGMDVWGQGT VTVSSGGGSGGGSGGGSSYELT QPLSVSV ALGQTARITCGNNIGSQN VHWYQQKPGQAPVLVIYRDSNRPSG IPDRFSGSKSGNTATLTISRAGDEA DYYCQVWDSSSTVVFGGGTQLTVL

SEQ ID NO:	Designation	Sequence
1052	MPK20298-F6_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVAPGQTARITCGGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTELTVL
1053	MPK20299-H3_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSIGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PLSVSV ALGQTARITCGGNNIGSKNV HWYQQKPGQAPVLAIRNSNRPSGIP ERFTGSNSGNTATLTISRAQAGDESD YYCQIWDSSSTVVFGGGTKLTVL
1054	MPK20298-B9_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKKNYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSV ALGQTARISCGGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTQLTVL
1055	MPK20299-E2_SCFV	QVQLVESGGGVVQPGRSLRLSCAVS GFNFSNNGMHWVRQAPGKGLEWVA VISYDGSNKYYTDSVKGRFTISRDN KNTLYLQMNSLRTEDTAVYYCAKV YYGSGIYYKKRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSV ALGQTARITCEGNNIGSQN VHWYQQKPGQAPVLV MYRDSNRPS GIPERFSGSKSGNTATLAISRAQAGDE SDYYCQVWDGSAVVFGGGTKLTVL
1056	MPK20299-D6_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSIGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PLSVSV ALGQTARITCEGNNIGSQNV HWYQQKPGQAPVLV MYRDSNRPSGI

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		PERFSGSKSGNTATLAISRAQAGDES DYVCQVWDGSAVVFGGGTQLTVL
1057	MPK20299-A4_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYNRYYYGMDVWGQGT TVTVSSGGGSGGGGSGGGSSYEL TQPPSVSV ALGQTARITCGHNIGSK GVHWYQQKPGQAPVLVIYRNSNRPS GIPERFSGSNSGNTATLTISGTQAMDE ADYYCQAWDSGTVVFGGGTQLTVL
1058	MPK20300-G5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYNRYYYGMDVWGQGT TVTVSSGGGSGGGGSGGGSSYEL TQPPSVSV ALGQTARITCGANNIGSK NVHWYQQKPGQPPVLVIYRDFNRPS GIPERFSASNSGNTATLTISRQAGDE ADYYCQVWDSSTGNVVFGGGTKLT VL
1059	MPK20299-C3_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFIFSNYGFHWVRQTPGKGLEWVA ISYDGSNKYYADSVKGRFTISRDN NTLYLQMNSLRGEDITAVYYCARV YGSYSYKNRYYYGMDVWGQGT TVTVSSGGGSGGGGSGGGSSYELT QPPSVSVAPGQTARITCGNNIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTELTVL
1060	MPK20299-B7_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARV YGSIGIYKKRYYYGMDVWGQGT TVTVSSGGGSGGGGSGGGSSYELTQ SSSVSVAPGQTARITCGNNIGSKNV HWYQQKPGQAPVLVIYRDSNRPSGIP ERFSGSKSGTTATLTISRVEAGDEAD YYCQVWDSSSAHVIFGGGTKLTVL

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1061	MPK20299-A5_SCFV	QVQLVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSGSVALGQTARITCGGNNLGSKN VHWYQQKPGQAPVLVIYRNSNRPSG IPERFSGSNSGNTATLTISRAQAGDEA DYVCQVWDSSTVVFGGGTKLTVL
1062	MPK20299-D1_SCFV	QVQLVESGGGLVKPGGSLRLSCAAS GFTFSNNGMHWRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSVALGQTARITCGGNRIGSKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTKLTVL
1063	MPK20299-C5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSGGGGSGGGSGGGSSYEL TQLPSVSVALGQTARITCGGHNIGSK GVHWYQQKPGQAPVLVIYRNSNRPS GIPERFSGSNSGNTATLTISRAQAGDE ADYYCQVWDSSTVVFGGGTELTVL
1064	MPK20299-B5_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YGSIGIYYKNRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSVALGQTARITCGGHNIGSKGV HWYQQKPGQAPVLVIYRNSNRPSGIP ERFSGSNSGNTATLTISRAQAGDEAD YYCQVWDSSTVVFGGGTQLTVL
1065	MPK20299-G9_SCFV	QVQLVESGGDLVQPGRSLRLSCAAS GFTFSNNGMHWRQAPGKGLEWVA VISNDGSNKYYADSVRGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPLSVSVALGQTARITCGGNNIGSKN VHWYQQKPGQAPVLVIYRNSNRPSG

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		IPERFSGSNSGNTATLTLSRVQAGDE 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 YGSIGIYYKKRYYYGMDVWGQGT TVSSGGGGSGGGSGGGSSYELTQ PPSVSV ALGQTARITCGNNIGSQNV HWYQQKPGQAPVLVIYRDSNRPSGIP ERFSGSKSGNTATLAISRAQAGDES DYYCQVWDSSAVVFGGGTQLTVL
1069	MPK20299-F2_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFTLSSSGMHWVRQAPGKGLEWVA VISNDGSNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSGGGGSGGGSGGGSSYELT QPPSVSV ALGQTARISCGNNIGSKN VHWYQQKPGQAPVLVMYRDSNRPS GIPERFSGSNSGNTATLTISGTQAMDE ADYYCQAWDSGTVVFGGGTKLTVL

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1070	MPK20298-D4_SCFV	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSNYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYFCARVY YSGGIYYKKRYYYGMDVWGQGT TVSSGGGSGGGSGGGSSSYELTQ PPSVSV ALGQTARITCGGNNIGGKNV HWYQQKPGQAPVLVIYRDSNRPSGIP ERFSGSKSGNTATLTISRAQAGDESD YYCQVWDSSTVVFGGGTQLTVL
1071	MPK20297-F5_SCFV	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGGIYYKNYYYGMDVWGQGT VTVSSGGGSGGGSGGGSSSYELT QPLSVSV ALGQTARITCGGNNIGSKN VHWYQQKPGQAPVLVIYRNSNRPSG IPERFSGSNSGNTATLTISRAQAGDEA DYCQVWDSSTVVFGGGTKLTVL
1072	MPK20299-D9_SCFV	QVQLVESGGGLVKPGGSLRLSCAAS GFNFSRNGMHWVRQVPGRGLDWVA VISNDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYSGGIYYKNYYYGMDVWGQGT VTVSSGGGSGGGSGGGSSSYELT QPPSVSV ALGQTARISCGGNNIESKN VHWYQQKPGQAPVLVIYRDSNRPSG IPERFSGSKSGTTATLTISRAQAGDEA EYYCQVWDSSTVVFGGGTQLTVL
1073	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISRD DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRT EVTCTVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK

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1074	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNRNYLAWYHQKPGQSPK LLISWASTRESGVPDRFSGSGSGTDF LTINSLQAEDVAVYYCQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSS TLTSLKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
1075	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYDGSNRYYASSVKGRFTISRDNS KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1076	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z (mAb)_LC	SYELTQPPSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRAA NRPSGIPERFSGSNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFGGGTQ LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1077	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q_ M99E_W109F_S111A)_huIgG1z (mAb)_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYAGSNRYYAASVKGRFTISRDNS KNTLYLQMNSLRGEDITALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH

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		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 NRPSGIPERFSGNSGNTATLTISGTQ AEDEADYYCQAFDAGTVVFGGGTQ LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1079	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G _W109F_S111A)_huIgG1z (mAb)_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFTFSNYGFHWVRQTPGKGLEWVA VISYSGSNRYADSVKGRFTISRDNS KNTLYLQMNSLRGEDTALYYCARV YYGSGTYYKNRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1080	anti- huCCR8_44379(VH:D61S,VL:N67Q_M99G _W109F_S111A)_huIgG1z (mAb)_LC	SYELTQPPSVSVALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRQS NRPSGIPERFSGNSGNTATLTISGTQ AGDEADYYCQAFDAGTVVFGGGTQ LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

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1081	Hu anti-huCCR8 LIBC315615-1 Hulg1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDISTVVFGGGTEL TVLGQPKAAPSVTLPSPSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1082	Hu anti-huCCR8 LIBC315615-1 Hulg1z mAb_HC	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSNCGMHWVRQAPGKGLEWVA VISYDGGNKYHADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1083	Hu anti-huCCR8 LIBC317152-1 Hulg1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGSNSGKTATLTISRAQ AGDEADYYCQVWDSTTVFGGGTE LTVLGQPKAAPSVTLPSPSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1084	Hu anti-huCCR8 LIBC317152-1 Hulg1z mAb_HC	QVQLVESGGGVAQPGRSLRLSCAAS GFNFSNCGMHWVRQAPGKGLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQMDSLRTEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH

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		EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1085	Hu anti-huCCR8 LIBC317471-1 Hulg1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQKRPQGAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSNTVVFGGGTN LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1086	Hu anti-huCCR8 LIBC317471-1 Hulg1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCVVS GFNFSNNGMHWVRQAPGKLEWVA VISNDGSNKYYADSVRGRFTISRDNS KNTLYLQMNSLRAEDTAVYSCAKV YYGSGIYYKNYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1087	Hu anti-huCCR8 LIBC317977-1 Hulg1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKAGQAPVQVIYRNS NRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1088	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFNFNTYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN KSTLYLQMNSLRAEDTAVYYCARVY YSGSYKKNYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTWSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1089	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGGKNVHWYQKPGQAPVLVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDESDYYCQVWDSSTVVFGGGTTL TVLGQPKAAPSVTLPSPSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1090	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCAAS GFTLSSYGFWVRQTPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDN NTLYLQMNSLRGEDTAVYYCARVY YSGTYKKNYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTWSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK

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1091	Hu anti-huCCR8 LIBC319840-1 Hulg1z mAb_LC	SYELTQPLSVSEALGQTARITCGGNNI GSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSKSGNTATLTISRAQA GDEADYYCQVWDSSTVVFGGGTKV TVLGQPKAAPSVTLPFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1092	Hu anti-huCCR8 LIBC319840-1 Hulg1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCVVS GFNFINGMHWRQAPGKGLDWVA VISNDGSNKYYPDsvKGRFTISRDN KNTLYLQMNSLRAEDSAVYYCAKV YYGSGNYYKNYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1093	Hu anti-huCCR8 LIBC320212-1 Hulg1z mAb_LC	SYELTQPLSVSVALGQTARITCEGNNI GSQNVHWYQQKPGQAPVLVMYRDS NRPSGIPERFSGSKSGNTATLAISRAQ AGDESDYYCQVWDGSAVVFGGGTT LTVLGQPKAAPSVTLPFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1094	Hu anti-huCCR8 LIBC320212-1 Hulg1z mAb_HC	QMQVVESGGGVVQPGRSLRLSCAAS GFTFSSSGMHWRQAPGKGLEWVA VISHDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLGGEDTAVYYCAKV YYGSGIYYKNRYYYGMDVWGQGT VIVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH

SEQ ID NO:	Designation	Sequence
		EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1095	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGHN IGSKGVHWYQQKPGQAPVLVIYRNS NRPSGIPERFSGNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTE LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1096	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_HC	QVQLVESGGGV AQPGRSLRLSCAAS GFNFDSCGMHWVRQAPGKLEWVA VISYDGGNKYYADSVKGRFTISRDDS KNTLYLQTDLSRTEDTAVYYCAKVY YSGGIYYKNRYYYGMDVWGQGTIV TVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSHE DPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTP PVLDSGDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSP GK
1097	Hu anti-huCCR8 LIBC320689-1 HulgG1z mAb_LC	SYELTQPLSVSV ALGQTGRITCGGNN IGSKNVHWYQQKPGQAPVLVIYRSS NRPSGIPERFSGNSGNTATLTISRAQ AGDESDYYCQIWDSSSTVVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSP VKAGVETTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1098	Hu anti-huCCR8 LIBC320689-1 HuIgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVA VISFDGNNKYYADSVKGRFTISRDN KNTLYLQMNSLRGEDTAVYYCARV YYGSGSYKRNRYYYGMDVWGQGT TVTVSTASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKVK EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLS PGK
1099	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQRPGQAPVLVIYRDS NRPSGIPERLSGSKAGNTATLTISR AGDEADYYCQVWDSSTVVFGGGTE LTVQGQPKAAPSVTLPFPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1100	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAVS GFTFSSNGMHWVRQAPGKGLEWVA VISNDGSNKYYGDSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYRNYYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPS SSSLGTQTYICNVNHKPSNTKVDKVK EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLS PGK

SEQ ID NO:	Designation	Sequence
1101	Hu anti-huCCR8 LIBC321824-1 HulgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTVVFGGGTKLT VLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNKYAASSYLSLT PEQWKSHRSYSCQVTHEGSTVEKTV APTECS
1102	Hu anti-huCCR8 LIBC321824-1 HulgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFPISRDNS KNTLYLQMNSLRGEDITAVYYCARV YYGSGIYYKNRYYYGMDVWGQGT VAVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1103	Hu anti-huCCR8 LIBC321845-1 HulgG1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPILVIYRNTN RPSGIPERFSGSNSGNTATLTISRAQV GDESDYFCQVWDSSTVVFGGGTKLT VLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPV KAGVETTPSKQSNKYAASSYLSLT PEQWKSHRSYSCQVTHEGSTVEKTV APTECS
1104	Hu anti-huCCR8 LIBC321845-1 HulgG1z mAb_HC	QVQVVESGGGVVQPGRSLRLSCGAS GFTFSGYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNS 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 Hulg1z mAb_LC	SYDLTQPLSVSV ALGQTARITCGGNN IGDKNVHWYQQKPGQAPV LVIYRNN VRPSGIPERFSGSNSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
1106	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAAS GLNFSNFGMHWVRQAPGKGLDWVA VISYDGGNKYYADSVKGRFTVSRDN SKNTLFLQMNSLRAEDTALYYCAKV YYGSGSYKKRYYYGMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1107	Hu anti-huCCR8 LIBC323412-1 Hulg1z mAb_LC	SYELTQPLSVSV ALGQTARITCGGNN IGSKNVHWYQQKPGQAPV LVIYRDS NRPSGIPERFSGSKSGNTATLTISRAQ AGDEADYYCQVWDSSTVVFGGGAK LTVLGQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNKYAASSYLS LTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS

SEQ ID NO:	Designation	Sequence
1108	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC	QVQLVESGGGVVQPGRSLRLSCAAS GFNFSSCGMHWVRQAPGKGLEWVA VISYDGTNKYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCAKV YYGSGIYYKKNYYYGMDVWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTWSNSGALT SGVHTFPAVLQSSGLYSLSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGSPSVFL FPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLS PGK
1109	huCCR8_32360_huIgG1z mAb_HC	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSNARMGWVRQAPGKGLEWVG RIKSKTEGGTRDYAAPVKGRFTISR DSKNTLYLQMNSLKTEDTAVYYCTS YSGVWGQGTMTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCP APELLGSPSVFLFPPKPKDTLMISRT EVTCTVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
1110	huCCR8_32360_huIgG1z mAb_LC	DIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNKNYLAWYHQPGQSPK LLISWASTRESGVPDRFSGSGSGTDFT LTINSLQAEDVAVYYCQYYISIPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDYSLSS TLTSLKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC

SEQ ID NO:	Designation	Sequence
1111	MPK20298-A4_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGACTGGAGTGGGTGGCA GTTATTTCAAATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAACAGGAACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGGCGGCGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGACCGATT TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC AAGCTGACCGTCCTA
1112	MPK20299-D2_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACATATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGGCGGCGCTCCGGT

SEQ ID NO:	Designation	Sequence
		GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGACACAACATTGGAAG TAAAGGTGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGACCATCACCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC AAGCTGACCGTCCTA
1113	MPK20299-F11_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCACCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAAAACACGCTGTTTCTGCA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGAGTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
1114	MPK20298-H6_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGT CTGGATTACCTTCAGTAGCTCTGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAATAATA AATACTATGCGGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAACAGGTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCCTCATATGAGCTGA CTCAGCCACCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGACACAACATTGGAAG TAAAGGTGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCGTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA
1115	MPK20297-A4_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTACCATTTCCAGAGACA ATTCCAAGAACACACTGTATCTGCA AATGGACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
		GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGACACAACATTGGAAG TCAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAAGTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA
1116	MPK20299-H8_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGGA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTGAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGGCAGGCCAGGCCCTGTGCA GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGCGCGATT TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAGGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGTGGGACCA AGCTGACCGTCCTA

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

SEQ ID NO:	Designation	Sequence
		GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCACTGGC CCTGGGACAGACGGCCAGGCTTAC CTGTGAGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACTATTAGCAGAGTCC AAGCCGGGGATGAGGCTGACTATT ACTGTCAGGCGTGGGACAGCAGCA CTGTGGTATTCGGCGGAGGCACCC AGCTGACCGTCCTA
1119	MPK20297-E5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCCTGGTCAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTCATATCGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACTCTCAGTGTCAAGAGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTACT GGTCATCTATAGGGATAGCAACCG GCCCTCAGGGATCCCTGAGCGATTC TCTGGCTCCAACTCTGGGAACGCGG CCACCCTGACCATCAGTAGGGTCG AAGCCGGGGATGAGGCCGACTATT ACTGTCAGGTGTGGGATAGTAGCA GTGATCATGTGGTATTCGGCGGAG GCACCCAGCTGACCGTCCTA

SEQ ID NO:	Designation	Sequence
1120	MPK20299-A3_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCCTCATATGAGCTGA CTCAGCCACCCTCGGTGTCAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCGTACT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAACCTCTGGGAACACAG CCACTCTGACCATCAGCGGGACCC AGGCTATGGATGAGGCTGACTATT ACTGTCAGGCGTGGGACAGCAGCA ATGTGGTATTCGGCGGAGGCACCC AGCTGACCGTCCTA
1121	MPK20297-B4_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATACTACTATTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGCGGCGGCTCCGGT

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1122	MPK20298-F6_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCGA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAACCGCTATTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCGGTGTCAGTGGC CCCAGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAAGTCGGGGACCACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGAGTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGGACC GAGCTGACCGTCCTA

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1123	MPK20299-H3_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGGCGGCGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CACAGCCACTCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCGTGTGCT GGCCATCTATAGGAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC ACTGGCTCCAACCTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGTCTGACTAT TACTGTCAAATATGGGACAGCAGC ACTGTGGTATTCGGCGGAGGCACC AAGCTGACCGTCCTA
1124	MPK20298-B9_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCGGACTCCGTGAAG GGCCGATTACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGTATTTAT TATAAAAAGAACTACTACTACGGT ATGGACGTCTGGGGCCAAGGGACC ACGGTCACCGTCTCCTCAGGTGGTG GTGGTTCCTGGCGGGCGGCGCTCCG

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1125	MPK20299-E2_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTCATATCGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGAGGGAAACAACATTGGAAG TCAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATGTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAACGATTC TCTGGCTCCAAGTCGGGGAAACACG GCCACCCTGGCCATCAGCAGAGCC CAAGCCGGGGATGAGTCTGACTAT TACTGTCAGGTGTGGGACGGCAGT GCCGTGGTATTCGGCGGAGGGACC AAGCTGACCGTCCTA

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1127	MPK20299-A4_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAACTATGG CTTTCACTGGGTCCGCCAGACTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA GATACTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTCCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGCTATATTACTGTGCGAGA GTTTACTATGGTTCGGGGACTTATT ATAAAAACCGCTACTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTTCCTGGCGGGCGGCGGCTCCGGT

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1128	MPK20300-G5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAACTATGG CTTTCACTGGGTCCGCCAGACTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA GATACTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTCCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGCTATATTACTGTGCGAGA GTTTACTATGGTTCGGGGACTTATT ATAAAAACCGCTACTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGCAAACAACATTGGAAG TAAAAATGTTCACTGGTACCAGCA GAAGCCAGGCCAGCCCCCTGTGCT GGTCATCTATAGAGATTTCAACCGG CCCTCTGGGATCCCTGAGCGATTCT CTGCCTCCAACTCGGGGAACACGG CCACCCTGACCATCAGCAGAGGCC AAGCCGGGGATGAGGCTGACTATT ACTGTCAGGTGTGGGACAGCAGCA CTGGGAATGTGGTATTCGGCGGAG GGACCAAGCTGACCGTCCTA

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1130	MPK20299-B7_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTCTGTGCGAGA GTTTACTATGGTTCGGGGATTATT ATAAAAAGAGATACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGGCGGCGCTCCGGT

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1131	MPK20299-A5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGGAGCCT CTGGATTACCTTCAGTGGCTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGG GCCGATTACCATCTCAAGAGACA ATTCCAAGAACACGCTGTATCTGCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGGTGTATTACTGTGCGAG AGTTTATTATGGTTCGGGGATTTAT TATAAAAACCGCTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGGGTCAGTGGC CCTGGGACAGACGGCCAGGATCAC CTGTGGGGGAAACAACCTTGGAAG TAAAAATGTGCACTGGTACCAACA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAGGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTATTCGGCGGTGGGACC AAGCTGACCGTCCTA

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1133	MPK20299-C5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAACATATGG CTTTCACTGGGTCCGCCAGACTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCATATGATGGAAGTAATA GATACTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTCCA AATGAACAGCCTGAGAGGTGAGGA CACGGCGCTATATTACTGTGCGAGA GTTTACTATGGTTCGGGGACTTATT ATAAAAACCGCTACTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTTCCTGGCGGGCGGCGGCTCCGGT

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1134	MPK20299-B5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAACTATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAATGGGTGGCA GTTATATCATATGATGGAAGTAATA AATATTATGCAGACTCCGTGAAGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACGCTGTATCTACA AATGAACAGCCTGAGAGCTGAGGA CACGGCTGTGTATTTCTGTGCGAGA GTTTACTATGGTTCGGGGATTTATT ATAAAAACCGCTATTACTACGGTAT GGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCAGGTGGTGGT GGTCTGTGGCGGCGGCGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCACTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGACACAACATTGGAAG TAAAGGTGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGTAGT ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA

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1136	MPK20299-G5_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGTCT CTGGATTCAACTTCAGTAACAATGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGACTGGAGTGGGTGGCA GTTATTTCAAATGATGGCAGTAATA AATATTATGCAGATTCCGTGAGGG GCCGATTACCATCTCCAGAGACA ATTCCAAGAACACACTGTATCTGCA AATGGACAGCCTGAGAACTGAGGA CACGGCTGTGTATTACTGTGCGAAA GTTTACTATGGTTCGGGTATTTATT ATAAAAACAGGTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCCTGGCGGCGGCGGCTCCGGT

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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 CTCAGCCACCCTCAGTGTGAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGCT GGCCATCTATAGGAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATTC ACTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCGGGACC CAGGCTATGGATGAGGCTGACTATT ACTGTCAGGCGTGGGACAGCAGCA CTGTGGTATTCGGCGGAGGGACCA AGCTGACCGTCCTA

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1139	MPK20299-F2_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCCCTCAGTAGCTCTGG CATGCACTGGGTCCGCCAGGCTCCA GGCAAGGGGCTGGAGTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCGGACTCCGTGAAG GGCCGGTTCACCATCTCCAGAGAC GATTCCAAGAACACACTGTATCTGC AAATGGACAGCCTGAGAACTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGTATTTAT TATAAAAACAGGTACTACTACGGG ATGGACGTCTGGGGCCAAGGGACC ACGGTCACCGTCTCCTCAGGTGGTG GTGGTTCTGGCGGGCGGCGCTCCG

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

SEQ ID NO:	Designation	Sequence
1141	MPK20297-F5_SCFV	CAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGTAGTCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATAACTACTATTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACTCTCAGTGTCAGTGGC CCTGGGACAGACGGCCAGGATTAC CTGTGGGGGAAACAACATTGGAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCCGTGTGCT GGTCATCTATAGAAATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAACTCGGGGAACACG GCCACCCTGACCATCAGCAGAGCC CAGGCCGGGGATGAGGCTGACTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGTGGGACCA AGCTGACCGTCCTA
1142	MPK20299-D9_SCFV	CAGGTGCAGCTGGTGGAGTCCGGG GGAGGCTTGGTCAAGCCTGGAGGG TCCCTGAGACTCTCCTGTGCAGCCT CTGGATTCAACTTCAGTAGGAATGG CATGCACTGGGTCCGCCAGGTTCCA GGCAGGGGGCTAGATTGGGTGGCA GTTATATCAAATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAG GGCCGATTACCATCTCCAGAGAC AATTCCAAGAACACGCTGTATCTGC AAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGTGCGAA AGTTTACTATGGTTCGGGGATTTAT TATAAAAATAACTACTACTACGGTA TGGACGTCTGGGGCCAAGGGACCA CGGTCACCGTCTCCTCAGGTGGTGG TGGTTCTGGCGGCGGCGGCTCCGGT

SEQ ID NO:	Designation	Sequence
		GGTGGTGGTTCTTCATATGAGCTGA CTCAGCCACCCTCAGTGTCAAGTGGC CCTGGGACAGACGGCCAGGATTTC CTGTGGGGGAAACAACATTGAAAG TAAAAATGTGCACTGGTACCAGCA GAAGCCAGGCCAGGCCCTGTGTT GGTCATCTATAGGGATAGCAACCG GCCCTCTGGGATCCCTGAGCGATT TCTGGCTCCAAGTCGGGGACCACG GCCACCCTGACCATCAGCAGAGCC CAAGCCGGGGATGAGGCTGAGTAT TACTGTCAGGTGTGGGACAGCAGC ACTGTGGTTTTTCGGCGGAGGCACCC AGCTGACCGTCCTA
1143	huCCR8_32360_huIgG1z mAb(LC:K38R)_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGAGGTGC AGCTGGTGGAGTCTGGGGGAGGCT TGGTAAAGCCTGGGGGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT TACTTTCAGTAACGCCCGGATGGGC TGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTTGGCCGTATT AAAAGCAAACTGAAGGTGGGACA AGAGACTACGCTGCACCCGTGAAA GGCAGATTCACCATCTCAAGAGAT GATTCAAAAAACACGCTGTATCTGC AAATGAACAGCCTGAAAACCGAGG ACACAGCCGTGTATTATTGTACCTC GTATAGTGGGGTCTGGGGCCAAGG GACAATGGTCACCGTGTCTTCAGCC TCCACCAAGGGCCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGAAC TCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCTACAGT CCTCAGGACTCTACTCCCTCAGCAG CGTGGTGACCGTGCCCTCCAGCAGC TTGGGCACCCAGACCTACATCTGCA ACGTGAATCACAAGCCCAGCAACA CCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAACCTCACAC ATGCCCACCGTGCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTC CTCTTCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGA

SEQ ID NO:	Designation	Sequence
		GGTCACATGCGTGGTGGTGGACGT GAGCCACGAAGACCCTGAGGTCAA GTTCAACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGACAAA GCCGCGGGAGGAGCAGTACAACAG CACGTACCGTGTGGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGCCCTCCAGCCC CCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAC AGGTGTACACCCTGCCCCATCCCG GGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCG GAGAACAACATAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCT TCTTCCTCTATAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTC CGGGCAAATAG
1144	huCCR8_32360_huIgG1z mAb(LC:K38R)_LC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGACATCG TGATGACCCAGTCTCCAGACTCCCT GGCTGTGTCTCTGGGCGAGAGGGC CACCATCAACTGCAAGTCCAGCCA GAGTGTTTTATACAGTTCCAACAAT AGAACTACTTAGCTTGGTACCATC AGAAACCAGGACAGTCTCCTAAGC TGCTCATTTCTGCGCATCTACCCG GGAATCCGGGGTCCCTGACCGATTG AGTGGCAGCGGGTCTGGGACAGAT TTCACTCTCACCATCAACAGCCTGC AGGCTGAAGATGTGGCAGTTTATTA CTGTCAACAATATTATAGTATTCCG ATCACTTTCGGCGGAGGGACCAAG GTGGAGATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGC CATCTGATGAGCAGTTGAAATCTGG AACTGCCTCTGTTGIGTGCCTGCTG AATAACTTCTATCCCAGAGAGGCC AAAGTACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCCAGG AGAGTGTCACAGAGCAGGACAGCA

SEQ ID NO:	Designation	Sequence
		AGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTT CAACAGGGGAGAGTGTTAG
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 GAACACGCTGTATCTCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GCTATATTACTGTGCGAGAGTTTAC TATGGTTCCGGGGACTTATTATAAAA ACCGTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTGTCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACATG

SEQ ID NO:	Designation	Sequence
		CGTGGTGGTGGACGTGAGCCACGA AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCTCACCCTCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCTCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCTC TATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1146	anti- huCCR8_44379(VH:D72S,VL:N67A_S68A_ M99G_W109F_S111A)_huIgG1z(mAb)_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCATATGAGCTGACTCAG CCACCCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTACTGGTCAT CTATAGAGCCGCCAACCAGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCTGGGAACACAGCCACTCT GACCATCAGCGGGACCCAGGCTGG CGATGAGGCTGACTATTACTGTGAG GCGTTCGACGCCGGCACTGTGGTAT TCGGCGGAGGCACCCAGCTGACCG TCCTAGGTCAGCCCAAGGCTGCACC CTCGGTCACTCTGTTCCCGCCCTCC TCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATCAGTG ACTTCTACCCGGGAGCCGTGACAGT GGCTTGGAAGGCAGATAGCAGCCC CGTCAAGGCGGGAGTGGAACAC CACACCCTCCAAACAAAGCAACAA CAAGTACGCGGCCAGCAGCTATCT

SEQ ID NO:	Designation	Sequence
		GAGCCTGACGCCTGAGCAGTGGAA GTCCACAGAAGCTACAGCTGCCA GGTCACGCATGAAGGGAGCACCGT GGAGAAGACAGTGGCCCCCTACAGA ATGTTCATAG
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 GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCG TGCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1148	anti- huCCR8_44379(VH:D61A_D72A,VL:N67Q _M99E_W109F_S111A)_huIgG1z (mAb)_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCATATGAGCTGACTCAG CCACCCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTACTGGTCAT CTATAGACAGAGCAACCGGCCCTC TGGGATCCCTGAGCGATTCTCTGGC TCCAACCTCTGGGAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTG AAGATGAGGCTGACTATTACTGTCA GGCGTTCGACGCCGGCACTGTGGT ATTCGGCGGAGGCACCCAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
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 ACCGTGTCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACC CTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCT 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 CCACCCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTACTGGTCAT CTATAGACAGAGCAACCGGCCCTC TGGGATCCCTGAGCGATTCTCTGGC TCCAACCTCTGGGAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTG GCGATGAGGCTGACTATTACTGTCA GGCGTTCGACGCCGGCACTGTGGT ATTCCGGCGGAGGCACCCAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1151	Hu anti-huCCR8 LIBC315615-1 Hulg1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAACTGACTCAG CCACTCTCAGTGTGCTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACATCAGCACTGTGGTT TTCGGCGGAGGGACCGAGCTGACC GTCCTAGGTCAGCCCAAGGCTGCA CCCTCGGTCACTCTGTTCCCGCCCT CCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG

SEQ ID NO:	Designation	Sequence
1152	Hu anti-huCCR8 LIBC315615-1 HuIgG1z 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 CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGACACCTTCCC GGCTGTCCTACAGTCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCACCG TGCCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCCTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAG

SEQ ID NO:	Designation	Sequence
		ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1153	Hu anti-huCCR8 LIBC317152-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGACACAACATTGGAAGTAAAG GTGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAAAACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCGAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACCTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
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 ACGGTGTCTGTGGAATCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCCAAGGACACCCCTCATG 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
1155	Hu anti-huCCR8 LIBC317471-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGAAGAGGC CAGGCCAGGCCCCTGTGCTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAACACTGTGGT TTTCGGCGGAGGGACCAACCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA 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 CTATGGTTCGGAATTTATTACAAA AATAACTACTACTACGGTATGGAC GTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACC CTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCCAAGGACACCCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1157	Hu anti-huCCR8 LIBC317977-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTctATGAGCTGACTCAGC CACTCTCAGTGTCAGTGGCCCTGGG ACAGACGGCCAGGATTACCTGTGG GGGAAACAACATTGGAAGTAAAAA TGTGCACTGGTACCAGCAGAAGGC AGGCCAGGCCCTGTGCAGGTCAT CTATAGAAATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACCTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCAGGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGTGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1158	Hu anti-huCCR8 LIBC317977-1 HulgGlz mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CAACTTCAATACCTATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAAGTAATAAATATT ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAGCACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGC TGTGTATTACTGTGCGAGAGTTTAC TATGGTTCGGGGAGTTATTATAAAA AGAATTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCAGCACCTGAACCTCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCCTCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1159	Hu anti-huCCR8 LIBC318774-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGAAACAACATTGGAGGTA AAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTGCTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGTCTGACTATTACTGTCA GGTTTGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1160	Hu anti-huCCR8 LIBC318774-1 HulgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTCAGTAGTTATGGCTTTCAC TGGGTCCGCCAGACTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAAGTAATAAAAct ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTCCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GGTGTATTACTGTGCGAGAGTTTAC TATGGTTCGGGGACTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCTT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCAGCACCTGAACCTCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAG 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 GGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTACTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCAAGGTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1162	Hu anti-huCCR8 LIBC319840-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGTAGTCTCTGGATT CAACTTCATTAAACAATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGACTGGGTGGCAGTTATA TCAAATGATGGAAGTAATAAATAC TATCCAGACTCCGTGAAGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACTCGG CTGTGTATTACTGTGCGAAAGTTTA CTATGGTTCGGGAAATTATTATAAA AACAACTACTACTACGGTATGGAC GTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACC CTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGGAATCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGAGGA GATGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCC TCTATAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGC AAATAG
1163	Hu anti-huCCR8 LIBC320212-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG AGGGAAACAACATTGGAAGTCAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTGCTGGTCAT GTATAGGGATAGCAACCGGCCCTC TGGGATCCCTGAACGATTCTCTGGC TCCAAGTCGGGGAACACGGCCACC CTGGCCATCAGCAGAGCCCAAGCC GGGGATGAGTCTGACTATTACTGTC AGGTGTGGGACGGCAGTGCCGTGG TATTCGGCGGAGGGACACGCTGA CCGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA 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 ACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

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

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTTCATAG
1166	Hu anti-huCCR8 LIBC320384-1 HulgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGctGGTGGAGtctGGGGGAGGCGTG GCCCAGCCTGGGAGGTCCCTGAGA CTCTCCTGTGCAGCCTCTGGATTCA ACTTCAGTGattGTGGCATGCACTGG GTCCGCCaggCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATCATA TGATGGAGGTAATAAATATTATGC GGACTCCGTGAAGGGCCGGTTCAC CATCTCCAGAGacgATTCCAAGAAC ACACTGTAtcTGCAAcggacAGCCTG AGAACTGAGGACACGGCTGTGTAT TACTGTGCGAAAGTTTACTATGGTT CGGGTATTTATTATAAAAACAGGTA CTACTACGGGATGGACGTctggggCC AAGGGACCACGGTcaccgTCTCCTCA GCCTCCACCAAGGGGCCCATCGGTCT TCCCCCTGGCACCCCTCCTCCAAGAG CACCTCTGGGGGCACAGCGGCCCT GGGCTGCCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTCGTGG AACTCAGGCGCCCTGACCAGCGGC GTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAG CAGCGTGGTGACCGTGCCCTCCAGC AGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTG AGCCCAAATCTTGTGACAAAATC ACACATGCCCACCGTGCCCAGCAC CTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCAAAACCCAA GGACACCCTCATGATCTCCCGGACC CCTGAGGTACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAG

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

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1168	Hu anti-huCCR8 LIBC320689-1 HulgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAGCTATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAATAATAAATACT ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTATATCTGCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GGTGTATTACTGTGCGAGAGTTTAT TATGGTTCGGGGAGTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCACAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCCACCG TGCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1169	Hu anti-huCCR8 LIBC321408-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAACTGACTCAG CCACTCTCAGTGTGAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAACAACATTGGAAGTAAAA ATGTACACTGGTACCAGCAGAGGC CAGGCCAGGCCCCTGTGTTGGTCAT CTACAGGGATAGCAACCGGCCCTC TGGGATCCCTGAGCGATTATCTGGC TCCAAAGCGGGGAACACGGCCACC CTGACCATCAGCAGAGCCCACGCC GGGGATGAGGCTGACTATTACTGTC AGGTGTGGGACAGCAGCACTGTGG TTTTCGGCGGAGGGACCGAGCTGA CCGTCCAAGGTCAGCCCCAAGGCTG CACCTCGGTCACTCTGTTCCCGCC CTCCTCTGAGGAGCTTCAAGCCAAC AAGGCCACACTGGTGTGTCTCATCA GTGACTTCTACCCGGGAGCCGTGAC AGTGGCCTGGAAGGCAGATAGCAG CCCCGTCAAGGCGGGAGTGGAAC CACCACACCCCTCCAAACAAAGCAA CAACAAGTACGCGGCCAGCAGCTA

SEQ ID NO:	Designation	Sequence
		TCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTG CCAGGTCACGCATGAAGGGAGCAC CGTGGAGAAGACAGTGGCCCCCTAC AGAATGTTCATAG
1170	Hu anti-huCCR8 LIBC321408-1 HulgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AATTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCTCTGAG ACTCTCCTGTGCAGTCTCTGGATTG ACGTTCACTAGCAATGGCATGCACT GGGTCCGCCAGGCTCCAGGCAAGG GGCTGGAGTGGGTGGCAGTTATAT CAAATGATGGAAGTAATAAATATT ATGGAGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGC TGTGTATTACTGTGCGAAAGTTTAC TATGGTTCGGAATTTATTACAGAA ACAATACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCAGCACCTGAACCTCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCCTCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTG ACCTGCCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCGTGCT GGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGA AGAGCCTCTCCCTGTCTCCGGGCAA ATAG
1171	Hu anti-huCCR8 LIBC321824-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGAAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCATACTGGTCAT CTATAGGAATACCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGTCG GGGATGAGTCTGACTATTTCTGTCA GGTGTGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1172	Hu anti-huCCR8 LIBC321824-1 HulgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTctGGGGGAGGCGT GGTCCAGccTGGGAGGTcCTGAGA CTCTCCTGTGGAGCCTCTGGATTCA CcttCAGtggcTATGGCATgcACTGGGT CcgcCAggcTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGA TGGAAGTAATAAATACTATGCAGA CTCCGTgAAGGGCCGATTCCCCATC TCAAGAgAaCAATTCCAAGAACACGC TGTATCTGCAAATGAACAGcCTGAG AGGTGAGGACACGGCGGTGTATTA CTGTgcGAGAGTTTATTATGGTTTCGG GGATTATTATAAAAACCGCTacTaC TACGGTAtgGACGtctGGGGCCAAGG GACCACGGTcgcCGTCTCCTCAGCCT CCACCAAGGGGCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACC TCTGGGGGGCACAGCGGCCCTGGGC TGCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAAC CAGGCGCCCTGACCAGCGGCGTGC ACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCT TGGGCACCCAGACCTACATCTGCA ACGTGAATCACAAAGCCCAGCAACA CCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAACACAC ATGCCCACCGTGCCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTC CTCTTCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGT GAGCCACGAAGACCTGAGGTCAA

SEQ ID NO:	Designation	Sequence
		GTTCAACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGACAAA GCCGCGGGAGGAGCAGTACAACAG CACGTACCGTGTGGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAC AGGTGTACACCCTGCCCCATCCCG GGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCG GAGAACAACATAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCT TCTTCTCTATAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCAACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTC CGGGCAAATAG
1173	Hu anti-huCCR8 LIBC321845-1 HuIgG1z mAb_LC	ATGGCCTGGGCTCTGCTGCTCCTCA CCCTCCTCACTCAGGGCACAGGGTC CTGGGCCTCCTATGAGCTGACTCAG CCACTCTCAGTGTCAGTGGCCCTGG GACAGACGGCCAGGATTACCTGTG GGGGAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTATACTGGTCAT CTATAGGAATACCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACCTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGTCG GGGATGAGTCTGACTATTTCTGTCA GGTGTGGGACAGCAGCACTGTGGT ATTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACCTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1174	Hu anti-huCCR8 LIBC321845-1 HulG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGGTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGGAGCCTCTGGATT CACCTTCAGTGGCTATGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGAT TCACCATCTCAAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGGTGAGGACACGGC GGTGTATTACTGTGCGAGAGTTTAT TATGGTTCGGGGATTTATTATAAAA ACCGCTACTACTACGGTATGGACGT CTGGGGCCAAGGGACCACGGTCGC CGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGAC AAGAAAGTTGAGCCCAAATCTTGT GACAAAACCTCACACATGCCACCG TGCCAGCACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCC CAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGA

SEQ ID NO:	Designation	Sequence
		AGACCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGCGGGA GGAGCAGTACAACAGCACGTACCG TGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTGTCCAAC AAAGCCCTCCCAGCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAG 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 GGGAAACAACATTGGAGATAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCCTGTGCTGGTCAT CTATAGGAATAACGTCCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAACTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGACCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1176	Hu anti-huCCR8 LIBC322176-1 Hulg1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAAATCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGGCT CAACTTCAGTAACTTTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGACTGGGTGGCAGTTATA TCATATGATGGAGGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGAT TCACCGTCTCCAGAGACAATTCCAA GAACACGCTCTTTCTGCAAATGAAC AGCCTGAGAGCTGAGGACACGGCT CTGTATTACTGTGCGAAAGTTTACT ATGGCTCGGGCAGTTATTATAAAA AGAGGTACTACTACGGTATGGACG TCTGGGGCCAGGGGACCACGGTCA CCGTCTCCTCAGCCTCCACCAAGGG CCCATCGGTCTTCCCCCTGGCACCC TCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAATCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACG

SEQ ID NO:	Designation	Sequence
		AAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGG AGGAGCAGTACAACAGCACGTACC GTGTGGTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGGTGTCCAA CAAAGCCCTCCCAGCCCCATCGA GAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTA CACCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCT 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 GGGGAACAACATTGGAAGTAAAA ATGTGCACTGGTACCAGCAGAAGC CAGGCCAGGCCCTGTGCTGGTCAT CTATAGGGATAGCAACCGGCCCTCT GGGATCCCTGAGCGATTCTCTGGCT CCAAGTCGGGGAACACGGCCACCC TGACCATCAGCAGAGCCCAAGCCG GGGATGAGGCTGACTATTACTGTCA GGTGTGGGACAGCAGCACTGTGGT TTTCGGCGGAGGGGCCAAGCTGAC CGTCCTAGGTCAGCCCAAGGCTGC ACCCTCGGTCACTCTGTTCCCGCCC TCCTCTGAGGAGCTTCAAGCCAACA AGGCCACACTGGTGTGTCTCATCAG TGACTTCTACCCGGGAGCCGTGACA GTGGCCTGGAAGGCAGATAGCAGC CCCGTCAAGGCGGGAGTGGAACC ACCACACCCTCCAAACAAAGCAAC AACAAGTACGCGGCCAGCAGCTAT

SEQ ID NO:	Designation	Sequence
		CTGAGCCTGACGCCTGAGCAGTGG AAGTCCCACAGAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCCTACA GAATGTTCATAG
1178	Hu anti-huCCR8 LIBC323412-1 HuIgG1z mAb_HC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTCAGGTGC AGCTGGTGGAGTCTGGGGGAGGCG TGGTCCAGCCTGGGAGGTCCCTGA GACTCTCCTGTGCAGCCTCTGGATT CAACTTCAGTAGCTGTGGCATGCAC TGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATA TCATATGATGGAATAATAAATACT ATGCGGACTCCGTGAAGGGCCGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGC TGTGTATTACTGTGCGAAAGTTTAC TATGGTTCGGGTATTTATTATAAAA AGAACTACTACTACGGTATGGACG TCTGGGGCCAAGGGACCACGGTCA CCGTCTCCTCAGCCTCCACCAAGGG CCCATCGGTCTTCCCCCTGGCACCC TCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGGAATCAGGCGCC CTGACCAGCGGCGTGCACACCTTCC CGGCTGTCCTACAGTCCTCAGGACT CTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTT GTGACAAAACCTCACACATGCCCCAC CGTGCCCAAGCACCTGAACTCCTGGG GGGACCGTCAGTCTTCTCTTCCCC CCAAAACCCAAGGACACCCTCATG 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 TACTTTCAGTAACGCCCCGATGGGC TGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTTGGCCGTATT AAAAGCAAACTGAAGGTGGGACA AGAGACTACGCTGCACCCGTGAAA GGCAGATTACCATCTCAAGAGAT GATTCAAAAACACGCTGTATCTGC AAATGAACAGCCTGAAAACCGAGG ACACAGCCGTGTATTATTGTACCTC GTATAGTGGGGTCTGGGGCCAAGG GACAATGGTCACCGTCTCTTCAGCC TCCACCAAGGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCAC CTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAAC TCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCTACAGT

SEQ ID NO:	Designation	Sequence
		CCTCAGGACTCTACTCCCTCAGCAG CGTGGTGACCGTGCCCTCCAGCAGC TTGGGCACCCAGACCTACATCTGCA ACGTGAATCACAAGCCCAGCAACA CCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAACCTCACAC ATGCCCACCGTGCCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTC CTCTTCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGT GAGCCACGAAGACCTGAGGTCAA GTTCAACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGACAAA GCCGCGGGAGGAGCAGTACAACAG CACGTACCGTGTGGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAC AGGTGTACACCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCG GAGAACAACCTACAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCT TCTTCTCTATAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTC CGGGCAAATAG
1180	huCCR8_32360_huIgG1z mAb_LC	ATGGACATGAGGGTGCCCGCTCAG CTCCTGGGGCTCCTGCTGCTGTGGC TGAGAGGTGCGCGCTGTGACATCG TGATGACCCAGTCTCCAGACTCCCT GGCTGTGTCTCTGGGCGAGAGGGC CACCATCAACTGCAAGTCCAGCCA GAGTGTTTTATACAGTTCCAACAAT AAGAACTACTTAGCTTGGTACCATC AGAAACCAGGACAGTCTCCTAAGC TGCTCATTTCTGGGCATCTACCCG GGAATCCGGGGTCCCTGACCGATT AGTGGCAGCGGGTCTGGGACAGAT TTCACTCTCACCATCAACAGCCTGC 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 C κ or C λ 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 C κ or C λ .
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 C κ or C λ , 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 C κ or C λ 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, C κ and/or C λ 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 C κ or C λ .

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 C λ -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 C λ -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 Cκ, wherein the first VL and Cκ 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-Ck 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-Ck 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 $RX_2X_3X_4RPS$ (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, 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.