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[Continued on next page]

(54) Title: CHIMERIC ANTIGEN RECEPTORS TARGETING FC RECEPTOR-LIKE 5 AND USES THEREOF

(57) Abstract: The presently disclosed subject matter provides for methods and compositions for treating a neoplasia (*e.g.*, multiple myeloma). It relates to chimeric antigen receptors (CARs) that specifically target Fc Receptor-like 5 (FcRL5), *e.g.*, domain 9 of FcRL5, and immunoresponsive cells comprising such CARs. The presently disclosed FcRL5-targeted CARs have enhanced immune-activating properties, including anti-tumor activity.

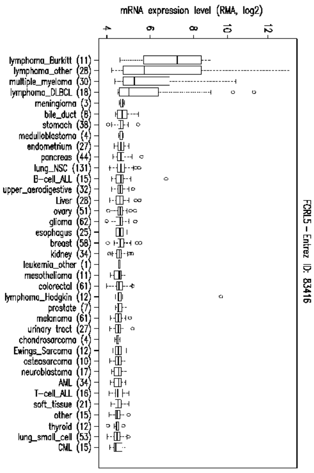

FIG. 1

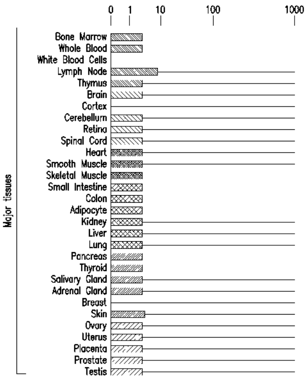

FIG. 1 (continued)

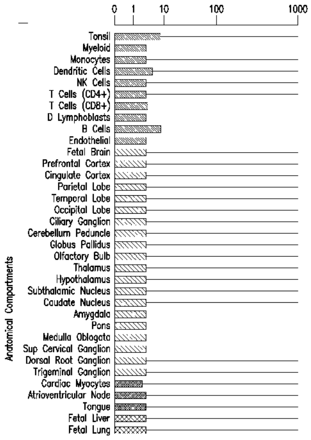

FIG. 1 (continued)

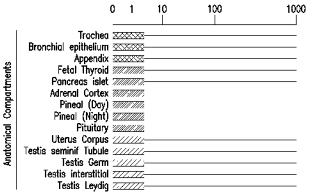

FIG. 1 (continued)

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CHIMERIC ANTIGEN RECEPTORS TARGETING FC RECEPTOR-LIKE 5 AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Patent Application Serial No. 62/088,164, filed December 5, 2014, the content of which is incorporated by reference in its entirety, and to which priority is claimed.

INTRODUCTION

The presently disclosed subject matter provides for methods and compositions for treating cancer. It relates to chimeric antigen receptors (CARs) that specifically target Fc Receptor-like 5 (FcRL5), *e.g.*, domain 9 of FcRL5, immunoresponsive cells comprising such CARs, and methods of using such cells for treating cancer (*e.g.*, multiple myeloma).

BACKGROUND OF THE INVENTION

Cell-based immunotherapy is a therapy with curative potential for the treatment of cancer. T cells and other immune cells may be modified to target tumor antigens through the introduction of genetic material coding for artificial or synthetic receptors for antigen, termed Chimeric Antigen Receptors (CARs), specific to selected antigens. Targeted T cell therapy using CARs has shown recent clinical success in treating hematologic malignancies.

Multiple myeloma (MM) is the second most common hematologic malignancy mortality (Siegel *et al.*, *CA:a cancer journal for clinicians* 63, 11-30 (2013)). Approximately 25% of patients have high-risk cytogenetics, which portends a median survival of less then 2 years (Boyd *et al.*, *Genes, chromosomes & cancer* 50, 765-774 (2011); Shaughnessy *et al.*, *Blood* 109, 2276-2284 (2007)). While recent strides have been made, regardless of cytogenetics, the disease is still considered incurable outside the immuno-therapeutic graft versus myeloma (GvM) effect of an allogeneic transplant. However, allogeneic transplants are limited by ineligibility and high rates of transplant-associated morbidity and mortality (Gahrton *et al.*, *The New England journal of medicine* 325, 1267-1273 (1991)). Similar to the GvM effect, a potentially curative T cell effect may be achieved with minimal toxicity through autologous adoptive T cell therapy.

Myeloma is expected to be an ideal disease to test adoptive T cell therapy. First, allogeneic transplants demonstrate that the T cell can be a curative treatment, even with minimal or no concomitant chemotherapy such as after non-myeloablative transplants or post-transplantation donor lymphocyte infusions. Second, conditioning chemotherapy, possibly through the mechanism of depleting regulatory T cells (Tregs), enhances the efficacy of adoptive T cell therapy (Brentjens *et al.*, *Blood* 118, 4817-4828 (2011) and Pegram *et al.*, *Blood* 119, 4133-4141 (2012)) as such, the immediate post-autologous transplant period could be an optimal time to administer T cells, and myeloma is one of the few diseases where autologous stem cell transplantation is the standard of care. Third, the immunomodulatory drug lenalidomide may improve CAR based therapy, as has been shown in mice (Bertilaccio *et al.*, *Blood* 122, 4171 (2013)), and lenalidomide is commonly used to treat MM. Fourth, adoptive T cell therapy works best in bone marrow predominant disease such as ALL (Brentjens *et al.*, *Science translational medicine* 5, 177ra138 (2013); Davila *et al.*, *Science translational medicine* 6, 224ra225 (2014)), when compared to solid tumors or extra-medullary CLL (Brentjens *et al.* (2011)) and similar to ALL, myeloma is a disease of the bone marrow.

While there are various reasons to expect that adoptive T cell therapy may work well in MM, expanding adoptive T cell therapy to myeloma poses unique challenges. Unlike other B-cell malignancies, CD19 expression is seen in only 2% of myeloma patients (Bataille *et al.*, *Haematologica* 91, 1234-1240 (2006)). Furthermore, unlike CD19, the common extracellular immunophenotypic markers in myeloma (CD138, CD38, and CD56) are all co-expressed on other essential cell types, and CARs to any of these targets could lead to unacceptable "off tumor, on target" toxicity (Brentjens *et al.* (2013)) which can be fatal even in targets where antibodies are well tolerated, as was the case with a HER2 targeted CAR (Morgan *et al.*, *Molecular therapy: the journal of the American Society of Gene Therapy* 18, 843-851 (2010)). Accordingly, there are needs for novel therapeutic strategies to design CARs targeting antigens that are highly expressed in MM cells and limited expression in normal tissues for treating multiple myeloma, which strategies capable of inducing potent tumor eradication with minimal toxicity and immunogenicity.

SUMMARY OF THE INVENTION

The presently disclosed subject matter generally provides chimeric antigen receptors (CARs) that specifically target Fc Receptor-like 5 (FcRL5), immunoresponsive cells comprising such CARs, and uses of these CARs and immunoresponsive cells for treating multiple myeloma.

The presently disclosed subject matter provides CARs. In one non-limiting example, the CAR comprises an extracellular antigen-binding domain, a transmembrane domain and an intracellular domain, where the extracellular antigen-binding domain specifically binds to FcRL5. In certain embodiments, the extracellular antigen-binding domain binds to domain 9 of FcRL5.

In certain non-limiting embodiments, the extracellular antigen-binding domain is a single-chain variable fragment (scFv). In certain embodiments, the extracellular antigen-binding domain is a murine scFv. In certain embodiments, the extracellular antigen-binding domain is a human scFv. In certain non-limiting embodiments, the extracellular antigen-binding domain is a Fab, which is optionally crosslinked. In certain non-limiting embodiments, the extracellular binding domain is a $F(ab)_2$. In certain non-limiting embodiments, any of the foregoing molecules can be comprised in a fusion protein with a heterologous sequence to form the extracellular antigen-binding domain. In certain embodiments, the extracellular antigen-binding domain specifically binds to FcRL5 with a binding affinity (K_d) of from about 1×10^{-11} M to about 3×10^{-6} M, 1×10^{-10} M to about 3×10^{-6} M or 1×10^{-9} M to about 3×10^{-6} M. In certain embodiments, the extracellular antigen-binding domain specifically binds to domain 8 or 9 of FcRL5 with a K_d of from about 1×10^{-9} M to about 3×10^{-6} M.

In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID

NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917 and SEQ ID NO:921, wherein the extracellular antigen-binding domain binds to FcRL5.

In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:915 and SEQ ID NO:919, wherein the extracellular antigen-binding domain binds to FcRL5.

In certain embodiments, the extracellular antigen-binding domain comprises (a) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917 and SEQ ID NO:921; and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID

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In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917, SEQ ID NO:921 and conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16,

SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:915, SEQ ID NO:919 and conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:915. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:917. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:919. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:921. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:144. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:143. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:216. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:215. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:220. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:219. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:236. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:235. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:268. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:267. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:116. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:115. In certain embodiments, the extracellular antigen-binding domain comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:172. In certain embodiments, the extracellular antigen-binding domain comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:171.

In certain embodiments, the extracellular antigen-binding domain comprises (a) a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ

ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917, SEQ ID NO:921 and conservative modifications thereof; and (b) a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:915, SEQ ID NO:919 and conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:915; and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:917. In certain embodiments, the extracellular antigen-binding domain comprises extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:919; and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:921. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:144, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:143. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:216, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:215. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:220, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:219. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:236, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:235. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:268, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:267. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:116, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:115. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:172, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:171.

In certain non-limiting embodiments, the extracellular antigen-binding domain comprises both of said heavy and light chains, optionally with a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. For example, in certain non-limiting embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:915, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:917, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:919 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:92, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:144 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:143, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:216 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:215, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:220 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:219, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:236 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:235, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:268 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:267, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:116 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:115, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region. In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:172 and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:171, optionally with (c) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 311, 317, 323, 328, 334, 337, 342, 347, 351, 356, 362, 368, 374, 376, 380, 384, 389, 394, 396, 400, 405, 408, 412, 415, 422, 427, 432, 437, 442, 446, 451, 453, 456, 458, 459, 463, 464, 467, 473, 476, 482, 486, 489, 492, 494, 497, 502, 507, 512, 517, 522, 527, 529, 532, 536, 539, 543, 546, 550, 553, 555, 561, 567, 570, 574, 577, 578, 579, 584, 578, 587, 591, 925 and 931; and (b) a light chain variable region CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 314, 320, 325, 331, 339, 345, 350, 353, 359, 365, 371, 377, 383, 386, 392, 395, 399, 402, 407, 410, 414, 418, 419, 424, 430, 435, 439, 443, 449, 452, 455, 457, 462, 465, 470, 479, 485, 488, 491, 493, 495, 499, 505, 509, 514, 519, 524, 528, 530, 531, 535, 541, 542, 545, 549, 554, 558, 564, 569, 573, 576, 581, 592, 928 and 934.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 309, 315, 321, 326, 332, 335, 340, 346, 354, 360, 366, 372, 378, 387, 393, 403, 411, 420, 425, 436, 440, 444, 471, 480, 500, 510, 515, 520, 525, 537, 551, 559, 565, 582, 589, 923 and 929; (b) a heavy chain variable region CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 310, 316, 322, 327, 333, 336, 341, 355, 361, 367, 373, 379, 388, 404, 412, 421, 426, 431, 441, 445, 450, 466, 472, 475, 481, 496, 501, 506, 511, 516, 521, 526, 538, 552, 560, 566, 583, 590, 924 and 930; (c) a heavy chain variable region CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 311, 317, 323, 328, 334, 337, 342, 347, 351, 356, 362, 368, 374, 376, 380, 384, 389, 394, 396, 400, 405, 408, 412, 415, 422, 427, 432, 437, 442, 446, 451, 453, 456, 458, 459, 463, 464, 467, 473, 476, 482, 486, 489, 492, 494, 497, 502, 507, 512, 517, 522, 527, 529, 532, 536, 539, 543, 546, 550, 553, 555, 561, 567, 570, 574, 577, 578, 579, 584, 578, 587, 591, 925 and 931; (d) a light chain variable region CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 312, 318, 324, 329, 338, 343, 348, 352, 357, 363, 369, 381, 390, 397, 401, 406, 416, 423, 428, 433, 447, 460, 468, 474, 477, 483, 490, 498, 503, 508, 518, 533, 540, 544, 547, 556, 562, 568, 571, 580, 585, 588, 926 and 932; (e) a light chain variable region CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 313, 319, 330, 344, 349, 358, 364, 370, 382, 385, 391, 398, 409, 417, 429, 434, 438, 448, 454, 461, 469, 478, 484, 487, 504, 513, 523, 534, 429, 448, 548, 557, 563, 572, 575, 586, 927 and 933; and (f) a light chain variable region CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 314, 320, 325, 331, 339, 345, 350, 353, 359, 365, 371, 377, 383, 386, 392, 395, 399, 402, 407, 410, 414, 418, 419, 424, 430, 435, 439, 443, 449, 452, 455, 457, 462, 465, 470, 479, 485, 488, 491, 493, 495, 499, 505, 509, 514, 519, 524, 528, 530, 531, 535, 541, 542, 545, 549, 554, 558, 564, 569, 573, 576, 581, 592, 928 and 934.

In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:923 or conservative modifications thereof, (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:924 or conservative modifications thereof, and (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:925 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises (a) a light chain variable region

CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:926 or conservative modifications thereof, (b) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:927 or conservative modifications thereof, and (c) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:928 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:929 or conservative modifications thereof, (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:930 or conservative modifications thereof, and (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:931 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises (a) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:932 or conservative modifications thereof, (b) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:933 or conservative modifications thereof, and (c) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:934 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:923 or conservative modifications thereof, (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:924 or conservative modifications thereof, (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:925 or conservative modifications thereof, (d) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:926 or conservative modifications thereof, (e) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:927 or conservative modifications thereof, and (f) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:928 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises:

(a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:929 or conservative modifications thereof, (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:930 or conservative modifications thereof, (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:931 or conservative modifications thereof, (d) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:932 or conservative modifications thereof, (e) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:933 or conservative modifications thereof, and (f) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:934 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:463 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:419 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:515 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:516 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:517 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:531 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:403 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:404 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:532 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:533 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:534 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:535.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:543 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:544 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:448 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:545 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:372 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:475 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:570 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:571 thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:572 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:573 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:440 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:441 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:442 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:329 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:330 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:443 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:309 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:310 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:489 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:490 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:313 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:491 or conservative modifications thereof.

In certain non-limiting embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:664 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:700 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:702 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:710 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:726 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:650 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises amino acids having the sequence set forth in SEQ ID NO:678 or conservative modifications thereof.

In certain non-limiting embodiments, the extracellular antigen-binding domain comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:923 or conservative modifications thereof, a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:924 or conservative modifications thereof, and a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:925 or conservative modifications thereof, and (ii) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:926 or conservative modifications thereof, a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:927 or conservative modifications thereof, and a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:928 or conservative modifications thereof, optionally with (iii) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In another non-limiting embodiment, the extracellular antigen-binding domain comprises (i) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:929 or conservative modifications thereof, a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:930 or conservative modifications thereof, and a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:931 or conservative modifications thereof, and (ii) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:932 or conservative modifications thereof, a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:933 or conservative modifications thereof, and a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:934 or conservative modifications thereof, optionally with (iii) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:463 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:419 or conservative modifications thereof, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:515 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:516 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:517 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:531 or conservative modifications thereof, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:403 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:404 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:532 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:533

or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:534 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:535, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:543 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:544 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:448 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:545 or conservative modifications thereof, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:372 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:475 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:570 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:571 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:572 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:573 or conservative modifications thereof, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises:

(a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:440 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:441 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:442 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:329 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:330 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:443 or conservative modifications thereof, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the extracellular antigen-binding domain comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:309 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:310 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:489 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:490 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:313 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:491 or conservative modifications thereof, optionally with (g) a linker sequence, for example a linker peptide, between the heavy chain variable region and the light chain variable region.

In certain embodiments, the linker peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:307 and SEQ ID NO:897.

In certain embodiments, the extracellular antigen-binding domain binds to FcRL5 comprising the amino acid sequence set forth in SEQ ID NO:899. In certain embodiments, the extracellular antigen-binding domain binds to an epitope comprising the amino acid sequence set forth in SEQ ID NO:964. In certain embodiments, the extracellular antigen-binding domain binds to an epitope comprising the amino acid sequence set forth in SEQ ID NO:965.

In accordance with the presently disclosed subject matter, the extracellular antigen-binding domain is covalently joined to a transmembrane domain. The extracellular antigen-binding domain can comprise a signal peptide that is covalently joined to the 5' terminus of the extracellular antigen-binding domain. In certain embodiments, the transmembrane domain of the CAR comprises a CD8 polypeptide, a CD28 polypeptide, a CD3ζ polypeptide, a CD4 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a CTLA-4 polypeptide, a PD-1 polypeptide, a LAG-3 polypeptide, a 2B4 polypeptide, a BTLA polypeptide, a synthetic peptide (not based on a protein associated with the immune response), or a combination thereof. In a non-limiting embodiment, the transmembrane domain comprises a CD8 polypeptide. In certain embodiments, the transmembrane domain comprises a CD28 polypeptide.

In accordance with the presently disclosed subject matter, in certain embodiments, the intracellular domain comprises a CD3ζ polypeptide. In certain embodiments, the intracellular domain further comprises at least one signaling region. In certain embodiments, the at least one signaling region comprises a CD28 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a DAP-10 polypeptide, a PD-1 polypeptide, a CTLA-4 polypeptide, a LAG-3 polypeptide, a 2B4 polypeptide, a BTLA polypeptide, a synthetic peptide (not based on a protein associated with the immune response), or a combination thereof. In certain embodiments, the signaling region is a co-stimulatory signaling region. In certain embodiments, the co-stimulatory signaling region comprises a CD28 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a DAP-10 polypeptide, or a combination thereof. In certain embodiments, the at least one co-stimulatory signaling region comprises a CD28 polypeptide. In certain non-limiting embodiments, the transmembrane domain comprises a CD28 polypeptide, the intracellular domain comprises a CD3ζ polypeptide, and the co-stimulatory signaling domain comprises a CD28 polypeptide. In certain non-limiting embodiments, the transmembrane domain comprises a CD8 polypeptide, the intracellular domain comprises a CD3ζ polypeptide, and the co-stimulatory signaling domain comprises a 4-1BB polypeptide.

In certain embodiments, the CAR is recombinantly expressed. The CAR can be expressed from a vector. In certain embodiments, the vector is a γ-retroviral rector.

The presently disclosed subject matter also provides isolated immunoresponsive cells comprising the above-described CARs. In certain embodiments, the isolated immunoresponsive cell is transduced with the CAR, for example, the CAR is constitutively expressed on the surface of the immunoresponsive cell. In certain embodiments, the isolated immunoresponsive cell is further transduced with at least one co-stimulatory ligand such that the immunoresponsive cell expresses the at least one co-stimulatory ligand. In certain embodiments, the at least one co-stimulatory ligand is selected from the group consisting of 4-1BBL, CD80, CD86, CD70, OX40L, CD48, TNFRSF14, and combinations thereof. In certain embodiments, the isolated immunoresponsive cell is further transduced with at least one cytokine such that the immunoresponsive cell secrets the at least one cytokine. In certain embodiments, the at least one cytokine is selected from the group consisting of IL-2, IL-3, IL-6, IL-7, IL-11, IL-12, IL-15, IL-17, IL-21, and combinations thereof. In certain embodiments, the isolated immunoresponsive cell is selected from the group consisting of a T cell, a Natural Killer (NK) cell, a cytotoxic T lymphocyte (CTL), a regulatory T cell, a human embryonic stem cell, a lymphoid progenitor cell, a T cell-precursor cell, and a pluripotent stem cell from which lymphoid cells may be differentiated. In certain embodiments, the immunoresponsive cell is a T cell.

The presently disclosed subject matter further provides nucleic acid molecules encoding the presently disclosed CARs, vectors comprising the nucleic acid molecules, and host cells expressing such nucleic acid molecules. In certain embodiments, the nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:951. In certain embodiments, the nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:952. In certain embodiments, the vector is a γ-retroviral vector. In certain embodiments, the host cell is a T cell.

Furthermore, the presently disclosed subject matter provides methods of using the above-described immunoresponsive cell for reducing tumor burden in a subject. For example, the presently disclosed subject matter provides methods of reducing tumor burden in a subject, where the method comprises administering an effective amount of the presently disclosed immunoresponsive cell to the subject, thereby inducing tumor cell death in the subject. In certain embodiments, the method reduces the number of tumor cells. In another embodiment, the method reduces the tumor size. In yet another embodiment, the method eradicates the tumor in the subject. In certain embodiments, the tumor is selected from the group consisting of multiple myeloma, Non-Hodgkin Lymphoma (especially Mantle Cell), Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burketts Lymphoma, and Waldenstrom's Macroglobulinemia. In certain embodiments, the tumor is multiple myeloma. In certain embodiments, the subject is a human. In certain embodiments, the immunoresponsive cell is a T cell.

Furthermore, the presently disclosed subject matter provides methods of using the above-described immunoresponsive cell for increasing or lengthening survival of a subject having neoplasia. For example, the presently disclosed subject matter provides methods of increasing or lengthening survival of a subject having neoplasia, where the method comprises administering an effective amount of the presently disclosed immunoresponsive cell to the subject, thereby increasing or lengthening survival of the subject. In certain embodiments, the neoplasia is selected from the group consisting of multiple myeloma, Non-Hodgkin Lymphoma (especially Mantle Cell), Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burketts Lymphoma, and Waldenstrom's Macroglobulinemia. In certain embodiments, the neoplasia is multiple myeloma. In certain embodiments, the method reduces or eradicates tumor burden in the subject.

The presently disclosed subject matter also provides methods for producing an immunoresponsive cell that binds to Fc Receptor-like 5 (FcRL5), *e.g.*, domain 9 of FcRL5. In one non-limiting example, the method comprises introducing into the immunoresponsive cell a nucleic acid sequence that encodes a chimeric antigen receptor (CAR), which comprises an extracellular antigen-binding domain, a transmembrane domain and an intracellular domain, wherein the extracellular antigen-binding domain specifically binds to Fc Receptor-like 5 (FcRL5). In a specific non-limiting embodiment, the extracellular antigen-binding domain is an scFv.

The presently disclosed subject matter further provides pharmaceutical compositions comprising an effective amount of the presently disclosed immunoresponsive cells and a pharmaceutically acceptable excipient. In certain embodiments, the pharmaceutical compositions are for treating a neoplasia. In certain embodiments, the neoplasia is selected from the group consisting of multiple myeloma, Non-Hodgkin Lymphoma (especially Mantle Cell), Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burketts Lymphoma, and Waldenstrom's Macroglobulinemia. In certain embodiments, the neoplasia is multiple myeloma.

The presently disclosed subject matter further provides kits for treating a neoplasia, comprising the presently disclosed immunoresponsive cells. In certain embodiments, the kit further include written instructions for using the immunoresponsive cell for treating a neoplasia. In certain embodiments, the neoplasia is selected from the group consisting of multiple myeloma, Non-Hodgkin Lymphoma (especially Mantle Cell), Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burketts Lymphoma, and Waldenstrom's Macroglobulinemia. In certain embodiments, the neoplasia is multiple myeloma.

In a first aspect, the present invention provides a chimeric antigen receptor (CAR), comprising an extracellular antigen-binding domain that binds to Fc Receptor-like 5 (FcRL5), a transmembrane domain, and an intracellular domain, wherein the extracellular antigen-binding domain comprises:

(aa) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:311;

(ab) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:320; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 315, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:316, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:317;

(ac) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 324, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:325 and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 321, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:322, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:323;

(ad) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NOs: 329, 330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:331; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 326, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:328;

(ae) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:331; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 332, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:333, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:334;

(af) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 338, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:339; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 335, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:336, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:337;

(ag) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 343, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:344, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:345; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 340, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:341, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:342;

(ah) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 348, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:349, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:350; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:347;

(ai) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 352, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:344, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:353; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:351;

(aj) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 357, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:358, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:359; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 354, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:355, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:356;

(ak) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 363, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:364, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:365; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NOs: 360, 361, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:362;

(al) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 369, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:370, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:371; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 366, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:367, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:368;

(am) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:375; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:373, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:374;

(an) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:377; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:376;

(ao) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 381, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:382, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:383; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 378, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:379, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:380;

(ap) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:385, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:386; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:384;

(aq) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 390, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:391, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:392; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 387, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:389;

(ar) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:395; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 393, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:355, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:394;

(as) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 397, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:399; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:396;

(at) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 401, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:402; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:400;

(au) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:407; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:405;

(av) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:409, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:410; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:408;

(aw) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:414; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:413;

(ax) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 416, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:417, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:418; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:415;

(ay) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:419 and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:349;

(az) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 423, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:358, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:424; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 420, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:421, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:422;

(ba) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 428, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:429, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:430; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 425, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:426, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:427;

(bb) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 433, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:434, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:435; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:431, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:432;

(bc) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 423, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:438, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:439; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 436, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:437;

(bd) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:443 and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 440, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:441, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:442;

(be) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 447, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:448, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:449; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 444, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:445, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:446;

(bf) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:452 and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:450, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:451;

(bg) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 369, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:454, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:455; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:453;

(bh) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:457; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:456;

(bi) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:331; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:458;

(bj) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 460, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:461, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:462; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:459;

(bk) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:419; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:463;

(bl) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 423, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:438, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:465; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 436, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:464;

(bm) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 468, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:469, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:470; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:466, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:467;

(bn) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 474, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:358, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:465; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 471, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:472, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:473;

(bo) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 477, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:478, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:479; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:475, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:476;

(bp) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 483, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:484, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:485; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 480, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:481, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:482;

(bq) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 433, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:487, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:488; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:486;

(br) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 490, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:491; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:489;

(bs) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:493; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:492;

(bt) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 490, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:349, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:495; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:494;

(bu) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 498, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:344, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:499; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:496, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:497;

(bv) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 503, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:504, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:505; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 500, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:501, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:502;

(bw) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 508, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:349, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:509; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:506, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:507;

(bx) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:513, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:514; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 510, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:511, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:512;

(by) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 518, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:519; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 515, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:516, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:517;

(bz) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 348, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:523, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:524; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 520, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:521, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:522;

(ca) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:528; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 525, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:526, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:527;

(cb) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:530; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:529;

(cc) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:531; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 515, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:516, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:517;

(cd) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 533, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:534, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:535; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:532;

(ce) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 428, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:429, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:430; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 425, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:426, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:536;

(cf) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 540, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:541; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 537, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:538, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:539;

(cg) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:542; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 537, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:538, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:539;

(ch) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 544, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:448, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:545; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:543;

(ci) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 547, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:548, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:549; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:546;

(cj) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:550;

(ck) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:513, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:550;

(cl) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:554; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 551, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:552, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:553;

(cm) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 556, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:557, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:558; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:555;

(cn) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 562, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:563, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:564; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 559, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:560, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:561;

(co) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 568, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:504, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:569; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 565, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:566, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:567;

(cp) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 571, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:572, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:573; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:475, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:570;

(cq) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 343, a CDR2 comprising the amino acid sequence set forth in

SEQ ID NO:575, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:576; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NOs: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:574;

(cr) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:577;

(cs) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:578;

(ct) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 580, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:438, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:581; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 436, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:579;

(cu) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 585, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 582, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:583, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:584;

(cv) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:586, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID

NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:578;

(cw) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 588, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:385, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:375; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:587;

(cx) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:592; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 589, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:590, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:591;

(cy) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 926, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:927, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:928; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 923, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:924, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:925; or

(cz) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 932, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:933, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:934; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 929, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:930, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:931.

In a second aspect, the present invention provides a chimeric antigen receptor (CAR), comprising an extracellular antigen-binding domain that binds to Fc Receptor-like 5 (FcRL5), a transmembrane domain, and an intracellular domain, wherein the extracellular antigen-binding domain comprises:

(aa) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:3, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth

in SEQ ID NO:4;

(ab) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:7, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:8;

(ac) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:11, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:12;

(ad) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:299, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:300;

(ae) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:15, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:16;

(af) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:19, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:20;

(ag) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:23, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:24;

(ah) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:27, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:28;

(ai) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:31, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:32;

(aj) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:35, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:36;

(ak) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:39, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:40;

(al) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:43, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:44;

(am) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:47, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:48;

(an) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:51, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:52;

(ao) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:55, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:56;

(ap) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:59, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:60;

(aq) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:63, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:64;

(ar) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light

chain variable region sequence set forth in SEQ ID NO:67, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:68;

(as) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:71, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:72;

(at) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:75, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:76;

(au) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:79, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:80;

(av) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:83, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:84;

(aw) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:87, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:88;

(ax) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:91, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:92;

(ay) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:95, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:96;

(az) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:99, and a heavy chain variable region

comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:100;

(ba) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:103, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:104;

(bb) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:107, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:108;

(bc) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:111, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:112;

(bd) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:115, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:116;

(be) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:119, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:120;

(bf) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:123, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:124;

(bg) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:127, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:128;

(bh) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:131, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth

in SEQ ID NO:132;

(bi) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:135, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:136;

(bj) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:139, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:140;

(bk) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:143, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:144;

(bl) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:147, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:148;

(bm) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:151, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:152;

(bn) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:155, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:156;

(bo) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:159, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:160;

(bp) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:163, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:164;

(bq) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:167, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:168;

(br) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:171, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:172;

(bs) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:175, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:176;

(bt) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:179, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:180;

(bu) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:183, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:184;

(bv) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:187, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:188;

(bw) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:191, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:192;

(bx) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:195, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:196;

(by) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light

chain variable region sequence set forth in SEQ ID NO:199, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:200;

(bz) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:203, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:204;

(ca) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:207, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:208;

(cb) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:211, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:212;

(cc) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:215, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:216;

(cd) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:219, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:220;

(ce) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:223, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:224;

(cf) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:227, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:228;

(cg) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:231, and a heavy chain variable region

comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:232;

(ch) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:235, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:236;

(ci) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:239, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:240;

(cj) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:243, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:244;

(ck) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:247, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:248;

(cl) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:251, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:252;

(cm) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:255, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:256;

(cn) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:259, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:260;

(co) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:263, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth

in SEQ ID NO:264;

(cp) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:267, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:268;

(cq) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:271, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:272;

(cr) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:275, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:276;

(cs) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:279, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:280;

(ct) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:283, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:284;

(cu) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:287, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:288;

(cv) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:291, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:292;

(cw) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:303, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:304;

(cx) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:295, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:296;

(cy) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:915, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:917; or

(cz) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:919, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:921.

In a third aspect, the present invention provides a nucleic acid molecule encoding the chimeric antigen receptor (CAR) of the first or second aspect.

In a fourth aspect, the present invention provides a vector comprising the nucleic acid molecule of the third aspect.

In a fifth aspect, the present invention provides an immunoresponsive cell comprising the CAR of the first or second aspect, the nucleic acid molecule of the third aspect or the vector of the fourth aspect.

In a sixth aspect, the present invention provides a T cell comprising the CAR of the first or second aspect, the nucleic acid molecule of the third aspect or the vector of the fourth aspect.

In a seventh aspect, the present invention provides a method of reducing tumor burden or increasing or lengthening survival of a subject having a tumor expressing FcRL5, comprising administering to the subject an effective amount of the immunoresponsive cell of the fifth aspect or the T cell of the sixth aspect.

In an eighth aspect, the present invention provides a method for producing an immunoresponsive cell that binds to Fc Receptor-like 5 (FcRL5), comprising introducing into the immunoresponsive cell a nucleic acid sequence that encodes the chimeric antigen receptor (CAR) of the first or second aspect, the nucleic acid molecule of the third aspect or the vector of the fourth aspect.

In a ninth aspect, the present invention provides an immunoresponsive cell that binds to Fc Receptor-like 5 (FcRL5) produced by the method of the eighth aspect.

In a tenth aspect, the present invention provides a pharmaceutical composition comprising an effective amount of the immunoresponsive cell of the fifth or ninth aspect or the T cell of the sixth aspect.

In an eleventh aspect, the present invention provides a kit for treating a tumor expressing FcRL5, comprising the immunoresponsive cell of the fifth aspect or the T cell of the sixth aspect.

In a twelfth aspect, the present invention provides the use of an effective amount of the immunoresponsive cell of the fifth aspect or the T cell of the sixth aspect in the manufacture of a medicament for treating a tumor expressing FcRL5 in a subject.

BRIEF DESCRIPTION OF THE FIGURES

The following Detailed Description, given by way of example, but not intended to limit the invention to specific embodiments described, may be understood in conjunction with the accompanying drawings.

Figure 1 depicts the FcRL5 expression in various normal tissues and human cancer cell lines.

Figure 2 depicts the screening of anti-FcRL5 scFvs using 3T3 cells expressing FcRL5 or FcRL1, 2, 3, 4 or 6.

Figure 3A-D. (A) A representation of the domains of FcRL5 and the soluble, glycosylphosphatidylinositol (GPI)-anchored and transmembrane forms of FcRL5. (B) A representation of the vector used to express a mutated form of FcRL5 that lacks domain 9 (also referred to herein as FcRL5Δdom9). (C) The nucleotide sequences of full length FcRL5 and the form of FcRL5 that lacks domain 9. (D) A representation of the differences in the nucleotide sequences of full length FcRL5 and the mutated form of FcRL5 in which domain 9 is deleted (referred to herein as "FcRL5Δdom9").

Figure 4 depicts the screening of anti-FcRL5 scFv ET200-39 on 3T3 cells expressing FcRL5Δdom9.

[Text continues on page 26.]

Figure 5 depicts the screening of anti-FcRL5 scFv ET200-104 on 3T3 cells expressing FcRL5Δdom9.

Figure 6 depicts the screening of anti-FcRL5 scFv ET200-105 on 3T3 cells expressing FcRL5Δdom9.

Figure 7 depicts the screening of anti-FcRL5 scFv ET200-109 on 3T3 cells expressing FcRL5Δdom9.

Figure 8 depicts the screening of anti-FcRL5 scFv ET200-117 on 3T3 cells expressing FcRL5Δdom9.

Figure 9A-B. Schematics of chimeric antigen receptor targeting FcRL5 in accordance with non-limiting embodiments of the presently disclosed subject matter. (A) Schematic of FcRL5-targeted CAR with CD28 co-stimulatory domain and CD3zeta. (B) Schematic of FcRL5-targeted CAR with 4-1BB co-stimulatory domain and CD3zeta.

Figure 10 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-31 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 11 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-39 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 12 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-69 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 13 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-104 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 14 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-105 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 15 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-109 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 16 depicts the vector map of a chimeric antigen receptor targeting FcRL5 using scFV ET200-117 in accordance with one non-limiting embodiment of the presently disclosed subject matter.

Figure 17 depicts the expression of FcRL5-targeted chimeric antigen receptors on the surface of transduced T cells.

Figure 18 depicts the cytotoxicity of FcRL5-targeted chimeric antigen receptor T cells for FcRL5-expressing cells.

Figure 19 depicts the induction of cytokine secretion of FcRL5-targeted chimeric antigen receptor T cells.

Figure 20 depicts the proliferation of FcRL5-targeted chimeric antigen receptor T cells upon antigen stimulation.

Figure 21 illustrates the CLIPS technology. The CLIPS reaction takes place between bromo groups of the CLIPS scaffold and thiol sidechains of cysteines. The reaction is fast and specific under mild conditions. Using this elegant chemistry, native protein sequences are transformed into CLIPS constructs with a range of structures. From left to right: two different single T2 loops, T3 double loop, conjugated T2+T3 loops, stabilized beta sheet, and stabilized alpha helix (Timmerman et al., J. Mol. Recognit. 2007; 20: 283-29).

Figure 22 illustrates combinatorial clips library screening. The target protein (left) containing a discontinuous conformational epitope is converted into a matrix library (middle). Combinatorial peptides are synthesized on a proprietary minicard and chemically converted into spatially defined CLIPS constructs (right).

Figure 23 depicts T3 looped CLIPSTM construct.

Figure 24A-D illustrates heat map technology. (A) Table of combined peptides, with two sub-sequences indicated as “Loop 1” and “Loop 2.” (B) Data from A displayed as a matrix. (C) Color bar indication of the heat map representation. (D) Heat map visualization of data from A.

Figure 25 shows heatmap analysis of data recorded for Herceptin.

Figure 26 shows heatmap analysis of data recorded for ET200-104.

Figure 27 illustrates a 3D model of amino acid residues 380-731 of FcRL55 with peptide stretch $_{657}$SRPILTFRAPR$_{667}$ highlighted.

DETAILED DESCRIPTION OF THE INVENTION

The presently disclosed subject matter generally provides FcRL5-targeted chimeric antigen receptors (CARs). In one non-limiting example, the CAR comprises an extracellular antigen-binding domain, a transmembrane domain and an intracellular domain, where the extracellular antigen-binding domain specifically binds to FcRL5. In certain embodiments, the extracellular antigen-binding domain specifically binds to domain 7, 8 or 9 of FcRL5. The presently disclosed subject matter also provides immunoresponsive cells (*e.g.*, T cell, a Natural Killer (NK) cell, a cytotoxic T lymphocyte (CTL), a regulatory T cell, a human embryonic stem cell, a lymphoid progenitor cell, a T cell-precursor cell, and a pluripotent stem cell from which lymphoid cells may be differentiated) expressing the FcRL5-targeted CARs, and methods of using such immunoresponsive cells for treating a tumor, *e.g.*, multiple myeloma.

I. Definitions

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton et al., Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); The Glossary of Genetics, 5th Ed., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, The Harper Collins Dictionary of Biology (1991). As used herein, the following terms have the meanings ascribed to them below, unless specified otherwise.

As used herein, the term "about" or "approximately" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, *i.e.*, the limitations of the measurement system. For example, "about" can mean within 3 or more than 3 standard deviations, per the practice in the art. Alternatively, "about" can mean a range of up to 20%, preferably up to 10%, more preferably up to 5%, and more preferably still up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 5-fold, and more preferably within 2-fold, of a value.

As used herein, the term "cell population" refers to a group of at least two cells expressing similar or different phenotypes. In non-limiting examples, a cell population can include at least about 10, at least about 100, at least about 200, at least about 300, at least about 400, at least about 500, at least about 600, at least about 700, at least about 800, at least about 900, at least about 1000 cells expressing similar or different phenotypes.

As used herein, the term "antibody" means not only intact antibody molecules, but also fragments of antibody molecules that retain immunogen-binding ability. Such fragments are also well known in the art and are regularly employed both *in vitro* and *in vivo*. Accordingly, as used herein, the term "antibody" means not only intact immunoglobulin molecules but also the well-known active fragments F(ab')$_2$, and Fab. F(ab')$_2$, and Fab fragments that lack the Fe fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding of an intact antibody (Wahl et al., *J. Nucl. Med.* 24:316-325 (1983). The antibodies of the invention comprise whole native antibodies, bispecific antibodies; chimeric antibodies; Fab, Fab', single chain V region fragments (scFv), fusion polypeptides, and unconventional antibodies.

As used herein, the term "single-chain variable fragment" or "scFv" is a fusion protein of the variable regions of the heavy (V_H) and light chains (V_L) of an immunoglobulin (*e.g.*, mouse or human) covalently linked to form a V_H::VL heterodimer. The heavy (V_H) and light chains (V_L) are either joined directly or joined by a peptide-encoding linker (*e.g.*, 10, 15, 20, 25 amino acids), which connects the N-terminus of the V_H with the C-terminus of the V_L, or the C-terminus of the V_H with the N-terminus of the V_L. The linker is usually rich in glycine for flexibility, as well as serine or threonine for solubility. The linker can link the heavy chain variable region and the light chain variable region of the extracellular antigen-binding domain. Non-limiting examples of linkers are disclosed in Shen et al., Anal. Chem. 80(6):1910-1917 (2008) and WO 2014/087010, the contents of which are hereby incorporated by reference in their entireties. In certain embodiments, the linker is a G4S linker.

In a non-limiting example, the linker comprises amino acids having the sequence set forth in SEQ ID NO:897 as provided below.

`GGGGSGGGGSGGGGS [SEQ ID NO: 897].` In certain embodiments, the nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:897 is set forth in SEQ ID NO:898, which is provided below:

`GGTGGAGGTGGATCAGGTGGAGGTGGATCTGGTGGAGGTGGATCT [SEQ ID NO:898].`

In another non-limiting example, the linker comprises amino acids having the sequence set forth in SEQ ID NO:307 as provided below: `SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO:307].` In certain embodiments, the nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:307 is set forth in SEQ ID NO:305, which is provided below: `TCTAGAGGTGGTGGTGGTAGCGGCGGCGGCGGCTCTGGTGGTGGTGGATCCCTCGAGATGGCC [SEQ ID NO: 305].`

Despite removal of the constant regions and the introduction of a linker, scFv proteins retain the specificity of the original immunoglobulin. Single chain Fv polypeptide antibodies can be expressed from a nucleic acid comprising V_H - and V_L -encoding sequences as described by Huston, et al. (Proc. Nat. Acad. Sci. USA, 85:5879-5883, 1988). See, also, U.S. Patent Nos. 5,091,513, 5,132,405 and 4,956,778; and U.S. Patent Publication Nos. 20050196754 and 20050196754. Antagonistic scFvs having inhibitory activity have been described (see, *e.g.*, Zhao et al., Hyrbidoma (Larchmt) 2008 27(6):455-51; Peter et al., J Cachexia Sarcopenia Muscle 2012 August 12; Shieh et al., J Imunol2009 183(4):2277-85; Giomarelli et al., Thromb Haemost 2007 97(6):955-63; Fife eta., J Clin Invst 2006 116(8):2252-61; Brocks et al., Immunotechnology 1997 3(3):173-84; Moosmayer et al., Ther Immunol 1995 2(10:31-40). Agonistic scFvs having stimulatory activity have been described (see, *e.g.*, Peter et al., J Bioi Chern 2003 25278(38):36740-7; Xie et al., Nat Biotech 1997 15(8):768-71; Ledbetter et al., Crit Rev Immunol1997 17(5-6):427-55; Ho et al., BioChim Biophys Acta 2003 1638(3):257-66).

As used herein, “F(ab)” refers to a fragment of an antibody structure that binds to an antigen but is monovalent and does not have a Fc portion, for example, an antibody digested by the enzyme papain yields two F(ab) fragments and an Fc fragment (*e.g.*, a heavy (H) chain constant region; Fc region that does not bind to an antigen).

As used herein, “$F(ab')_2$” refers to an antibody fragment generated by pepsin digestion of whole IgG antibodies, wherein this fragment has two antigen binding (ab’) (bivalent) regions, wherein each (ab’) region comprises two separate amino acid chains, a part of a H chain and a light (L) chain linked by an S-S bond for binding an antigen and where the remaining H chain portions are linked together. A “$F(ab')_2$” fragment can be split into two individual Fab’ fragments.

As used herein, the term “vector” refers to any genetic element, such as a plasmid, phage, transposon, cosmid, chromosome, virus, virion, etc., which is capable of replication when associated with the proper control elements and which can transfer gene sequences into cells. Thus, the term includes cloning and expression vehicles, as well as viral vectors and plasmid vectors.

As used herein, the term "expression vector" refers to a recombinant nucleic acid sequence, *i.e.*, recombinant DNA molecule, containing a desired coding sequence and appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequence in a particular host organism. Nucleic acid sequences necessary for expression in prokaryotes usually include a promoter, an operator (optional), and a ribosome binding site, often along with other sequences. Eukaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals.

As used herein, "CDRs" are defined as the complementarity determining region amino acid sequences of an antibody which are the hypervariable regions of immunoglobulin heavy and light chains. See, *e.g.*, Kabat et al., Sequences of Proteins of Immunological Interest, 4th U. S. Department of Health and Human Services, National Institutes of Health (1987). Generally, antibodies comprise three heavy chain and three light chain CDRs or CDR regions in the variable region. CDRs provide the majority of contact residues for the binding of the antibody to the antigen or epitope. In certain embodiments, the CDRs regions are delineated using the Kabat system (Kabat, E. A., et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242).

As used herein, the term "affinity" is meant a measure of binding strength. Without being bound to theory, affinity depends on the closeness of stereochemical fit between antibody combining sites and antigen determinants, on the size of the area of contact between them, and on the distribution of charged and hydrophobic groups. Affinity also includes the term "avidity," which refers to the strength of the antigen-antibody bond after formation of reversible complexes. Methods for calculating the affinity of an antibody for an antigen are known in the art, comprising use of binding experiments to calculate affinity. Antibody activity in functional assays (*e.g.*, flow cytometry assay) is also reflective of antibody affinity. Antibodies and affinities can be phenotypically characterized and compared using functional assays (*e.g.*, flow cytometry assay).

Nucleic acid molecules useful in the methods of the invention include any nucleic acid molecule that encodes a polypeptide of the invention or a fragment thereof. Such nucleic acid molecules need not be 100% identical with an endogenous nucleic acid sequence, but will typically exhibit substantial identity. Polynucleotides having "substantial identity" to an endogenous sequence are typically capable of hybridizing with at least one strand of a double-stranded nucleic acid molecule. By "hybridize" is meant pair to form a double-stranded molecule between complementary polynucleotide sequences (*e.g.*, a gene described herein), or portions thereof, under various conditions of stringency. (See, *e.g.*, Wahl, G. M. and S. L. Berger (1987) Methods Enzymol. 152:399; Kimmel, A. R. (1987) Methods Enzymol. 152:507).

For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and more preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, *e.g.*, formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and more preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, *e.g.*, sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred: embodiment, hybridization will occur at 30° C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37° C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 μg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42° C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50% formamide, and 200 μg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

For most applications, washing steps that follow hybridization will also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include a temperature of at least about 25° C, more preferably of at least about 42° C, and even more preferably of at least about 68° C. In a preferred embodiment, wash steps will occur at 25° C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42° C. in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 68° C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art. Hybridization techniques are well known to those skilled in the art and are described, for example, in Benton and Davis (Science 196:180, 1977); Grunstein and Rogness (Proc. Natl. Acad. Sci., USA 72:3961, 1975); Ausubel et al. (Current Protocols in Molecular Biology, Wiley Interscience, New York, 2001); Berger and Kimmel (Guide to Molecular Cloning Techniques, 1987, Academic Press, New York); and Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York.

By “substantially identical” is meant a polypeptide or nucleic acid molecule exhibiting at least 50% identity to a reference amino acid sequence (for example, any one of the amino acid sequences described herein) or nucleic acid sequence (for example, any one of the nucleic acid sequences described herein). Preferably, such a sequence is at least 60%, more preferably 80% or 85%, and more preferably 90%, 95% or even 99% identical at the amino acid level or nucleic acid to the sequence used for comparison.

Sequence identity is typically measured using sequence analysis software (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wis. 53705, BLAST, BESTFIT, GAP, or PILEUP/PRETTYBOX programs). Such software matches identical or similar sequences by assigning degrees of homology to various substitutions, deletions, and/or other modifications. In an exemplary approach to determining the degree of identity, a BLAST program may be used, with a probability score between e-3 and e-100 indicating a closely related sequence.

As used herein, the term “analog” refers to a structurally related polypeptide or nucleic acid molecule having the function of a reference polypeptide or nucleic acid molecule.

As used herein, the term “ligand” refers to a molecule that binds to a receptor. In particular, the ligand binds a receptor on another cell, allowing for cell-to-cell recognition and/or interaction.

As used herein, the term “disease” refers to any condition or disorder that damages or interferes with the normal function of a cell, tissue, or organ. Examples of diseases include neoplasia or pathogen infection of cell.

As used herein, the term “effective amount” refers to an amount sufficient to have a therapeutic effect. In certain embodiments, an “effective amount” is an amount sufficient to arrest, ameliorate, or inhibit the continued proliferation, growth, or metastasis (*e.g.*, invasion, or migration) of a neoplasia.

As used herein, the term “heterologous nucleic acid molecule or polypeptide” refers to a nucleic acid molecule (*e.g.*, a cDNA, DNA or RNA molecule) or polypeptide that is not normally present in a cell or sample obtained from a cell. This nucleic acid may be from another organism, or it may be, for example, an mRNA molecule that is not normally expressed in a cell or sample.

As used herein, the term “immunoresponsive cell” refers to a cell that functions in an immune response or a progenitor, or progeny thereof.

As used herein, the term “modulate” refers positively or negatively alter. Exemplary modulations include an about 1%, about 2%, about 5%, about 10%, about 25%, about 50%, about 75%, or about 100% change.

As used herein, the term “increase” refers to alter positively by at least about 5%, including, but not limited to, alter positively by about 5%, by about 10%, by about 25%, by about 30%, by about 50%, by about 75%, or by about 100%.

As used herein, the term “reduce” refers to alter negatively by at least about 5% including, but not limited to, alter negatively by about 5%, by about 10%, by about 25%, by about 30%, by about 50%, by about 75%, or by about 100%.

As used herein, the term “isolated cell” refers to a cell that is separated from the molecular and/or cellular components that naturally accompany the cell.

As used herein, the term "isolated," "purified," or "biologically pure" refers to material that is free to varying degrees from components which normally accompany it as found in its native state. "Isolate" denotes a degree of separation from original source or surroundings. "Purify" denotes a degree of separation that is higher than isolation. A "purified" or "biologically pure" protein is sufficiently free of other materials such that any impurities do not materially affect the biological properties of the protein or cause other adverse consequences. That is, a nucleic acid or peptide of this invention is purified if it is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Purity and homogeneity are typically determined using analytical chemistry techniques, for example, polyacrylamide gel electrophoresis or high performance liquid chromatography. The term "purified" can denote that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. For a protein that can be subjected to modifications, for example, phosphorylation or glycosylation, different modifications may give rise to different isolated proteins, which can be separately purified.

As used herein, the term "secreted" is meant a polypeptide that is released from a cell via the secretory pathway through the endoplasmic reticulum, Golgi apparatus, and as a vesicle that transiently fuses at the cell plasma membrane, releasing the proteins outside of the cell.

As used herein, the term "specifically binds" or "specifically binds to" or "specifically target" is meant a polypeptide or fragment thereof that recognizes and binds a biological molecule of interest (*e.g.*, a polypeptide), but which does not substantially recognize and bind other molecules in a sample, for example, a biological sample, which naturally includes a polypeptide of the invention.

As used herein, the term "treating" or "treatment" refers to clinical intervention in an attempt to alter the disease course of the individual or cell being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Therapeutic effects of treatment include, without limitation, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastases, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. By preventing progression of a disease or disorder, a treatment can prevent deterioration due to a disorder in an affected or diagnosed subject or a subject suspected of having the disorder, but also a treatment may prevent the onset of the disorder or a symptom of the disorder in a subject at risk for the disorder or suspected of having the disorder.

As used herein, the term “subject” refers to any animal (*e.g.*, a mammal), including, but not limited to, humans, non-human primates, rodents, and the like (*e.g.*, which is to be the recipient of a particular treatment, or from whom cells are harvested).

II. Fc Receptor-Like 5 (FcRL5)

Fc Receptor-Like 5 (FcRL5) (also known as “CD307e” or “IRTA2”) is a rational target for treating multiple myeloma as it is expressed on B cells and plasma cells. FcRL5 binds to the Fc portion of IgG and contributes to B cell receptor signaling and B cell proliferation (Franco *et al.*, *Journal of immunology* 190, 5739-5746 (2013); Dement-Brown *et al.*, *Journal of leukocyte biology* 91, 59-67 (2012). FcRL5 was found to be an alternative to CD138 as a FACS marker for malignant plasma cells from fresh or frozen patient samples with a mean relative MFI between 10-55 (n=23) (Ise *et al.*, *Leukemia* 21, 169-174 (2007)). Another study confirmed cell surface expression of FcRL5 by FACS on primary patient samples from most chronic lymphocytic leukemia (CLL), and mantle cell lymphoma cases, and all multiple myeloma (MM) (n=8) cases tested (Ise *et al.* (2007)). A third group found high surface staining on plasma cells from normal bone marrows (n=7), in MGUS (n=16), and in MM (n=16), (MFI similar in all three groups, ~1000 fold increase compared to isotype control) (Elkins *et al.*, *Molecular cancer therapeutics* 11, 2222-2232 (2012)). FcRL5 is on 1q21 and has been found to be involved in 1q21 abnormalities in B cell malignancies (Hatzivassiliou *et al.*, *Immunity* 14, 277-289 (2001)). Amplification of 1q21 is found in 48% of MM patients at diagnosis and 67% of patients at relapse, and correlates with a worse prognosis (An *et al.*, *Haematologica* 99, 353-359 (2014)). An antibody-drug conjugate targeting FcRL5 was effective in treating an *in vivo* murine model of MM (Elkins *et al.* (2012)).

Non-limiting examples of human FcRL5 amino acid sequences can be found under GenBank Protein Accession Nos: AAI01070.1; XP_011508332.1; XP_011508334.1; XP_011508333.1; XP_011508332.1; and NP_001182317.1.

In certain non-limiting embodiments, FcRL5 is human FcRL5 having the amino acid sequence set forth in SEQ ID NO:899, or fragments thereof. SEQ ID NO:899 is provided below:

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYLGKEILRE
TPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVVLRCRAKAEVTLNNTIYKN
DNVLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSNTVKIQVQEPFTRPVLRASSFQPISGNPV
TLTCETQLSLERSDVPLRFRFFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRS
WIQVQIPASHPVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSL
TTENSGNYYCTADNGLGAKPSKAVSLSVTVPVSHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQF
HHEDAALERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHPVLTLSSAEAL
TFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYYCTADNGFGPQRS
EVVSLFVTVPVSRPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGEASFN
LSLTAEHSGNYSCEANNGLVAQHSDTISLSVIVPVSRPILTFRAPRAQAVVGDLLELHCEALRGSSPIL
YWFYHEDVTLGKISAPSGGGASFNLSLTTEHSGIYSCEADNGLEAQRSEMVTLKVAVPVSRPVLTLRAP
GTHAAVGDLLELHCEALRGSPLILYRFFHEDVTLGNRSSPSGGASLNLSLTAEHSGNYSCEADNGLGAQ
RSETVTLYITGLTANRSGPFATGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPSDSDSQEP
TYHNVPAWEELQPVYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVASTPVSG
SLFLASSAPHR [SEQ ID NO:899].

In certain embodiments, FcRL5 comprises 9 immunoglobulin (Ig)-like domains, *e.g.*, domain 1, domain 2, domain 3, domain 4, domain 5, domain 6, domain 7, domain 8 and domain 9 (*see* Figure 3A and 3C). In certain embodiments, domain 9 of FcRL5 comprises the amino acid sequence set forth in SEQ ID NO:900. SEQ ID NO:900 is provided below.

RPVLTLRAPGTHAAVGDLLELHCEALRGSPLILYRFFHEDVTLGNRSSPSGGASLNLSLTAEHSGNYSC
EADNGLGAQRSETVTLYI [SEQ ID NO:900].

In certain embodiments, domain 9 of FcRL5 can have the amino acid sequence set forth in SEQ ID NO:963, or fragments thereof. SEQ ID NO:963 is provided below:

GTHAAVGDLLELHCEALRGSPLILYRFFHEDVTLGNRSSPSGGASLNLSLTAEHSGNYSCEADNGLGAQ
RSETVTLYI [SEQ ID NO:963].

In certain embodiments, domain 1 can comprise amino acids 23-100 of SEQ ID NO:899; domain 2 can comprise amino acids 105-185 of SEQ ID NO:899; domain 3 can comprise amino acids 191-273 of SEQ ID NO:899; domain 4 can comprise amino acids 287-373 of SEQ ID NO:899; domain 5 can comprise amino acids 380-466 of SEQ ID NO:899; domain 6 can comprise amino acids 490-555 of SEQ ID NO:899; domain 7 can comprise amino acids 565-638 of SEQ ID NO:899; domain 8 can comprise amino acids 658-731 of SEQ ID NO:899; and domain 9 can comprise amino acids 754-835 of SEQ ID NO:899.

In certain embodiments, domain 9 of FcRL5 comprises an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence of SEQ ID NO:900 or 963.

III. Chimeric Antigen Receptor (CAR).

Chimeric antigen receptors (CARs) are engineered receptors, which graft or confer a specificity of interest onto an immune effector cell. CARs can be used to graft the specificity of a monoclonal antibody onto a T cell; with transfer of their coding sequence facilitated by retroviral vectors.

There are three generations of CARs. “First generation” CARs are typically composed of an extracellular antigen binding domain (*e.g.*, a single-chain variable fragments (scFv)) fused to a transmembrane domain, fused to cytoplasmic/intracellular domain of the T cell receptor chain. “First generation” CARs typically have the intracellular domain from the CD3ξ- chain, which is the primary transmitter of signals from endogenous TCRs. “First generation” CARs can provide *de novo* antigen recognition and cause activation of both CD4$^+$ and CD8$^+$ T cells through their CD3ζ chain signaling domain in a single fusion molecule, independent of HLA-mediated antigen presentation. “Second generation” CARs add intracellular domains from various co-stimulatory molecules (*e.g.*, CD28, 4-1BB, ICOS, OX40) to the cytoplasmic tail of the CAR to provide additional signals to the T cell. “Second generation” CARs comprise those that provide both co-stimulation (*e.g.*, CD28 or 4-1BB) and activation (CD3ζ). Preclinical studies have indicated that “Second Generation” CARs can improve the anti-tumor activity of T cells. For example, robust efficacy of “Second Generation” CAR modified T cells was demonstrated in clinical trials targeting the CD19 molecule in patients with chronic lymphoblastic leukemia (CLL) and acute lymphoblastic leukemia (ALL). “Third generation” CARs comprise those that provide multiple co-stimulation (*e.g.*, CD28 and 4-1BB) and activation (CD3ζ).

In accordance with the presently disclosed subject matter, the CARs comprise an extracellular antigen-binding domain, a transmembrane domain and an intracellular domain, where the extracellular antigen-binding domain binds to FcRL5. In a specific non-limiting embodiment, the extracellular antigen-binding domain is a scFv. In a specific non-limiting embodiment, the extracellular antigen-binding domain is a Fab, which is optionally crosslinked. In a specific non-limiting embodiment, the extracellular binding domain is a $F(ab)_2$. In a specific non-limiting embodiment, any of the foregoing molecules may be comprised in a fusion protein with a heterologous sequence to form the extracellular antigen-binding domain.

In certain non-limiting embodiments, the extracellular antigen-binding domain of a CAR of the present disclosure has a high binding specificity as well as high binding affinity to FcRL5 or domain 9 of FcRL5. In certain non-limiting embodiments, the extracellular antigen-binding domain of a CAR of the present disclosure has a high binding specificity as well as high binding affinity to domain 8 of FcRL5. In certain non-limiting embodiments, the extracellular antigen-binding domain of a CAR of the present disclosure has a high binding specificity as well as high binding affinity to domain 7 of FcRL5. For example, in such embodiments, the extracellular antigen-binding domain of the CAR (embodied, for example, in an scFv or an analog thereof) binds to FcRL5 (or domain 8 or domain 9 of FcRL5) with a dissociation constant (K_d) of about 3×10^{-6} M or less. In certain embodiments, the K_d is about 1×10^{-6} M or less, about 1×10^{-7} M or less, about 1×10^{-8} M or less, about 1×10^{-9} M or less, about 1×10^{-10} M or less or about 1×10^{-11} M or less. In certain embodiments, the K_d is from about 1×10^{-11} M to about 3×10^{-6} M, 1×10^{-10} M to about 3×10^{-6} M or from about 1×10^{-9} M to about 3×10^{-6} M, such as from about 1×10^{-9} M to about 1×10^{-8} M, from about 1×10^{-8} M to about 1×10^{-7} M, or from about 1×10^{-7} M to about 1×10^{-6} M, or from about 1×10^{-6} M to about 3×10^{-6} M.

Binding of the extracellular antigen-binding domain (embodiment, for example, in an scFv or an analog thereof) of a presently disclosed CAR to FcRL5 (or domain 8 or domain 9 of FcRL5) can be confirmed by, for example, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), FACS analysis, bioassay (*e.g.*, growth inhibition), or Western Blot assay. Each of these assays generally detect the presence of protein-antibody complexes of particular interest by employing a labeled reagent (*e.g.*, an antibody, or an scFv) specific for the complex of interest. For example, the scFv can be radioactively labeled and used in a radioimmunoassay (RIA) (see, for example, Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope can be detected by such means as the use of a γ counter or a scintillation counter or by autoradiography. In certain embodiments, the FcRL5-targeted extracellular antigen-binding domain is labeled with a fluorescent marker. Non-limiting examples of fluorescent markers include green fluorescent protein (GFP), blue fluorescent protein (*e.g.*, EBFP, EBFP2, Azurite, and mKalama1), cyan fluorescent protein (*e.g.*, ECFP, Cerulean, and CyPet), and yellow fluorescent protein (*e.g.*, YFP, Citrine, Venus, and YPet). In certain embodiments, the FcRL5-targeted human scFv is labeled with GFP.

In certain embodiments, the extracellular antigen-binding domain of a presently disclosed CAR comprises a single-chain variable fragment (scFv). In one specific embodiment, the extracellular antigen-binding domain of a presently disclosed CAR comprises a human scFv that specifically binds to human FcRL5. In another specific embodiment, the extracellular antigen-binding domain of a presently disclosed CAR comprises a murine scFv that specifically binds to human FcRL5. In certain embodiments, the extracellular antigen-binding domain of a presently disclosed CAR comprises a scFv that specifically binds to at least a portion of domain 7 of FcRL5. In certain embodiments, the extracellular antigen-binding domain of a presently disclosed CAR comprises a scFv that specifically binds to at least a portion of domain 8 of FcRL5. In certain embodiments, the extracellular antigen-binding domain of a presently disclosed CAR comprises a scFv that specifically binds to at least a portion of domain 9 of FcRL5. For example, and not by way of limitation, domain 9 of FcRL5 comprises the amino acid sequence set forth in SEQ ID NO:900 or 963, or fragments thereof.

In certain embodiments, the extracellular antigen-binding domain is a murine scFv obtained from two commercially available mouse hybridomas binding different extracellular epitopes on human FcRL5, which have been characterized in the Franco *et al.*, *Journal of Immunology* (2013);190:5739-5746; Ise *et al.*, *Clinical cancer research: an official fournal of the American Association for Cancer Research* (2005);11:87-96; and Ise *et al.*, *Clinical chemistry and laboratory medicine: CCLM/FESCC* (2006);44:594-602, each of which are herein incorporated by reference in their entireties. In certain embodiments, the extracellular antigen-binding domain is a murine scFv that is derived from a heavy chain variable region and a light chain variable region of an antibody that binds to human FcRL5, *e.g.*, antibodies F56 and F119 as disclosed in Ise *et al.* (2005), which is herein incorporated by reference in its entirety.

Extracellular Antigen-Binding Domain of A CAR

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917 and SEQ ID NO:921, wherein the scFv antibody binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ

ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:915 and SEQ ID NO:919.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:915 as provided below.

VKLQESGGGLVQPGGSRKLSCAASGFTFSIFGLHWVRQAPEKGLEWVAYISGDSNTIYYADTVKGRFTI
SRDNPKNTLFLQMTSLRSEDTAMYYCARNSYYALDYWGQGTTVTVSS [SEQ ID NO: 915]

The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:915 is set forth in SEQ ID NO:916 as provided below.

GTGAAGCTGCAGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCGGAAACTCTCCTGTGCAGCC
TCTGGATTCACTTTCAGTATCTTTGGATTGCACTGGGTTCGTCAGGCTCCAGAGAAGGGGCTGGAGTGG
GTCGCATACATTAGTGGTGACAGTAATACCATCTACTATGCAGACACAGTGAAGGGCCGATTCACCATC
TCCAGAGACAATCCCAAGAACACCCTGTTCCTGCAAATGACCAGTCTAAGGTCTGAGGACACGGCCATG
TATTACTGTGCAAGAAATAGCTACTATGCTCTGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCC
TCA [SEQ ID NO:916]

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:917 as provided below.

DIELTQSPAIMSVSPGEKVTMTCRASSSVSSSYLHWYQQRSGASPKIWIYSTSNLASGVPARFSGSGTG
TSYSLTISSVEAEDAATYYCQQYSGYPWTFGGGTKLEI [SEQ ID NO:917]

The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:917 is set forth in SEQ ID NO:918 as provided below.

GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGTATCTCCAGGTGAAAAGGTCACCATGACCTGC
AGGGCCAGCTCAAGTGTCAGTTCCAGTTACTTGCACTGGTACCAGCAGAGGTCAGGTGCCTCCCCCAAA
ATCTGGATTTATAGCACATCCAACTTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGACTGGG
ACCTCTTACTCTCTCACAATCAGCAGTGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTAC
AGTGGTTACCCGTGGACGTTCGGTGGAGGGACCAAGCTGGAGATC [SEQ ID NO:918]

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:919 as provided below.

VQLQESGGGLVQPGGSRKLSCTASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSNNIYFADTVKGRFTI
SRDNPKNTLFLQMTSLRSEDTAMYYCARSEYYGSSHMDYWGQGTTVTVSS [SEQ ID NO:919]

The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:3 is set forth in SEQ ID NO:920 as provided below.

GTCCAACTGCAGGAGTCAGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCGGAAACTCTCCTGTACAGCC
TCTGGATTCACTTTCAGTAGCTTTGGAATGCACTGGGTTCGTCAGGCTCCAGAGAAGGGGCTGGAGTGG
GTCGCATACATTAGTAGTGGCAGTAATAACATCTACTTTGCGGACACAGTGAAGGGCCGATTCACCATC
TCCAGAGACAATCCCAAGAACACCCTGTTCCTGCAAATGACCAGTCTAAGGTCTGAGGACACGGCCATG
TATTACTGTGCAAGATCGGAATACTACGGTAGTAGCCATATGGACTACTGGGGCCAAGGGACCACGGTC
ACCGTCTCCTCA [SEQ ID NO:920]

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:921 as provided below.

DIELTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKPLIYSATYRNSGVPDRFTGSGSGT
DFTLTITNVQSKDLADYFCQQYNRYPYTSGGGTKLEI [SEQ ID NO:921]

The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:921 is set forth in SEQ ID NO:922 as provided below.

GACATTGAGCTCACCCAGTCTCCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGC
AAGGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACCA
CTGATTTACTCGGCAACCTACCGGAACAGTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACA
GATTTCACTCTCACCATCACTAACGTGCAGTCTAAAGACTTGGCAGACTATTTCTGTCAACAATATAAC
AGGTATCCGTACACGTCCGGAGGGGGGACCAAGCTGGAGATC [SEQ ID NO:922]

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:144. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:144 is set forth in SEQ ID NO:142.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:143. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:143 is set forth in SEQ ID NO:141.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:216. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:216 is set forth in SEQ ID NO:214.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:215. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:215 is set forth in SEQ ID NO:213.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:220. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:220 is set forth in SEQ ID NO:218.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:219. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:219 is set forth in SEQ ID NO:217.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:236. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:236 is set forth in SEQ ID NO:234.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:235. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:235 is set forth in SEQ ID NO:232.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:268. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:268 is set forth in SEQ ID NO:266.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:267. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:267 is set forth in SEQ ID NO:265.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:172. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:172 is set forth in SEQ ID NO:170.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv)

comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:171. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:171 is set forth in SEQ ID NO:169.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:116. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:116 is set forth in SEQ ID NO:114.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:115. The nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:115 is set forth in SEQ ID NO:113.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917, SEQ ID NO:921 and (b) a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40,

SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:917 and SEQ ID NO:921, wherein the extracellular binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:3, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:4.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:7, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:8.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:11, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:12.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:15, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:16.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv)

comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:19, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:20.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:23, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:24.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:27, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:28.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:31, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:32.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:35, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:36.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:39, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:40.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:43, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:44.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:47, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:48.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence

set forth in SEQ ID NO:51, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:52.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:55, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:56.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:59, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:60.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:63, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:64.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:67, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:68.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:71, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:72.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:75, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:76.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:79, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:80.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:83, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:84.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:87, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:88.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:91, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:92.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:95, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:96.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:99, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:100.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:103, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:104.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:107, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:108.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:111, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:112.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:115, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:116.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:119, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:120.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:123, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:124.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:127, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:128.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:131, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:132.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:135, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:136.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:139, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:140.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:143, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:144.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:147, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:148.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv)

comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:151, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:152.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:155, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:156.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:159, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:160.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:163, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:164.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:167, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:168.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:171, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:172.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:175, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:176.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:179, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:180.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence

set forth in SEQ ID NO:183, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:184.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:187, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:188.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:191, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:192.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:195, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:196.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:199, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:200.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:203, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:204.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:207, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:208.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:211, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:212.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:215, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:216.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:219, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:220.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:223, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:224.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:227, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:228.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:231, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:232.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:235, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:236.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:239, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:240.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:243, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:244.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:247, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:248.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:251, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:252.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:255, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:256.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:259, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:260.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:263, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:264.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:267, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:268.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:271, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:272.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:275, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:276.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:279, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:280.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv)

comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:283, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:284.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:287, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:288.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:291, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:292.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:279, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:280.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:283, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:284.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:287, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:288.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:291, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:292.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:295, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:296.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence

set forth in SEQ ID NO:299, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:300.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:303, and (b) a heavy chain variable region comprising amino acids having a sequence set forth in SEQ ID NO:304.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:915, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:917.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:919, and (b) a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:921.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises heavy and light chain variable regions comprising amino acid sequences that are homologous to the amino acid sequences described herein and as disclosed in Tables 1-76. For example, and not by way of limitation, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID

NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917 and SEQ ID NO:921.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:915 and SEQ ID NO:919.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:19, SEQ ID NO:23, SEQ ID NO:27, SEQ ID NO:31,

SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:71, SEQ ID NO:75, SEQ ID NO:79, SEQ ID NO:83, SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:95, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:119, SEQ ID NO:123, SEQ ID NO:127, SEQ ID NO:131, SEQ ID NO:135, SEQ ID NO:139, SEQ ID NO:143, SEQ ID NO:147, SEQ ID NO:151, SEQ ID NO:155, SEQ ID NO:159, SEQ ID NO:163, SEQ ID NO:167, SEQ ID NO:171, SEQ ID NO:175, SEQ ID NO:179, SEQ ID NO:183, SEQ ID NO:187, SEQ ID NO:191, SEQ ID NO:195, SEQ ID NO:199, SEQ ID NO:203, SEQ ID NO:207, SEQ ID NO:211, SEQ ID NO:215, SEQ ID NO:219, SEQ ID NO:223, SEQ ID NO:227, SEQ ID NO:231, SEQ ID NO:235, SEQ ID NO:239, SEQ ID NO:243, SEQ ID NO:247, SEQ ID NO:251, SEQ ID NO:255, SEQ ID NO:259, SEQ ID NO:263, SEQ ID NO:267, SEQ ID NO:271, SEQ ID NO:275, SEQ ID NO:279, SEQ ID NO:283, SEQ ID NO:287, SEQ ID NO:291, SEQ ID NO:295, SEQ ID NO:299, SEQ ID NO:303, SEQ ID NO:917 and SEQ ID NO:921; and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, SEQ ID NO:272, SEQ ID NO:276, SEQ ID NO:280, SEQ ID

NO:284, SEQ ID NO:288, SEQ ID NO:292, SEQ ID NO:296, SEQ ID NO:300, SEQ ID NO:304, SEQ ID NO:915 and SEQ ID NO:919.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:143, and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:144, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:215, and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:216, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:219, and (b) a heavy chain variable comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:220, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:235, and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:236, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:267, and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:268, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:915, and (b) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:917, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:919, and (b) a light chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:921, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv)

comprises (a) a light chain variable comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:115, and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:116, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:171, and (b) a heavy chain variable region comprising an amino acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the amino acid sequence set forth in SEQ ID NO:172, wherein the extracellular antigen-binding domain binds to an FcRL5 polypeptide.

An extracellular antigen-binding domain (*e.g.*, scFv) comprising V_H and/or V_L regions having high (*i.e.*, 80% or greater) homology to the V_H and V_L regions of the sequences set forth above, can be obtained by mutagenesis (*e.g.*, site-directed or PCR-mediated mutagenesis), followed by testing of the encoded altered scFv for retained function (*i.e.*, the binding affinity) using the binding assays described herein. In certain embodiments, a V_L sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity contains substitutions (*e.g.*, conservative substitutions to generate conservative modifications of a sequence), insertions or deletions relative to the reference sequence, but an extracellular antigen-binding domain (*e.g.*, scFv) comprising that sequence retains the ability to bind to FcRL5. In certain embodiments, a V_H sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity contains substitutions (*e.g.*, conservative substitutions), insertions or deletions relative to the reference sequence, but an extracellular antigen-binding domain (*e.g.*, scFv) comprising that sequence retains the ability to bind to FcRL5. In certain embodiments, a total of about 1 to about 10 amino acids have been substituted, inserted and/or deleted in the disclosed sequences.

For example, and not by way of limitation, a V_H sequence or a V_L sequence, can have up to about one, up to about two, up to about three, up to about four, up to about five, up to about six, up to about seven, up to about eight, up to about nine or up to about ten amino acid residues that are modified and/or substituted. Non-limiting examples of conservative modifications are provided below, *e.g.*, within Table 231.

The presently disclosed subject matter further provides extracellular antigen-binding domains (*e.g.*, scFv) that comprise heavy chain variable region and light chain variable region CDRs, *e.g.*, CDR1s, CDR2s and CDR3s, as disclosed herein in Tables 229 and 230. The CDR regions are delineated using the Kabat system (Kabat, E. A., et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). The present disclosure further provides extracellular antigen-binding domains (*e.g.*, scFv) that comprise conservative modifications of the antibody sequences disclosed herein. For example, and not by way of limitation, an extracellular antigen-binding domains (*e.g.*, scFv) of the presently disclosed subject matter comprises a heavy chain variable region comprising CDR1, CDR2 and CDR3 sequences and a light chain variable region comprising CDR1, CDR2 and CDR3 sequences, wherein one or more of these CDR sequences comprise specified amino acid sequences disclosed herein, or conservative modifications thereof, and wherein the extracellular antigen-binding domains retain the desired functional properties. *See* Tables 229 and 230.

In certain embodiments, the presently disclosed subject matter provides an extracellular antigen-binding domain (*e.g.*, scFv) comprising a light chain variable region, wherein the light chain variable region comprises: (a) a CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 312, 3118, 324, 329, 338, 343, 348, 352, 357, 363, 369, 381, 390, 397, 401, 406, 416, 423, 428, 433, 447, 460, 468, 474, 477, 483, 490, 498, 503, 508, 518, 533, 540, 544, 547, 556, 562, 568, 571, 580, 585, 588, 926 and 932, and conservative modifications thereof; (b) a CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:313, 319, 330, 344, 349, 358, 364, 370, 382, 385, 391, 398, 409, 417, 429, 434, 438, 448, 454, 461, 469, 478, 484, 487, 504, 513, 523, 534, 429, 448, 548, 557, 563, 572, 575, 586, 927 and 933, and conservative modifications thereof; and (c) a CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 314, 320, 325, 331, 339, 345, 350, 353, 359, 365, 371, 377, 383, 386, 392, 395, 399, 402, 407, 410, 414, 418, 419, 424, 430, 435, 439, 443, 449, 452, 455, 457, 462, 465, 470, 479, 485, 488, 491, 493, 495, 499, 505, 509, 514, 519, 524, 528, 530, 531, 535, 541, 542, 545, 549, 554, 558, 564, 569, 573, 576, 581, 592, 928 and 934, and conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region, wherein the heavy chain variable region comprises: (a) a CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 309, 315, 321, 326, 332, 335, 340, 346, 354, 360, 366, 372, 378, 387, 393, 403, 411, 420, 425, 436, 440, 444, 471, 480, 500, 510, 515, 520, 525, 537, 551, 559, 565, 582, 589, 923 and 929 and conservative modifications thereof; (b) a CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 310, 316, 322, 327, 333, 336, 341, 355, 361, 367, 373, 379, 388, 404, 412, 421, 426, 431, 441, 445, 450, 466, 472, 475, 481, 496, 501, 506, 511, 516, 521, 526, 538, 552, 560, 566, 583, 590, 924 and 930 and conservative modifications thereof; and (c) a CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 311, 317, 323, 328, 334, 337, 342, 347, 351, 356, 362, 368, 374, 376, 380, 384, 389, 394, 396, 400, 405, 408, 412, 415, 422, 427, 432, 437, 442, 446, 451, 453, 456, 458, 459, 463, 464, 467, 473, 476, 482, 486, 489, 492, 494, 497, 502, 507, 512, 517, 522, 527, 529, 532, 536, 539, 543, 546, 550, 553, 555, 561, 567, 570, 574, 577, 578, 579, 584, 578, 587, 591, 925 and 931, and conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:463 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:419 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:515 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:516 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:517 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:531 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:403 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:404 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:532 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:533 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:534 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:535 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:543 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:544 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:448 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:545 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:372 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:475 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:570 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:571 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:572 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:573 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:440 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:441 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:442 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:329 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:330 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:443 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:309 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:310 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:489 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:490 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:313 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:491 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:923 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:924 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:925 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises (a) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:926 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:927 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:928 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:929 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:930 or conservative modifications thereof; and (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ

ID NO:931 or conservative modifications thereof. In certain embodiments, the extracellular antigen-binding domain comprises (a) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:932 or conservative modifications thereof; (b) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO: 933 or conservative modifications thereof; and (c) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:934 or conservative modifications thereof.

The presently disclosed subject matter provides an extracellular antigen-binding domain (*e.g.*, scFv) comprising a heavy chain variable region comprising CDR1, CDR2, and CDR3 sequences and a light chain variable region comprising CDR1, CDR2, and CDR3 sequences, wherein: (a) the heavy chain variable region CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 311, 317, 323, 328, 334, 337, 342, 347, 351, 356, 362, 368, 374, 376, 380, 384, 389, 394, 396, 400, 405, 408, 412, 415, 422, 427, 432, 437, 442, 446, 451, 453, 456, 458, 459, 463, 464, 467, 473, 476, 482, 486, 489, 492, 494, 497, 502, 507, 512, 517, 522, 527, 529, 532, 536, 539, 543, 546, 550, 553, 555, 561, 567, 570, 574, 577, 578, 579, 584, 578, 587, 591, 925 and 931, and conservative modifications thereof; and (b) the light chain variable region CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 314, 320, 325, 331, 339, 345, 350, 353, 359, 365, 371, 377, 383, 386, 392, 395, 399, 402, 407, 410, 414, 418, 419, 424, 430, 435, 439, 443, 449, 452, 455, 457, 462, 465, 470, 479, 485, 488, 491, 493, 495, 499, 505, 509, 514, 519, 524, 528, 530, 531, 535, 541, 542, 545, 549, 554, 558, 564, 569, 573, 576, 581, 592, 928 and 934 and conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds to human FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:463 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:419 or conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:517 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:531 or conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:532 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:535 or conservative modifications thereof; wherein the antibody or antigen-binding fragment thereof specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:543 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:545 or conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:570 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:573 or conservative modifications thereof; wherein the antibody or antigen-binding fragment thereof specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:925 or conservative modifications thereof; and (b) and a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:928 or conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:931 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:934 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:442 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:443 or conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:489 or conservative modifications thereof; and (b) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:491 or conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the presently disclosed subject matter provides an extracellular antigen-binding domain (*e.g.*, scFv) comprising a heavy chain variable region comprising CDR1, CDR2, and CDR3 sequences and a light chain variable region comprising CDR1, CDR2, and CDR3 sequences, wherein: (a) the heavy chain variable region CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 309, 315, 321, 326, 332, 335, 340, 346, 354, 360, 366, 372, 378, 387, 393, 403, 411, 420, 425, 436, 440, 444, 471, 480, 500, 510, 515, 520, 525, 537, 551, 559, 565, 582, 589, 923 and 929, and conservative modifications thereof; (b) the heavy chain variable region CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 310, 316, 322, 327, 333, 336, 341, 355, 361, 367, 373, 379, 388, 404, 412, 421, 426, 431, 441, 445, 450, 466, 472, 475, 481, 496, 501, 506, 511, 516, 521, 526, 538, 552, 560, 566, 583, 590, 924 and 930, and conservative modifications thereof; (c) the heavy chain variable region CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 311, 317, 323, 328, 334, 337, 342, 347, 351, 356, 362, 368, 374, 376, 380, 384, 389, 394, 396, 400, 405, 408, 412, 415, 422, 427, 432, 437, 442, 446, 451, 453, 456, 458, 459, 463, 464, 467, 473, 476, 482, 486, 489, 492, 494, 497, 502, 507, 512, 517, 522, 527, 529, 532, 536, 539, 543, 546, 550, 553, 555, 561, 567, 570, 574, 577, 578, 579, 584, 578, 587, 591, 925 and 931 and conservative modifications thereof; (d) the light chain variable region CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 312, 3118, 324, 329, 338, 343, 348, 352, 357, 363, 369, 381, 390, 397, 401, 406, 416, 423, 428, 433, 447, 460, 468, 474, 477, 483, 490, 498, 503, 508, 518, 533, 540, 544, 547, 556, 562, 568, 571, 580, 585, 588, 926 and 932 and conservative modifications thereof; (e) the light chain variable region CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:313, 319, 330, 344, 349, 358, 364, 370, 382, 385, 391, 398, 409, 417, 429, 434, 438, 448, 454, 461, 469, 478, 484, 487, 504, 513, 523, 534, 429, 448, 548, 557, 563, 572, 575, 586, 927 and 933 and conservative modifications thereof; and (f) the light chain variable region CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 314, 320, 325, 331, 339, 345, 350, 353, 359, 365, 371, 377, 383, 386, 392, 395, 399, 402, 407, 410, 414, 418, 419, 424, 430, 435, 439, 443, 449, 452, 455, 457, 462, 465, 470, 479, 485, 488, 491, 493, 495, 499, 505, 509, 514, 519, 524, 528, 530, 531, 535, 541, 542, 545, 549, 554, 558, 564, 569, 573, 576, 581, 592, 928 and 934 and conservative modifications thereof; wherein the extracellular antigen-binding domain specifically binds FcRL5.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:463 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:419 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:515 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:516 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:517 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:318 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:319 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:531 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:403 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:404 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:532 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:533 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:534 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:535 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:411 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:412 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:543 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:544 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:448 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:545 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:372 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:475 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:570 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:571 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:572 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:573 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:923 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:924 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:925 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:926 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:927 or conservative modifications thereof; and (f) and a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:928 or conservative modifications thereof.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises (a) a heavy chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:929 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:930 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:931 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising amino acids having the sequence set forth in SEQ ID NO:932 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising amino acids having the sequence set forth in SEQ ID NO:933 or conservative modifications thereof, and (f) a light chain variable region CDR3 comprising amino acids having the sequence set forth in SEQ ID NO:934 or conservative modifications thereof.

In certain embodiments, a presently disclosed anti-FcRL5 antibody or antigen-binding fragment thereof comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:440 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:441 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:442 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:329 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:330 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:443 or conservative modifications thereof.

In certain embodiments, a presently disclosed anti-FcRL5 antibody or antigen-binding fragment thereof comprises: (a) a heavy chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:309 or conservative modifications thereof; (b) a heavy chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:310 or conservative modifications thereof; (c) a heavy chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:489 or conservative modifications thereof; (d) a light chain variable region CDR1 comprising the amino acid sequence of SEQ ID NO:490 or conservative modifications thereof; (e) a light chain variable region CDR2 comprising the amino acid sequence of SEQ ID NO:313 or conservative modifications thereof; and (f) a light chain variable region CDR3 comprising the amino acid sequence of SEQ ID NO:491 or conservative modifications thereof.

As used herein, the terms “conservative sequence modifications” and “conservative modifications” refers to amino acid modifications that do not significantly affect or alter the binding characteristics of the presently disclosed CAR (*e.g.*, the extracellular antigen-binding domain) comprising the amino acid sequence. Such conservative modifications include amino acid substitutions, additions and deletions. Modifications can be introduced into the human scFv of the presently disclosed subject matter by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Amino acids can be classified into groups according to their physicochemical properties such as charge and polarity.

Conservative amino acid substitutions are ones in which the amino acid residue is replaced with an amino acid within the same group. For example, amino acids can be classified by charge: positively-charged amino acids include lysine, arginine, histidine, negatively-charged amino acids include aspartic acid, glutamic acid, neutral charge amino acids include alanine, asparagine, cysteine, glutamine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. In addition, amino acids can be classified by polarity: polar amino acids include arginine (basic polar), asparagine, aspartic acid (acidic polar), glutamic acid (acidic polar), glutamine, histidine (basic polar), lysine (basic polar), serine, threonine, and tyrosine; non-polar amino acids include alanine, cysteine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, tryptophan, and valine. Thus, one or more amino acid residues within a CDR region can be replaced with other amino acid residues from the same group and the altered antibody can be tested for retained function (*i.e.*, the functions set forth in (c) through (l) above) using the functional assays described herein. In certain embodiments, no more than one, no more than two, no more than three, no more than four, no more than five residues within a specified sequence or a CDR region are altered. Exemplary conservative amino acid substitutions are shown in Table 231.

Table 231

Original Residue	**Exemplary conservative amino acid Substitutions**
Ala (A)	Val; Leu; Ile
Arg (R)	Lys; Gln; Asn
Asn (N)	Gln; His; Asp, Lys; Arg
Asp (D)	Glu; Asn
Cys (C)	Ser; Ala
Gln (Q)	Asn; Glu
Glu (E)	Asp; Gln
Gly (G)	Ala
His (H)	Asn; Gln; Lys; Arg
Ile (I)	Leu; Val; Met; Ala; Phe

Original Residue	Exemplary conservative amino acid Substitutions
Leu (L)	Ile; Val; Met; Ala; Phe
Lys (K)	Arg; Gln; Asn
Met (M)	Leu; Phe; Ile
Phe (F)	Trp; Leu; Val; Ile; Ala; Tyr
Pro (P)	Ala
Ser (S)	Thr
Thr (T)	Val; Ser
Trp (W)	Tyr; Phe
Tyr (Y)	Trp; Phe; Thr; Ser
Val (V)	Ile; Leu; Met; Phe; Ala

In certain non-limiting embodiments, an extracellular antigen-binding domain of the CAR can comprise a linker connecting the heavy chain variable region and light chain variable region of the extracellular antigen-binding domain. As used herein, the term “linker” refers to a functional group (*e.g.*, chemical or polypeptide) that covalently attaches two or more polypeptides or nucleic acids so that they are connected to one another. As used herein, a “peptide linker” refers to one or more amino acids used to couple two proteins together (*e.g.*, to couple V_H and V_L domains). Non-limiting examples of peptide linkers are disclosed in Shen et al., Anal. Chem. 80(6):1910-1917 (2008).

In one non-limiting example, the linker is a G4S linker that comprises amino acids having the sequence set forth in SEQ ID NO:897. In certain embodiments, the nucleotide sequence encoding the amino acid sequence of SEQ ID NO:897 is set forth in SEQ ID NO:898. In one non-limiting example, the linker comprises amino acids having the sequence set forth in SEQ ID NO:307. In certain embodiments, the nucleotide sequence encoding the amino acid sequence of SEQ ID NO:307 is set forth in SEQ ID NO:305.

In certain embodiments, the linker comprises amino acids having the sequence set forth in SEQ ID NO:901 as provided below.

`GGGGS [SEQ ID NO:901].`

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:902 as provided below.

SGGSGGS [SEQ ID NO:902].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:903 as provided below.

GGGGSGGGS [SEQ ID NO:903].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:904 as provided below.

GGGGSGGGGS [SEQ ID NO:904].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:905 as provided below.

GGGGSGGGGSGGGGGGGS [SEQ ID NO:905].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:906 as provided below.

GGGGSGGGGSGGGGSGGGGS [SEQ ID NO:906].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:907 as provided below.

GGGGSGGGGSGGGGSGGGGSGGGGS [SEQ ID NO:907].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:908 as provided below.

GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS [SEQ ID NO:908].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:909 as provided below.

GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS [SEQ ID NO:909].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:910 as provided below.

EPKSCDKTHTCPPCP [SEQ ID NO:910].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:911 as provided below.

GGGGSGGGSEPKSCDKTHTCPPCP [SEQ ID NO:911].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:912 as provided below.

ELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCP [SEQ ID NO:912].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:913 as provided below.

GSGSGS [SEQ ID NO:913].

In certain embodiments, the the linker comprises amino acids having the sequence set forth in SEQ ID NO:914 as provided below.

`AAA [SEQ ID NO:914].`

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) comprises a heavy chain variable region, a light chain variable region and a linker peptide between the heavy chain variable region and the light chain variable region. Non-limiting examples of extracellular antigen-binding domains, *e.g.*, scFvs, of the present disclosure that comprise a heavy chain variable region, a light chain variable region and a linker peptide are disclosed in Tables 77-152. For example, and not by way of limitation, the extracellular antigen-binding domain comprising a heavy chain variable region, a light chain variable region and a linker peptide of the present disclosure comprises an amino acid sequence selected from the group consisting of SEQ ID NO:594, SEQ ID NO:596, SEQ ID NO:598, SEQ ID NO:600, SEQ ID NO:602, SEQ ID NO:604, SEQ ID NO:606, SEQ ID NO:608, SEQ ID NO:610, SEQ ID NO:612, SEQ ID NO:614, SEQ ID NO:616, SEQ ID NO:618, SEQ ID NO:620, SEQ ID NO:622, SEQ ID NO:624, SEQ ID NO:626, SEQ ID NO:628, SEQ ID NO:630, SEQ ID NO:632, SEQ ID NO:634, SEQ ID NO:636, SEQ ID NO:638, SEQ ID NO:640, SEQ ID NO:642, SEQ ID NO:644, SEQ ID NO:646, SEQ ID NO:648, SEQ ID NO:650, SEQ ID NO:652, SEQ ID NO:654, SEQ ID NO:656, SEQ ID NO:658, SEQ ID NO:660, SEQ ID NO:662, SEQ ID NO:664, SEQ ID NO:666, SEQ ID NO:668, SEQ ID NO:670, SEQ ID NO:672, SEQ ID NO:674, SEQ ID NO:676, SEQ ID NO:678, SEQ ID NO:680, SEQ ID NO:682, SEQ ID NO:684, SEQ ID NO:686, SEQ ID NO:688, SEQ ID NO:690, SEQ ID NO:692, SEQ ID NO:694, SEQ ID NO:696, SEQ ID NO:698, SEQ ID NO:700, SEQ ID NO:702, SEQ ID NO:704, SEQ ID NO:706, SEQ ID NO:708, SEQ ID NO:710, SEQ ID NO:712, SEQ ID NO:714, SEQ ID NO:716, SEQ ID NO:718, SEQ ID NO:720, SEQ ID NO:722, SEQ ID NO:724, SEQ ID NO:726, SEQ ID NO:728, SEQ ID NO:730, SEQ ID NO:732, SEQ ID NO:734, SEQ ID NO:736, SEQ ID NO:738, SEQ ID NO:740, SEQ ID NO:742, SEQ ID NO:744 and conservative modifications of (as shown in Tables 77-152).

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:650 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:664 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:678 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:700 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:702 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:710 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:726 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:650 or conservative modifications of.

In certain embodiments, the extracellular antigen-binding domain (*e.g.*, scFv) having a heavy chain variable region, a light chain variable region and a linker peptide comprises the amino acid sequence of SEQ ID NO:678 or conservative modifications of.

In addition, the extracellular antigen-binding domain can comprise a leader or a signal peptide that directs the nascent protein into the endoplasmic reticulum. Signal peptide or leader can be essential if the CAR is to be glycosylated and anchored in the cell membrane. The signal sequence or leader can be a peptide sequence (about 5, about 10, about 15, about 20, about 25, or about 30 amino acids long) present at the N-terminus of newly synthesized proteins that directs their entry to the secretory pathway. In non-limiting examples, the signal peptide is covalently joined to the 5' terminus of the extracellular antigen-binding domain. In certain embodiments, the signal peptide comprises a CD8 polypeptide comprising amino acids having the sequence set forth in SEQ ID NO:26 as provided below.

`MALPVTALLLPLALLLHAAR [SEQ ID NO:935]`

The nucleotide sequence encoding the amino acid sequence of SEQ ID NO:935 is set forth in SEQ ID NO:936, which is provided below:

`ATGGCTCTCCCAGTGACTGCCCTACTGCTTCCCCTAGCGCTTCTCCTGCATGCAGCTCGT [SEQ ID NO:936]`

In another embodiment, the signal peptide comprises amino acids having the sequence set forth in SEQ ID NO:937 as provided below.

`METDTLLLWVLLLWVPGSTG [SEQ ID NO:937]`

The nucleotide sequence encoding the amino acid sequence of SEQ ID NO:937 is set forth in SEQ ID NO:938, which is provided below:

`ATGGAAACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGA [SEQ ID NO:938]`

In certain embodiments, the extracellular antigen-binding domain, *e.g.*, the human scFv, comprises a heavy chain variable region, a light chain variable region, a linker peptide between the heavy chain variable region and the light chain variable region, and an His-tag and an HA-tag. In certain embodiments, the amino acid sequence of the His-tag and HA-tag comprises the amino acid sequence of SEQ ID NO:308. The nucleotide sequence encoding SEQ ID NO: 308 is SEQ ID NO: 306.

In certain embodiments, the extracellular antigen-binding domain, *e.g.*, the human scFv, binds to a human FcRL5 polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 899. In certain embodiments, the extracellular antigen-binding domain, *e.g.*, the human scFv, binds to an epitope in domain 9 (*e.g.*, amino acids 754-835 of SEQ ID NO:899). In certain embodiments, the extracellular antigen-binding domain, *e.g.*, the human scFv, binds to an epitope in domain 8 (*e.g.*, amino acids 658-731 of SEQ ID NO:899). In certain embodiments, the extracellular antigen-binding domain, *e.g.*, the human scFv, binds to an epitope within domain 9 comprising amino acids 829-840 of SEQ ID NO:899. In certain embodiments, the extracellular antigen-binding domain, *e.g.*, the human scFv, binds to an epitope within domain 8 comprising amino acids 657-667 of SEQ ID NO:899. For example, and not by way of limitation, the extracellular antigen-binding domain, *e.g.*, the human scFv, binds to an epitope comprising the amino acid sequence RSETVTLYITGL (SEQ ID NO:964). In certain embodiments, In certain embodiments, an antibody or an antigen-binding fragment thereof of the present disclosure binds to an epitope comprising the amino acid sequence SRPILTFRAPR (SEQ ID NO:965).

Transmembrane Domain of a CAR

In certain non-limiting embodiments, the transmembrane domain of the CAR comprises a hydrophobic alpha helix that spans at least a portion of the membrane. Different transmembrane domains result in different receptor stability. After antigen recognition, receptors cluster and a signal is transmitted to the cell. In accordance with the presently disclosed subject matter, the transmembrane domain of the CAR can comprise a CD8 polypeptide, a CD28 polypeptide, a CD3ζ polypeptide, a CD4 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a CTLA-4 polypeptide, a PD-1 polypeptide, a LAG-3 polypeptide, a 2B4 polypeptide, a BTLA polypeptide, a synthetic peptide (not based on a protein associated with the immune response), or a combination thereof.

In certain embodiments, the transmembrane domain of a presently disclosed CAR comprises a CD28 polypeptide. The CD28 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or 100% homologous to the sequence having a NCBI Reference No: P10747 or NP_006130 (SEQ ID NO:939), or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions. In non-limiting embodiments, the CD28 polypeptide can have an amino acid sequence that is a consecutive portion of SEQ ID NO:939 which is at least 20, or at least 30, or at least 40, or at least 50, and up to 220 amino acids in length. Alternatively or additionally, in non-limiting various embodiments, the CD28 polypeptide has an amino acid sequence of amino acids 1 to 220, 1 to 50, 50 to 100, 100 to 150, 150 to 200, or 200 to 220 of SEQ ID NO:939. In certain embodiments, the CAR of the presently disclosed subject matter comprises a transmembrane domain comprising a CD28 polypeptide, and an intracellular domain comprising a co-stimulatory signaling region that comprises a CD28 polypeptide. In certain embodiments, the CD28 polypeptide comprised in the transmembrane domain and the intracellular domain has an amino acid sequence of amino acids 114 to 220 of SEQ ID NO:939.

SEQ ID NO:939 is provided below:

```
1   MLRLLLALNL FPSIQVTGNK ILVKQSPMLV AYDNAVNLSC KYSYNLFSRE FRASLHKGLD
61  SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP
121 PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR
181 SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS [SEQ ID NO:939]
```

In accordance with the presently disclosed subject matter, a "CD28 nucleic acid molecule" refers to a polynucleotide encoding a CD28 polypeptide. In certain embodiments, the CD28 nucleic acid molecule encoding the CD28 polypeptide comprised in the transmembrane domain and the intracellular domain (*e.g.*, the co-stimulatory signaling region) of the presently disclosed CAR (amino acids 114 to 220 of SEQ ID NO:939) comprises nucleic acids having the sequence set forth in SEQ ID NO:940 as provided below.

```
ATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAGAGCAATGGAACCATTATCCATGTGAAA
GGGAAACACCTTTGTCCAAGTCCCCTATTTCCCGGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTT
GGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTTTCTGGGTGAGGAGTAAG
AGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCC [SEQ ID NO:940].
```

In certain embodiments, the transmembrane domain of a presently disclosed CAR comprises a CD8 polypeptide. The CD8 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or 100% homologous to the sequence having a NCBI Reference No: AAH25715 (SEQ ID NO:960), or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions. In non-limiting embodiments, the CD8 polypeptide can have an amino acid sequence that is a consecutive portion of SEQ ID NO:960 which is at least 20, or at least 30, or at least 40, or at least 50, or at least 70, or at least 100, or at least 150, or at least 200 and up to 235 amino acids in length. Alternatively or additionally, in non-limiting various embodiments, the CD8 polypeptide has an amino acid sequence of amino acids 1 to 235, 1 to 50, 50 to 100, 100 to 150, 150 to 200, 130 to 210, or 200 to 235 of SEQ ID NO:960. In certain embodiments, the CAR of the presently disclosed subject matter comprises a transmembrane domain comprising a CD8 polypeptide. In certain embodiments, the CD8 polypeptide comprised in the transmembrane domain has an amino acid sequence of amino acids 137 to 207 of SEQ ID NO:960.

SEQ ID NO:960 is provided below:

```
1   malpvtalll plalllhaar psqfrvspld rtwnlgetve lkcqvllsnp tsgcswlfqp
61  rgaaasptfl lylsqnkpka aegldtqrfs gkrlgdtfvl tlsdfrrene gcyfcsalsn
121 simyfshfvp vflpakpttt paprpptpap tiasqplslr peacrpaagg avhtrgldfa
181 cdiyiwapla gtcgvlllsl vitlycnhrn rrrvckcprp vvksgdkpsl saryv [SEQ
ID NO:960]
```

In accordance with the presently disclosed subject matter, a “CD8 nucleic acid molecule” refers to a polynucleotide encoding a CD8 polypeptide. In certain embodiments, the CD8 nucleic acid molecule encoding the CD8 polypeptide comprised in the transmembrane domain and the intracellular domain (*e.g.*, the co-stimulatory signaling region) of the presently disclosed CAR (amino acids 137 to 207 of SEQ ID NO:960) comprises nucleic acids having the sequence set forth in SEQ ID NO:961 as provided below.

```
CCCACCACGACGCCAGCGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGTCCCTG
CGCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGAT
ATCTACATCTGGGCGCCCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTAC
TGCAAC [SEQ ID NO:961]
```

In certain non-limiting embodiments, a CAR can also comprise a spacer region that links the extracellular antigen-binding domain to the transmembrane domain. The spacer region can be flexible enough to allow the antigen binding domain to orient in different directions to facilitate antigen recognition. The spacer region can be the hinge region from IgG1, or the CH_2CH_3 region of immunoglobulin and portions of CD3.

Intracellular Domain of a CAR

In certain non-limiting embodiments, an intracellular domain of the CAR can comprise a CD3ζ polypeptide, which can activate or stimulate a cell (*e.g.*, a cell of the lymphoid lineage, *e.g.*, a T cell). CD3ζ comprises three ITAMs, and transmits an activation signal to the cell (*e.g.*, a cell of the lymphoid lineage, *e.g.*, a T cell) after antigen is bound. The CD3ζ polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100% homologous to the sequence set forth in SEQ ID NO:941, or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions. In non-limiting embodiments, the CD3ζ polypeptide can have an amino acid sequence that is a consecutive portion of SEQ ID NO:941 which is at least 20, or at least 30, or at least 40, or at least 50, and up to 163 amino acids in length. Alternatively or additionally, in non-limiting various embodiments, the CD3ζ polypeptide has an amino acid sequence of amino acids 1 to 163, 1 to 50, 50 to 100, 100 to 150, or 150 to 163 of SEQ ID NO:941. In certain embodiments, the CD3ζ polypeptide comprised in the intracellular domain of a presently disclosed CAR has an amino acid sequence of amino acids 52 to 163 of SEQ ID NO: 941.

SEQ ID NO: 941 is provided below:

```
1   MKWKALFTAA ILQAQLPITE AQSFGLLDPK LCYLLDGILF IYGVILTALF LRVKFSRSAD
61  APAYQQGQNQ LYNELNLGRR EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE
121 AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR [SEQ ID NO:941]
```

In accordance with the presently disclosed subject matter, a "CD3ζ nucleic acid molecule" refers to a polynucleotide encoding a CD3ζ polypeptide. In certain embodiments, the CD3ζ nucleic acid molecule encoding the CD3ζ polypeptide comprised in the intracellular domain of a presently disclosed CARs (amino acids 52 to 163 of SEQ ID NO: 941) comprises nucleic acids having the sequence set forth in SEQ ID NO:942 as provided below.

```
AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAG
CTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGG
GGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAG
GCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGT
CTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAA   [SEQ
ID NO:942]
```

In certain non-limiting embodiments, an intracellular domain of the CAR further comprises at least one signaling region. The at least one signaling region can include a CD28 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a DAP-10 polypeptide, a PD-1 polypeptide, a CTLA-4 polypeptide, a LAG-3 polypeptide, a 2B4 polypeptide, a BTLA polypeptide, a synthetic peptide (not based on a protein associated with the immune response), or a combination thereof.

In certain embodiments, the signaling region is a co-stimulatory signaling region. In certain embodiments, the co-stimulatory region comprises at least one co-stimulatory molecule, which can provide optimal lymphocyte activation. As used herein, "co-stimulatory molecules" refer to cell surface molecules other than antigen receptors or their ligands that are required for an efficient response of lymphocytes to antigen. The at least one co-stimulatory signaling region can include a CD28 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a DAP-10 polypeptide, or a combination thereof. The co-stimulatory molecule can bind to a co-stimulatory ligand, which is a protein expressed on cell surface that upon binding to its receptor produces a co-stimulatory response, *i.e.*, an intracellular response that effects the stimulation provided when an antigen binds to its CAR molecule. Co-stimulatory ligands, include, but are not limited to CD80, CD86, CD70, OX40L, 4-1BBL, CD48, TNFRSF14, and PD-L1. As one example, a 4-1BB ligand (*i.e.*, 4-1BBL) may bind to 4-1BB (also known as "CD137") for providing an intracellular signal that in combination with a CAR signal induces an effector cell function of the CAR$^+$ T cell. CARs comprising an intracellular domain that comprises a co-stimulatory signaling region comprising 4-1BB, ICOS or DAP-10 are disclosed in U.S. 7,446,190 (*e.g.*, the nucleotide sequence encoding 4-1BB is set forth in SEQ ID NO:15, the nucleotide sequence encoding ICOS is set forth in SEQ ID NO:16, and the nucleotide sequence encoding DAP-10 is set forth in SEQ ID NO:17 in U.S.7,446,190), which is herein incorporated by reference in its entirety. In certain embodiments, the intracellular domain of the CAR comprises a co-stimulatory signaling region that comprises a CD28 polypeptide. In certain embodiments, the intracellular domain of the CAR comprises a co-stimulatory signaling region that comprises two co-stimulatory molecules:CD28 and 4-1BB or CD28 and OX40.

4-1BB can act as a tumor necrosis factor (TNF) ligand and have stimulatory activity. The 4-1BB polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or 100% homologous to the sequence having a NCBI Reference No: P41273 or NP_001552 (SEQ ID NO:943) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions. In certain embodiments, the 4-1BB polypeptide comprised in the intracellular domain of a presently disclosed CAR has an amino acid sequence of amino acids 214 to 255 of SEQ ID NO: 943. SEQ ID NO:943 is provided below:

1 MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSPCPP NSFSSAGGQR
61 TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS MCEQDCKQGQ ELTKKGCKDC
121 CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SVTPPAPARE
181 PGHSPQIISF FLALTSTALL FLLFFLTLRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG
241 CSCRFPEEEE GGCEL [SEQ ID NO:943]

In accordance with the presently disclosed subject matter, a “4-1BB nucleic acid molecule” refers to a polynucleotide encoding a 4-1BB polypeptide. In certain embodiments, the 4-1BB nucleic acid molecule encoding the 4-1BB polypeptide comprised in the intracellular domain of a presently disclosed CARs (amino acids 214 to 255 of SEQ ID NO: 943) comprises nucleic acids having the sequence set forth in SEQ ID NO: 962 as provided below.

AAACGGGGCAGAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAA
GAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTG [SEQ ID NO:
962]

An OX40 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or 100% homologous to the sequence having a NCBI Reference No: P43489 or NP_003318 (SEQ ID NO:944), or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:944 is provided below:

1 MCVGARRLGR GPCAALLLLG LGLSTVTGLH CVGDTYPSND RCCHECRPGN GMVSRCSRSQ
61 NTVCRPCGPG FYNDVVSSKP CKPCTWCNLR SGSERKQLCT ATQDTVCRCR AGTQPLDSYK
121 PGVDCAPCPP GHFSPGDNQA CKPWTNCTLA GKHTLQPASN SSDAICEDRD PPATQPQETQ
181 GPPARPITVQ PTEAWPRTSQ GPSTRPVEVP GGRAVAAILG LGLVLGLLGP LAILLALYLL
241 RRDQRLPPDA HKPPGGGSFR TPIQEEQADA HSTLAKI [SEQ ID NO:944]

In accordance with the presently disclosed subject matter, an “OX40 nucleic acid molecule” refers to a polynucleotide encoding an OX40 polypeptide.

An ICOS polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or 100% homologous to the sequence having a NCBI Reference No: NP_036224 (SEQ ID NO:945) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:945 is provided below:

```
1   MKSGLWYFFL FCLRIKVLTG EINGSANYEM FIFHNGGVQI LCKYPDIVQQ FKMQLLKGGQ
61  ILCDLTKTKG SGNTVSIKSL KFCHSQLSNN SVSFFLYNLD HSHANYYFCN LSIFDPPPFK
121 VTLTGGYLHI YESQLCCQLK FWLPIGCAAF VVVCILGCIL ICWLTKKKYS SSVHDPNGEY
181 MFMRAVNTAK KSRLTDVTL [SEQ ID NO: 945]
```

In accordance with the presently disclosed subject matter, an “ICOS nucleic acid molecule” refers to a polynucleotide encoding an ICOS polypeptide.

CTLA-4 is an inhibitory receptor expressed by activated T cells, which when engaged by its corresponding ligands (CD80 and CD86; B7-1 and B7-2, respectively), mediates activated T cell inhibition or anergy. In both preclinical and clinical studies, CTLA-4 blockade by systemic antibody infusion, enhanced the endogenous anti-tumor response albeit, in the clinical setting, with significant unforeseen toxicities.

CTLA-4 contains an extracellular V domain, a transmembrane domain, and a cytoplasmic tail. Alternate splice variants, encoding different isoforms, have been characterized. The membrane-bound isoform functions as a homodimer interconnected by a disulfide bond, while the soluble isoform functions as a monomer. The intracellular domain is similar to that of CD28, in that it has no intrinsic catalytic activity and contains one YVKM motif able to bind PI3K, PP2A and SHP-2 and one proline-rich motif able to bind SH3 containing proteins. One role of CTLA-4 in inhibiting T cell responses seem to be directly via SHP-2 and PP2A dephosphorylation of TCR-proximal signaling proteins such as CD3 and LAT. CTLA-4 can also affect signaling indirectly via competing with CD28 for CD80/86 binding. CTLA-4 has also been shown to bind and/or interact with PI3K, CD80, AP2M1, and PPP2R5A.

In accordance with the presently disclosed subject matter, a CTLA-4 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100% homologous to UniProtKB/Swiss-Prot Ref. No.: P16410.3 (SEQ ID NO:946) (homology herein may be determined using standard software such as BLAST or FASTA) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:946 is provided below:

```
1   MACLGFQRHK AQLNLATRTW PCTLLFFLLF IPVFCKAMHV AQPAVVLASS RGIASFVCEY
61  ASPGKATEVR VTVLRQADSQ VTEVCAATYM MGNELTFLDD SICTGTSSGN QVNLTIQGLR
121 AMDTGLYICK VELMYPPPYY LGIGNGTQIY VIDPEPCPDS DFLLWILAAV SSGLFFYSFL
```

181 LTAVSLSKML KKRSPLTTGV YVKMPPTEPE CEKQFQPYFI PIN [SEQ ID NO:946]

In accordance with the presently disclosed subject matter, a "CTLA-4 nucleic acid molecule" refers to a polynucleotide encoding a CTLA-4 polypeptide.

PD-1 is a negative immune regulator of activated T cells upon engagement with its corresponding ligands PD-L1 and PD-L2 expressed on endogenous macrophages and dendritic cells. PD-1 is a type I membrane protein of 268 amino acids. PD-1 has two ligands, PD-L1 and PD-L2, which are members of the B7 family. The protein's structure comprises an extracellular IgV domain followed by a transmembrane region and an intracellular tail. The intracellular tail contains two phosphorylation sites located in an immunoreceptor tyrosine-based inhibitory motif and an immunoreceptor tyrosine- based switch motif, that PD-1 negatively regulates TCR signals. SHP- I and SHP-2 phosphatases bind to the cytoplasmic tail of PD-1 upon ligand binding. Upregulation of PD-L1 is one mechanism tumor cells may evade the host immune system. In pre- clinical and clinical trials, PD-1 blockade by antagonistic antibodies induced anti-tumor responses mediated through the host endogenous immune system.

In accordance with the presently disclosed subject matter, a PD-1 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100% homologous to NCBI Reference No: NP_005009.2 (SEQ ID NO:947) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:947 is provided below:

1 MQIPQAPWPV VWAVLQLGWR PGWFLDSPDR PWNPPTFSPA LLVVTEGDNA TFTCSFSNTS
61 ESFVLNWYRM SPSNQTDKLA AFPEDRSQPG QDCRFRVTQL PNGRDFHMSV VRARRNDSGT
121 YLCGAISLAP KAQIKESLRA ELRVTERRAE VPTAHPSPSP RPAGQFQTLV VGVVGGLLGS
181 LVLLVWVLAV ICSRAARGTI GARRTGQPLK EDPSAVPVFS VDYGELDFQW REKTPEPPVP
241 CVPEQTEYAT IVFPSGMGTS SPARRGSADG PRSAQPLRPE DGHCSWPL [SEQ ID NO:947]

In accordance with the presently disclosed subject matter, a "PD-1 nucleic acid molecule" refers to a polynucleotide encoding a PD-1 polypeptide.

Lymphocyte-activation protein 3 (LAG-3) is a negative immune regulator of immune cells. LAG-3 belongs to the immunoglobulin (lg) superfamily and contains 4 extracellular Ig-like domains. The LAG3 gene contains 8 exons. The sequence data, exon/intron organization, and chromosomal localization all indicate a close relationship of LAG3 to CD4. LAG3 has also been designated CD223 (cluster of differentiation 223).

In accordance with the the presently disclosed subject matter, a LAG-3 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100% homologous to UniProtKB/Swiss-Prot Ref. No.: P18627.5 (SEQ ID NO:948) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:948 is provided below:

```
1 MWEAQFLGLL FLQPLWVAPV KPLQPGAEVP VVWAQEGAPA QLPCSPTIPL QDLSLLRRAG
61 VTWQHQPDSG PPAAAPGHPL APGPHPAAPS SWGPRPRRYT VLSVGPGGLR SGRLPLQPRV
121 QLDERGRQRG DFSLWLRPAR RADAGEYRAA VHLRDRALSC RLRLRLGQAS MTASPPGSLR
181 ASDWVILNCS FSRPDRPASV HWFRNRGQGR VPVRESPHHH LAESFLFLPQ VSPMDSGPWG
241 CILTYRDGFN VSIMYNLTVL GLEPPTPLTV YAGAGSRVGL PCRLPAGVGT RSFLTAKWTP
301 PGGGPDLLVT GDNGDFTLRL EDVSQAQAGT YTCHIHLQEQ QLNATVTLAI ITVTPKSFGS
361 PGSLGKLLCE VTPVSGQERF VWSSLDTPSQ RSFSGPWLEA QEAQLLSQPW QCQLYQGERL
421 LGAAVYFTEL SSPGAQRSGR APGALPAGHL LLFLILGVLS LLLLVTGAFG FHLWRRQWRP
481 RRFSALEQGI HPPQAQSKIE ELEQEPEPEP EPEPEPEPEP EPEQL [SEQ ID NO:948]
```

In accordance with the presently disclosed subject matter, a “LAG-3 nucleic acid molecule” refers to a polynucleotide encoding a LAG-3 polypeptide.

Natural Killer Cell Receptor 2B4 (2B4) mediates non-MHC restricted cell killing on NK cells and subsets of T cells. To date, the function of 2B4 is still under investigation, with the 2B4-S isoform believed to be an activating receptor, and the 2B4- L isoform believed to be a negative immune regulator of immune cells. 2B4 becomes engaged upon binding its high-affinity ligand, CD48. 2B4 contains a tyrosine-based switch motif, a molecular switch that allows the protein to associate with various phosphatases. 2B4 has also been designated CD244 (cluster of differentiation 244).

In accordance with the presently disclosed subject matter, a 2B4 polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100% homologous to UniProtKB/Swiss-Prot Ref. No.: Q9BZW8.2 (SEQ ID NO:949) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:949 is provided below:

1 MLGQVVTLIL LLLLKVYQGK GCQGSADHVV SISGVPLQLQ PNSIQTKVDS IAWKKLLPSQ
61 NGFHHILKWE NGSLPSNTSN DRFSFIVKNL SLLIKAAQQQ DSGLYCLEVT SISGKVQTAT
121 FQVFVFESLL PDKVEKPRLQ GQGKILDRGR CQVALSCLVS RDGNVSYAWY RGSKLIQTAG
181 NLTYLDEEVD INGTHTYTCN VSNPVSWESH TLNLTQDCQN AHQEFRFWPF LVIIVILSAL
241 FLGTLACFCV WRRKRKEKQS ETSPKEFLTI YEDVKDLKTR RNHEQEQTFP GGGSTIYSMI
301 QSQSSAPTSQ EPAYTLYSLI QPSRKSGSRK RNHSPSFNST IYEVIGKSQP KAQNPARLSR
361 KELENFDVYS [SEQ ID NO:949]

In accordance with the presently disclosed subject matter, a “2B4 nucleic acid molecule” refers to a polynucleotide encoding a 2B4 polypeptide.

B- and T-lymphocyte attenuator (BTLA) expression is induced during activation of T cells, and BTLA remains expressed on Th1 cells but not Th2 cells. Like PD1 and CTLA4, BTLA interacts with a B7 homolog, B7H4. However, unlike PD-1 and CTLA-4, BTLA displays T-Cell inhibition via interaction with tumor necrosis family receptors (TNF-R), not just the B7 family of cell surface receptors. BTLA is a ligand for tumor necrosis factor (receptor) superfamily, member 14 (TNFRSF14), also known as herpes virus entry mediator (HVEM). BTLA-HVEM complexes negatively regulate T-cell immune responses. BTLA activation has been shown to inhibit the function of human $CD8^+$ cancer-specific T cells. BTLA has also been designated as CD272 (cluster of differentiation 272).

In accordance with the presently disclosed subject matter, a BTLA polypeptide can have an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100% homologous to UniProtKB/Swiss-Prot Ref. No.: Q7Z6A9.3 (SEQ ID NO:950) or fragments thereof, and/or may optionally comprise up to one or up to two or up to three conservative amino acid substitutions.

SEQ ID NO:950 is provided below:

1 MKTLPAMLGT GKLFWVFFLI PYLDIWNIHG KESCDVQLYI KRQSEHSILA GDPFELECPV
61 KYCANRPHVT WCKLNGTTCV KLEDRQTSWK EEKNISFFIL HFEPVLPNDN GSYRCSANFQ
121 SNLIESHSTT LYVTDVKSAS ERPSKDEMAS RPWLLYRLLP LGGLPLLITT CFCLFCCLRR
181 HQGKQNELSD TAGREINLVD AHLKSEQTEA STRQNSQVLL SETGIYDNDP DLCFRMQEGS
241 EVYSNPCLEE NKPGIVYASL NHSVIGPNSR LARNVKEAPT EYASICVRS [SEQ ID NO:950]

In accordance with the presently disclosed subject matter, a “BTLA nucleic acid molecule" refers to a polynucleotide encoding a BTLA polypeptide.

In certain embodiments, the CAR comprises an extracellular antigen-binding region that specifically binds to human FcRL5, a transmembrane domain comprising a CD28 polypeptide, and an intracellular domain comprising a CD3ζ polypeptide and a co-stimulatory signaling region that comprises a CD28 polypeptide, as shown in Figure 9. As shown in Figure 9, the CAR also comprises a signal peptide or a leader covalently joined to the 5' terminus of the extracellular antigen-binding domain. The signal peptide comprises a CD8 polypeptide.

In certain embodiments, the CAR of the presently disclosed subject matter can further comprise an inducible promoter, for expressing nucleic acid sequences in human cells. Promoters for use in expressing CAR genes can be a constitutive promoter, such as ubiquitin C (UbiC) promoter.

The presently disclosed subject matter also provides isolated nucleic acid molecule encoding the FcRL5-targeted CAR described herein or a functional portion thereof. In certain embodiments, the isolated nucleic acid molecule encodes a presently disclosed FcRL5-targeted CAR comprising an scFv that specifically binds to human FcRL5, a transmembrane domain comprising a CD28 polypeptide, and an intracellular domain comprising a CD3ξ polypeptide and a co-stimulatory signaling region comprising a CD28 polypeptide. In certain embodiments, the scFv is a fully human scFv. In certain embodiments, the scFv is a murine scFv. In certain non-limiting embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:951 provided below:

ATGGCTCTCCCAGTGACTGCCCTACTGCTTCCCCTAGCGCTTCTCCTGCATGCAGCTCGTGTGAAGCTG
CAGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCGGAAACTCTCCTGTGCAGCCTCTGGATTC
ACTTTCAGTATCTTTGGATTGCACTGGGTTCGTCAGGCTCCAGAGAAGGGGCTGGAGTGGGTCGCATAC
ATTAGTGGTGACAGTAATACCATCTACTATGCAGACACAGTGAAGGGCCGATTCACCATCTCCAGAGAC
AATCCCAAGAACACCCTGTTCCTGCAAATGACCAGTCTAAGGTCTGAGGACACGGCCATGTATTACTGT
GCAAGAAATAGCTACTATGCTCTGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA
GGTGGATCAGGTGGAGGTGGATCTGGTGGAGGTGGATCTGACATTGAGCTCACCCAGTCTCCAGCAATC
ATGTCTGTATCTCCAGGTGAAAAGGTCACCATGACCTGCAGGGCCAGCTCAAGTGTCAGTTCCAGTTAC
TTGCACTGGTACCAGCAGAGGTCAGGTGCCTCCCCCAAAATCTGGATTTATAGCACATCCAACTTGGCT
TCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGACTGGGACCTCTTACTCTCTCACAATCAGCAGTGTG
GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTACAGTGGTTACCCGTGGACGTTCGGTGGAGGG
ACCAAGCTGGAGATCGAACAAAAACTCATCTCAGAAGAGGATCTGGCGGCCGCAATTGAAGTTATGTAT
CCTCCTCCTTACCTAGACAATGAGAAGAGCAATGGAACCATTATCCATGTGAAAGGGAAACACCTTTGT

CCAAGTCCCCTATTTCCCGGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTTGGTGGAGTCCTGGCT
TGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCCTG
CACAGTGACTACATGAACATGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCATTACCAGCCCTATGCC
CCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTAC
CAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGAC
AAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTAC
AATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGG
GGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCAC
ATGCAGGCCCTGCCCCCTCGCTAA [SEQ ID NO:951] The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:951 encodes a FcRL-5-targeted CAR comprising a murine scFv that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:915, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:917, and a linker having an amino acid sequence of SEQ ID NO:897 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD28 polypeptide, and an intracellular domain comprising a CD3ξ polypeptide and a co-stimulatory signaling region comprising a CD28 polypeptide.

In another specific non-limiting example, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:952 provided below:

ATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACGTCCA
ACTGCAGGAGTCAGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCGGAAACTCTCCTGTACAGCCTCTGG
ATTCACTTTCAGTAGCTTTGGAATGCACTGGGTTCGTCAGGCTCCAGAGAAGGGGCTGGAGTGGGTCGC
ATACATTAGTAGTGGCAGTAATAACATCTACTTTGCGGACACAGTGAAGGGCCGATTCACCATCTCCAG
AGACAATCCCAAGAACACCCTGTTCCTGCAAATGACCAGTCTAAGGTCTGAGGACACGGCCATGTATTA
CTGTGCAAGATCGGAATACTACGGTAGTAGCCATATGGACTACTGGGGCCAAGGGACCACGGTCACCGT
CTCCTCAGGTGGAGGTGGATCAGGTGGAGGTGGATCTGGTGGAGGTGGATCTGACATTGAGCTCACCCA
GTCTCCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCAGTCAGAATGT
GGGTACTAATGTAGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACCACTGATTTACTCGGCAAC
CTACCGGAACAGTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCAT
CACTAACGTGCAGTCTAAAGACTTGGCAGACTATTTCTGTCAACAATATAACAGGTATCCGTACACGTC
CGGAGGGGGGACCAAGCTGGAGATCGAACAAAAACTCATCTCAGAAGAGGATCTGGCGGCCGCAATTGA
AGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAGAGCAATGGAACCATTATCCATGTGAAAGGGAA
ACACCTTTGTCCAAGTCCCCTATTTCCCGGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTTGGTGG
AGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTTTCTGGGTGAGGAGTAAGAGGAG
CAGGCTCCTGCACAGTGACTACATGAACATGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCATTACCA

GCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAGTTCAGCAGGAGCGCAGACGC
CCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGA
TGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGA
AGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGA
GCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGA
CGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAA [SEQ ID NO:952]. The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:952 encodes a FcRL-5-targeted CAR comprising a murine scFv that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:919, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:921, and a linker having an amino acid sequence of SEQ ID NO:897 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD28 polypeptide, and an intracellular domain comprising a CD3ξ polypeptide and a co-stimulatory signaling region comprising a CD28 polypeptide.

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:953 provided below:

CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGATACACTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGCTCCTATGTGC
TGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCAGGATTACCTGTGGGGGAAACAACA
TTGGAAGTAAAAGTGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCCTGTGCTGGTCATCTATTATG
ATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGA
CCATCAGCAGGGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTAGTGATT
ATGTCTTCGGAACTGGGACCAAGGTCACCGTCCTAGGTTCTAGAGGTGGTGGTGGTAGCGGCGGCGGCG
GCTCTGGTGGTGGTGGATCCCTCGAGATGGCCGAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTGGTCA
AGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCGTCAGTGACTACTACATGAGCT
GGATCCGCCAGGCTCCAGGGAAGGGCCTGGAGTGGATTTCATACATTAGTGGTAGTGGTAATAGCATAT
ACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGGATCTGC
AAATGACCAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGCGCTCTACTAAATTCGATTACT
GGGGTCAAGGTACTCTGGTGACCGTCTCCTCAGCGGCCGCACCCACCACGACGCCAGCGCCGCGACCAC
CAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGG
GGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTACATCTGGGCGCCCCTGGCCGGGA
CTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGCAACAAACGGGGCAGAAAGAAGCTCC
TGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGGCTGTAGCTGCC
GATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGCAGGAGCGCAGAGCCCCCCG

CGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTT
TGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCC
TGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCC
GGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCC
TTCACATGCAGGCCCTGCCCCCTCGCTAACAGCCACTCGAGGATCCGGATTAGTCCAATTTGTTAAAGA
CAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGA
GCCATAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAG
GTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAA
GTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG
TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTT
TCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACT
AACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACA
ACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCC
TCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACC
CGTCAGCGGGGGTCTTTCACACATGCAGCATGTATCAAAATTAATTTGGTTTTTTTTCTTAAGTATTTA
CATTAAATGGCCATAGTACTTAAAGTTACATTGGCTTCCTTGAAATAAACATGGAGTATTCAGAATGTG
TCATAAATATTTCTAATTTTAAGATAGTATCTCCATTGGCTTTCTACTTTTTCTTTTATTTTTTTTTGT
CCTCTGTCTTCCATTTGTTGTTGTTGTTGTTTGTTTGTTTGTTTGTTGGTTGGTTGGTTAATTTTTTTT
TAAAGATCCTACACTATAGTTCAAGCTAGACTATTAGCTACTCTGTAACCCAGGGTGACCTTGAAGTCA
TGGGTAGCCTGCTGTTTTAGCCTTCCCACATCTAAGATTACAGGTATGAGCTATCATTTTTGGTATATT
GATTGATTGATTGATTGATGTGTGTGTGTGTGATTGTGTTTGTGTGTGTGACTGTGAAAATGTGTGTAT
GGGTGTGTGTGAATGTGTGTATGTATGTGTGTGTGTGAGTGTGTGTGTGTGTGTGTGCATGTGTGTGTG
TGTGACTGTGTCTATGTGTATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTTGTGAAAAAATATTCTATGGTAGTGAGAGCCAACGCTCCGGCTCAGGTGTCAGGTTGGTTTTTGAGA
CAGAGTCTTTCACTTAGCTTGGAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGG
CGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCG
CACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCT
TACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATA
GTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATC
CGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAA
ACGCGCGATGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTT
CTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATAC
ATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGA
GTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTG
CTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCG
AACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCA
CTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCC
GCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCA
TGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGA

CAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTG
ATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAA
TGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAG
ACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTG
CTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGC
CCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCG
CTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGA
TTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCA
AAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTT
GAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTT
GTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAA
ATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACC
TCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACT
CAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCT
TGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCG
AAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTC
CAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTT
TGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGG
CCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTA
CCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGG
AAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGC
ACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATT
AGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAAT
TTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTTGCTCTTAGGAGTTTCCTAATACATCCC
AAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGGGGGCGGGGGGAAGCTAAGCCAGCTTT
TTTTAACATTTAAAATGTTAATTCCATTTTAAATGCACAGATGTTTTTATTTCATAAGGGTTTCAATGT
GCATGAATGCTGCAATATTCCTGTTACCAAAGCTAGTATAAATAAAAATAGATAAACGTGGAAATTACT
TAGAGTTTCTGTCATTAACGTTTCCTTCCTCAGTTGACAACATAAATGCGCTGCTGAGCAAGCCAGTTT
GCATCTGTCAGGATCAATTTCCCATTATGCCAGTCATATTAATTACTAGTCAATTAGTTGATTTTTATT
TTTGACATATACATGTGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTT
TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAGATGGAACA
GCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGAT
GGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGA
ACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGC
CCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCG
CGCGCTTATGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATT
GACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGC
TGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGGGGCTCG
TCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTT
ATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTA

ACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGA
GACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCTAAAATCCCGATCGTTTAGGA
CTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTC
CCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGTCTTGTCTGCTGCAGC
ATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATATGGGCCCGGGCTAGACT
GTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCG
GTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGG
CCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCG
CATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGG
GTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAA
CCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATA
TGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCTGACATGACAAGA
GTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAGA
CCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGA [SEQ ID NO:953]. The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:953 encodes a FcRL-5-targeted CAR (designated as 31 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-998 of SEQ ID NO:953) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:116, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:115, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 270-998 of SEQ ID NO: 953 encodes the human scFv. Nucleotides 1008-1220 of SEQ ID NO: 953 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1221-1346 of SEQ ID NO: 953 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1347-1685 of SEQ ID NO: 953 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 953 are shown in Table 232.

Table 232

Portions	Nucleotide Sequence	Number of Nucleotides

	Positions of SEQ ID NO: 953	
anti-FcRL5 scFv 31	207..998	792
CD8a TM	1008..1220	213
4-1BB	1221..1346	126
CD3zeta	1347..1685	339
LTR	1965..2434	470
M13 fwd	3133..3149	17
AmpR promoter	3624..3728	105
AmpR	3729..4589	861
ori	4760..5348	589
CAP binding site	5636..5657	22
lac promoter	5672..5702	31
lac operator	5710..5726	17
M13 rev	5734..5750	17
LTR	6159..6752	594
MMLV Psi	6815..7172	358
gag (truncated)	7237..7653	417

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:954 provided below:

CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGATACACTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGCAATTTTATGC
TGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGCAGTG
GCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAGTTCCCCCACCACTGTGATCT
ATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAGCTCCTCCAACT
CTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACGAGGCTGACTACTACTGTCAGTCTTATGATA
GCAGCAATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTTCTAGAGGTGGTGGTGGTAGCG
GCGGCGGCGGCTCTGGTGGTGGTGGATCCCTCGAGATGGCCGAGGTCCAGCTGGTGCAGTCTGGGGCTG
AGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATG
CTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTG
GTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAG
CCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGCTCTAACTACT
ACTACAACGATTACTGGGGTCAAGGTACTCTGGTGACCGTCTCCTCAGCGGCCGCACCCACCACGACGC

CAGCGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGT
GCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTACATCTGGG
CGCCCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGCAACAAACGGG
GCAGAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAG
ATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGCAGGA
GCGCAGAGCCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAG
AGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGA
ACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGA
TGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGG
ACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAACAGCCACTCGAGGATCCGGATTAGT
CCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCAGCTGAA
GCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAA
AGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATA
ACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGAT
ATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAA
CAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTC
CAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTG
TGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCA
ATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
GTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCT
GAGTGATTGACTACCCGTCAGCGGGGGTCTTTCACACATGCAGCATGTATCAAAATTAATTTGGTTTTT
TTTCTTAAGTATTTACATTAAATGGCCATAGTACTTAAAGTTACATTGGCTTCCTTGAAATAAACATGG
AGTATTCAGAATGTGTCATAAATATTTCTAATTTTAAGATAGTATCTCCATTGGCTTTCTACTTTTTCT
TTTATTTTTTTTTGTCCTCTGTCTTCCATTTGTTGTTGTTGTTGTTTGTTTGTTTGTTTGTTGGTTGGT
TGGTTAATTTTTTTTTAAAGATCCTACACTATAGTTCAAGCTAGACTATTAGCTACTCTGTAACCCAGG
GTGACCTTGAAGTCATGGGTAGCCTGCTGTTTTAGCCTTCCCACATCTAAGATTACAGGTATGAGCTAT
CATTTTTGGTATATTGATTGATTGATTGATTGATGTGTGTGTGTGTGATTGTGTTTGTGTGTGTGACTG
TGAAAATGTGTGTATGGGTGTGTGTGAATGTGTGTATGTATGTGTGTGTGTGAGTGTGTGTGTGTGTGT
GTGCATGTGTGTGTGTGTGTGACTGTGTCTATGTGTATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTTGTGAAAAAATATTCTATGGTAGTGAGAGCCAACGCTCCGGCTCAGGTGTCA
GGTTGGTTTTTGAGACAGAGTCTTTCACTTAGCTTGGAATTCACTGGCCGTCGTTTTACAACGTCGTGA
CTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAA
TAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGAT
GCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCTCAGTACAATCTG
CTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTG
TCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTC
ACCGTCATCACCGAAACGCGCGATGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCA
TGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTT
TATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAAT
ATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTT

GCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCAC
GAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTT
TTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAG
AGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGC
ATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGG
CCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATC
ATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCA
CGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCC
GGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGG
CTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGG
GGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAAC
GAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACT
CATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTG
ATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGA
TCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGC
TACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA
GAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAG
CACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTC
TTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGT
GCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAA
GCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGC
GCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGAC
TTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCT
TTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTG
TGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCG
AGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTC
ATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGA
GTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTG
TGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTTGCTCTTAGGAGT
TTCCTAATACATCCCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGGGGGCGGGGGGA
AGCTAAGCCAGCTTTTTTTAACATTTAAAATGTTAATTCCATTTTAAATGCACAGATGTTTTTATTTCA
TAAGGGTTTCAATGTGCATGAATGCTGCAATATTCCTGTTACCAAAGCTAGTATAAATAAAAATAGATA
AACGTGGAAATTACTTAGAGTTTCTGTCATTAACGTTTCCTTCCTCAGTTGACAACATAAATGCGCTGC
TGAGCAAGCCAGTTTGCATCTGTCAGGATCAATTTCCCATTATGCCAGTCATATTAATTACTAGTCAAT
TAGTTGATTTTTATTTTTGACATATACATGTGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCT
TAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCA
GGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCA
GGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCC
GGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAG
ATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCT

TCTCGCTTCTGTTCGCGCGCTTATGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGC
GCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCC
GACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTT
TCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAA
GCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGATTTTATGCGCCTGCGTC
GGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCG
GCCGCAACCCTGGGAGACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCTAAAAT
CCCGATCGTTTAGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAG
AACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGT
CTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATATG
GGCCCGGGCTAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATC
GCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTC
TTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTT
GACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCG
TCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCT
CTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGAC
CCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAG
CACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGA [SEQ ID NO:954].

The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:954 encodes a FcRL-5-targeted CAR (designated as 39 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-1013 of SEQ ID NO:954) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:144, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:143, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 207-1013 of SEQ ID NO: 954 encodes the human scFv. Nucleotides 1023-1235 of SEQ ID NO: 954 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1236-1361 of SEQ ID NO: 954 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1362-1700 of SEQ ID NO: 954 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 954 are shown in Table 233.

Table 233

Portions	Nucleotide Sequence Positions of SEQ ID NO: 954	Number of Nucleotides
anti-FcRL5 scFv 39	207..1013	807
CD8a TM	1023..1235	213
4-1BB	1236..1361	126
CD3zeta	1362..1700	339
LTR	1980..2449	470
M13 fwd	3148..3164	17
AmpR promoter	3639..3743	105
AmpR	3744..4604	861
ori	4775..5363	589
CAP binding site	5651..5672	22
lac promoter	5687..5717	31
lac operator	5725..5741	17
M13 rev	5749..5765	17
LTR	6174..6767	594
MMLV Psi	6830..7187	358
gag (truncated)	7252..7668	417

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:955 provided below:

CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGACAGTCTGTCG
TGACGCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCT
CCAACATCGGAAGTAATTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCT
ATAGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCT
CCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCC

TGAGTGGTTATGTCTTCGGAACTGGGACCAAGCTGACCGTCCTAGGTTCTAGAGGTGGTGGTGGTAGCG
GCGGCGGCGGCTCTGGTGGTGGTGGATCCCTCGAGATGGCCCAGGTGCAGCTACAGCAGTGGGGCGCAG
GACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACT
ACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAA
GCACCAACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCT
CCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGCGCCTGTACGAAGGTG
GTTACCATGGTTGGGGTTCTTGGCTGTCTTCTGATTCTTGGGGTCAAGGTACTCTGGTGACCGTCTCCT
CAGCGGCCGCACCCACCACGACGCCAGCGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGC
CCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACT
TCGCCTGTGATATCTACATCTGGGCGCCCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTA
TCACCCTTTACTGCAACAAACGGGGCAGAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGAC
CAGTACAAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTG
AACTGAGAGTGAAGTTCAGCAGGAGCGCAGAGCCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATA
ACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGA
TGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGG
CGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACC
AGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAAC
AGCCACTCGAGGATCCGGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTT
GACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATTTAG
TCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATT
TTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAAC
AGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTG
CCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTC
GCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGAT
TGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCG
CTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCACACATGCAGCA
TGTATCAAAATTAATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTACTTAAAGTTACA
TTGGCTTCCTTGAAATAAACATGGAGTATTCAGAATGTGTCATAAATATTTCTAATTTTAAGATAGTAT
CTCCATTGGCTTTCTACTTTTTCTTTTATTTTTTTTTGTCCTCTGTCTTCCATTTGTTGTTGTTGTTGT
TTGTTTGTTTGTTTGTTGGTTGGTTGGTTAATTTTTTTTTAAAGATCCTACACTATAGTTCAAGCTAGA
CTATTAGCTACTCTGTAACCCAGGGTGACCTTGAAGTCATGGGTAGCCTGCTGTTTTAGCCTTCCCACA
TCTAAGATTACAGGTATGAGCTATCATTTTTGGTATATTGATTGATTGATTGATTGATGTGTGTGTGTG
TGATTGTGTTTGTGTGTGTGACTGTGAAAATGTGTGTATGGGTGTGTGTGAATGTGTGTATGTATGTGT
GTGTGTGAGTGTGTGTGTGTGTGTGTGCATGTGTGTGTGTGACTGTGTCTATGTGTATGACTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGTGAAAAAATATTCTATGGTAGTGAGA
GCCAACGCTCCGGCTCAGGTGTCAGGTTGGTTTTTGAGACAGAGTCTTTCACTTAGCTTGGAATTCACT
GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACA
TCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAG

CCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCAT
ATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACC
CGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGG
GAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGATGACGAAAGGGCCTCGTGATAC
GCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAA
ATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAAT
AACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCC
TTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAG
ATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTG
AGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTAT
TATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTG
AGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCA
TAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCG
CTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCA
TACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTG
GCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGAC
CACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGT
CTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGG
GGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATT
GGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAA
GGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACT
GAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCT
GCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTT
TTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAG
GCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTG
CTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGC
GGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGAT
ACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAA
GCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTC
CTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTAT
GGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCT
TTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCC
GCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGC
CTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCA
GTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTC
CGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATT
ACGCCAAGCTTTGCTCTTAGGAGTTTCCTAATACATCCCAAACTCAAATATATAAAGCATTTGACTTGT
TCTATGCCCTAGGGGGCGGGGGGAAGCTAAGCCAGCTTTTTTTAACATTTAAAATGTTAATTCCATTTT
AAATGCACAGATGTTTTTATTTCATAAGGGTTTCAATGTGCATGAATGCTGCAATATTCCTGTTACCAA
AGCTAGTATAAATAAAAATAGATAAACGTGGAAATTACTTAGAGTTTCTGTCATTAACGTTTCCTTCCT

CAGTTGACAACATAAATGCGCTGCTGAGCAAGCCAGTTTGCATCTGTCAGGATCAATTTCCCATTATGC
CAGTCATATTAATTACTAGTCAATTAGTTGATTTTTATTTTTGACATATACATGTGAATGAAAGACCCC
ACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGA
ATAGAAAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTG
GTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATA
TCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTA
TTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTATGCTCCCCGAGCTCAATAAAAG
AGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCA
ATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGAT
TGACTACCCGTCAGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGAC
CACCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTA
TGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTG
GAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTCGGGGGCCGTTTTT
GTGGCCCGACCTGAGTCCTAAAATCCCGATCGTTTAGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTT
TGGGACCGAAGCCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTG
TTTCTGTATTTGTCTGAAAATATGGGCCCGGGCTAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGT
CACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACC
TTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTC
ATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATC
GTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCG
CCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCC
CTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCC
CCGCCCCTTGTAAACTTCCCTGACCCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCAC
TTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTG
GACCGA [SEQ ID NO:955]. The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:955 encodes a FcRL-5-targeted CAR (designated as 69 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-1037 of SEQ ID NO:955) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:172, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:171, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling

region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 207-1037 of SEQ ID NO: 955 encodes the human scFv. Nucleotides 1047-1259 of SEQ ID NO: 955 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1260-1385 of SEQ ID NO: 955 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1386-1724 of SEQ ID NO: 955 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 955 are shown in Table 234.

Table 234

Portions	Nucleotide Sequence Positions of SEQ ID NO: 955	Number of Nucleotides
anti-FcRL5 scFv 69	207..1037	831
CD8a TM	1047..1259	213
4-1BB	1260..1385	126
CD3zeta	1386..1724	339
LTR	2004..2473	470
M13 fwd	3172..3188	17
AmpR promoter	3663..3767	105
AmpR	3768..4628	861
ori	4799..5387	589
CAP binding site	5675..5696	22
lac promoter	5711..5741	31
lac operator	5749..5765	17
M13 rev	5773..5789	17
LTR	6198..6791	594
MMLV Psi	6854..7211	358
gag (truncated)	7276..7692	417

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:956 provided below:

CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGAAATTTTATGC
TGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGCAGTG
GCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGCAGCGCCCGGGCAGTGCCCCCACCACTGTGATCT
ATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAGCTCCTCCAACT
CTGCCTCCCTCACCATCTCTGGACTGAAGACTGAGGACGAGGCTGACTACTACTGTCAGTCTTATGATA
GCAGCAATGTGGTATTCGGCGGAGGGACCAAGGTCACCGTCCTAGGTTCTAGAGGTGGTGGTGGTAGCG
GCGGCGGCGGCTCTGGTGGTGGTGGATCCCTCGAGATGGCCGAGGTGCAGCTGGTGGAGTCTGGGGGAG
GCTTGGTACAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATG
AAATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTA
GTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCAC
TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCACGCTGGGACTACG
GTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCGGCCGCACCCACCACGACGCCAG
CGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCC
GGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTACATCTGGGCGC
CCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGCAACAAACGGGGCA
GAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATG
GCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGCAGGAGCG
CAGAGCCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGG
AGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGA
AAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACA
CCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAACAGCCACTCGAGGATCCGGATTAGTCCA
ATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCAGCTGAAGCC
TATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGA
CCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACT
GAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATC
TGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAG
GATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAG
CCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGC
CTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATA
AAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTA
TCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAG
TGATTGACTACCCGTCAGCGGGGGTCTTTCACACATGCAGCATGTATCAAAATTAATTTGGTTTTTTTT
CTTAAGTATTTACATTAAATGGCCATAGTACTTAAAGTTACATTGGCTTCCTTGAAATAAACATGGAGT
ATTCAGAATGTGTCATAAATATTTCTAATTTTAAGATAGTATCTCCATTGGCTTTCTACTTTTTCTTTT
ATTTTTTTTTGTCCTCTGTCTTCCATTTGTTGTTGTTGTTGTTTGTTTGTTTGTTTGTTGGTTGGTTGG
TTAATTTTTTTTTTAAAGATCCTACACTATAGTTCAAGCTAGACTATTAGCTACTCTGTAACCCAGGGTG

ACCTTGAAGTCATGGGTAGCCTGCTGTTTTAGCCTTCCCACATCTAAGATTACAGGTATGAGCTATCAT
TTTTGGTATATTGATTGATTGATTGATTGATGTGTGTGTGTGTGATTGTGTTTGTGTGTGTGACTGTGA
AAATGTGTGTATGGGTGTGTGTGAATGTGTGTATGTATGTGTGTGTGTGAGTGTGTGTGTGTGTGTGTG
CATGTGTGTGTGTGTGACTGTGTCTATGTGTATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTTGTGAAAAAATATTCTATGGTAGTGAGAGCCAACGCTCCGGCTCAGGTGTCAGGT
TGGTTTTTGAGACAGAGTCTTTCACTTAGCTTGGAATTCACTGGCCGTCGTTTTACAACGTCGTGACTG
GGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAG
CGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCG
GTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTC
TGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCT
GCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACC
GTCATCACCGAAACGCGCGATGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGA
TAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTAT
TTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATT
GAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCC
TTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAG
TGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTC
CAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGC
AACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATC
TTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCA
ACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATG
TAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGA
TGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGC
AACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTG
GCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGC
CAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAA
ATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCAT
ATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATA
ATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCA
AAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTAC
CAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAG
CGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAC
CGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTA
CCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCA
CACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCG
CCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCA
CGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG
AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTT
TACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGG
ATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGT

CAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATT
AATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTT
AGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGA
GCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTTGCTCTTAGGAGTTTC
CTAATACATCCCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGGGGGCGGGGGGAAGC
TAAGCCAGCTTTTTTTAACATTTAAAATGTTAATTCCATTTTAAATGCACAGATGTTTTTATTTCATAA
GGGTTTCAATGTGCATGAATGCTGCAATATTCCTGTTACCAAAGCTAGTATAAATAAAAATAGATAAAC
GTGGAAATTACTTAGAGTTTCTGTCATTAACGTTTCCTTCCTCAGTTGACAACATAAATGCGCTGCTGA
GCAAGCCAGTTTGCATCTGTCAGGATCAATTTCCCATTATGCCAGTCATATTAATTACTAGTCAATTAG
TTGATTTTTATTTTTGACATATACATGTGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAA
GTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGA
ACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
CCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGC
TCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATG
TTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCT
CGCTTCTGTTCGCGCGCTTATGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCC
AGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGAC
TTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCA
TTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAGCT
GGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGATTTTATGCGCCTGCGTCGGT
ACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCC
GCAACCCTGGGAGACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCTAAAATCCC
GATCGTTTAGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAAC
CTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGTCTT
GTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATATGGGC
CCGGGCTAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCT
CACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTT
AACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTT
TCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGAC
CCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCT
CTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTA
GGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCT
GACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCAC
GAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGA [SEQ ID NO:956].

The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:956 encodes a FcRL-5-targeted CAR (designated as 104 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-1010) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:216, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:215, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 207-1010 of SEQ ID NO: 956 encodes the human scFv. Nucleotides 1020-1232 of SEQ ID NO: 956 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1233-1358 of SEQ ID NO: 956 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1359-1697 of SEQ ID NO: 956 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 956 are shown in Table 235.

Table 235

Portions	Nucleotide Sequence Positions of SEQ ID NO: 956	Number of Nucleotides
antiFcRL5 scFv 104	207..1010	804
CD8a TM	1020..1232	213
4-1BB	1233..1358	126
CD3zeta	1359..1697	339
LTR	1977..2446	470
M13 fwd	3145..3161	17
AmpR promoter	3636..3740	105
AmpR	3741..4601	861
ori	4772..5360	589
CAP binding site	5648..5669	22
lac promoter	5684..5714	31
lac operator	5722..5738	17
M13 rev	5746..5762	17
LTR	6171..6764	594

MMLV Psi	6827..7184	358
gag (truncated)	7249..7665	417

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:957 provided below:

CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGATACACTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGCTCCTATGTGC
TGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGAT
TGACGAATAAATATGTTTCCTGGTATCAACAGAAGCCAGGCCAGTCCCCTGTGTTGGTCATCTATGAGG
ATGCCAAGCGGCCCTCAGGGATCCCTGCGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGA
CCATCAGCGGGACCCAGGCTATGGATGAGTCTGAATATTACTGTCAGGCGTGGGACAGCAGTGTGGTGG
TTTTTGGCGGAGGGACCAAGCTGACCGTCCTAGGTTCTAGAGGTGGTGGTGGTAGCGGCGGCGGCGGCT
CTGGTGGTGGTGGATCCCTCGAGATGGCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGC
CTGGCAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTTACCTTTGATGATTATGCCATGCACTGGG
TCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATTAGTTGGAATAGTGGTAGTATAGGCT
ATGCGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAA
TGAACAGTCTGAGAGATGAGGACACGGCCTTGTATTACTGTGCAAAAGACCGAGGGGGGGGAGTTATCG
TTAAGGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGCGGCCGCACCCACCA
CGACGCCAGCGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGTCCCTGCGCCCAG
AGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTACA
TCTGGGCGCCCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGCAACA
AACGGGGCAGAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAG
AGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCA
GCAGGAGCGCAGAGCCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGAC
GAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAA
GGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGA
TTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCA
CCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAACAGCCACTCGAGGATCCGG
ATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCA
GCTGAAGCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGG
AATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAA
TACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAA
CAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGG
GCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGAT
GCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATG
ACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCG
AGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT

ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTC
TCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCACACATGCAGCATGTATCAAAATTAATTTG
GTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTACTTAAAGTTACATTGGCTTCCTTGAAATAA
ACATGGAGTATTCAGAATGTGTCATAAATATTTCTAATTTTAAGATAGTATCTCCATTGGCTTTCTACT
TTTTCTTTTATTTTTTTTTGTCCTCTGTCTTCCATTTGTTGTTGTTGTTGTTTGTTTGTTTGTTTGTTG
GTTGGTTGGTTAATTTTTTTTTAAAGATCCTACACTATAGTTCAAGCTAGACTATTAGCTACTCTGTAA
CCCAGGGTGACCTTGAAGTCATGGGTAGCCTGCTGTTTTAGCCTTCCCACATCTAAGATTACAGGTATG
AGCTATCATTTTTGGTATATTGATTGATTGATTGATGTGTGTGTGTGTGTGTGATTGTGTTTGTGTGTG
TGACTGTGAAAATGTGTGTATGGGTGTGTGTGAATGTGTGTATGTATGTGTGTGTGTGAGTGTGTGTGT
GTGTGTGTGCATGTGTGTGTGTGTGACTGTGTCTATGTGTATGACTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTTGTGAAAAAATATTCTATGGTAGTGAGAGCCAACGCTCCGGCTCAG
GTGTCAGGTTGGTTTTTGAGACAGAGTCTTTCACTTAGCTTGGAATTCACTGGCCGTCGTTTTACAACG
TCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTG
GCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCG
CCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCTCAGTAC
AATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACG
GGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAG
GTTTTCACCGTCATCACCGAAACGCGCGATGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTA
ATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTA
TTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTC
AATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGG
CATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGG
GTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAG
AACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCG
GGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAG
AAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACA
CTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGG
GGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTG
ACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAG
CTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCC
TTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAG
CACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGG
ATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAG
TTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCC
TTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAG
AAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAAC
CACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCT
TCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACT
CTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGT
CGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGG

GTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATT
GAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAG
GAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACC
TCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG
CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTG
ATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGC
GCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGC
CGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTA
ATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTG
GAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTTGCTCTT
AGGAGTTTCCTAATACATCCCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGGGGGCG
GGGGGAAGCTAAGCCAGCTTTTTTTAACATTTAAAATGTTAATTCCATTTTAAATGCACAGATGTTTTT
ATTTCATAAGGGTTTCAATGTGCATGAATGCTGCAATATTCCTGTTACCAAAGCTAGTATAAATAAAAA
TAGATAAACGTGGAAATTACTTAGAGTTTCTGTCATTAACGTTTCCTTCCTCAGTTGACAACATAAATG
CGCTGCTGAGCAAGCCAGTTTGCATCTGTCAGGATCAATTTCCCATTATGCCAGTCATATTAATTACTA
GTCAATTAGTTGATTTTTATTTTTGACATATACATGTGAATGAAAGACCCCACCTGTAGGTTTGGCAAG
CTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCA
AGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCC
GGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCC
TGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAAC
CATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAG
TTCGCTTCTCGCTTCTGTTCGCGCGCTTATGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACT
CGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
GGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGG
AGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGATTTTATGCGCC
TGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAA
CACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCC
TAAAATCCCGATCGTTTAGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGA
GACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCC
GCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAA
AATATGGGCCCGGGCTAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAG
CGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGG
CCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATC
AAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTG
GCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCC
GCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACT
CCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTC
CCTGACCCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTA
GTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGA[SEQ ID

NO:957]. The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:957 encodes a FcRL-5-targeted CAR (designated as 105 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-1019) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:220, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:219, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 207-1019 of SEQ ID NO: 957 encodes the human scFv. Nucleotides 1029-1241 of SEQ ID NO: 957 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1242-1367 of SEQ ID NO: 957 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1368-1706 of SEQ ID NO: 957 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 957 are shown in Table 236.

Table 236

Portions	Nucleotide Sequence Positions of SEQ ID NO: 957	Number of Nucleotides
antiFcRL5 scFv 105	207..1019	813
CD8a TM	1029..1241	213
4-1BB	1242..1367	126
CD3zeta	1368..1706	339
LTR	1986..2455	470
M13 fwd	3154..3170	17
AmpR promoter	3645..3749	105
AmpR	3750..4610	861
ori	4781..5369	589

CAP binding site	5657..5678	22
lac promoter	5693..5723	31
lac operator	5731..5747	17
M13 rev	5755..5771	17
LTR	6180..6773	594
MMLV Psi	6836..7193	358
gag (truncated)	7258..7674	417

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:958 provided below:

CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGACTGCCTGTGC
TGACTCAGCCACCCTCAGCGTCTGCGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAACCACCT
CCAACATCGGAAGTAATACTGTACACTGGTACCAGCAGCTCCCAGGGACGGCCCCCAAACTCCTCATCT
ATAATAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCT
CCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTACATATTCCTGTGCAACATGGGATGACAGCC
TGAGTGGTGTGGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTTCTAGAGGTGGTGGTGGTAGCG
GCGGCGGCGGCTCTGGTGGTGGTGGATCCCTCGAGATGGCCGAGGTCCAGCTGGTGCAGTCTGGGGCTG
AGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATG
CTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTG
GTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAG
CCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCGCCT
ACGGTGACTACGAGTATGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGCGG
CCGCACCCACCACGACGCCAGCGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGT
CCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCT
GTGATATCTACATCTGGGCGCCCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCC
TTTACTGCAACAAACGGGGCAGAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGACCAGTAC
AAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGA
GAGTGAAGTTCAGCAGGAGCGCAGAGCCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGC
TCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGG
GAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGG
CCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTC
TCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAACAGCCAC
TCGAGGATCCGGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCA
ACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATTTAGTCTCCA

GAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAA
GGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGA
ATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAAC
AGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGC
TTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTG
AGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTC
CTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCACACATGCAGCATGTATC
AAAATTAATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTACTTAAAGTTACATTGGCT
TCCTTGAAATAAACATGGAGTATTCAGAATGTGTCATAAATATTTCTAATTTTAAGATAGTATCTCCAT
TGGCTTTCTACTTTTTCTTTTATTTTTTTTTGTCCTCTGTCTTCCATTTGTTGTTGTTGTTGTTTGTTT
GTTTGTTTGTTGGTTGGTTGGTTAATTTTTTTTTAAAGATCCTACACTATAGTTCAAGCTAGACTATTA
GCTACTCTGTAACCCAGGGTGACCTTGAAGTCATGGGTAGCCTGCTGTTTTAGCCTTCCCACATCTAAG
ATTACAGGTATGAGCTATCATTTTTGGTATATTGATTGATTGATTGATTGATGTGTGTGTGTGTGATTG
TGTTTGTGTGTGTGACTGTGAAAATGTGTGTATGGGTGTGTGTGAATGTGTGTATGTATGTGTGTGTGT
GAGTGTGTGTGTGTGTGTGTGTGCATGTGTGTGTGTGTGACTGTGTCTATGTGTATGACTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGTGAAAAAATATTCTATGGTAGTGAGAGCCAAC
GCTCCGGCTCAGGTGTCAGGTTGGTTTTTGAGACAGAGTCTTTCACTTAGCTTGGAATTCACTGGCCGT
CGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCC
TTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAA
TGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTG
CACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGA
CGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTG
CATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGATGACGAAAGGGCCTCGTGATACGCCTAT
TTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGC
GCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCT
GATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTC
CCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTG
AAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTT
TTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCC
GTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACT
CACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCA
TGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTT
TGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAA
ACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAAC
TACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTC
TGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCG
GTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTC
AGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAAC

TGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCT
AGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGT
CAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGC
AAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGA
AGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACC
ACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCA
GTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGG
GCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTAC
AGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCA
GGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCG
GGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAA
ACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTG
CGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCC
GAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCC
CCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGC
GCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTC
GTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCA
AGCTTTGCTCTTAGGAGTTTCCTAATACATCCCAAACTCAAATATATAAAGCATTTGACTTGTTCTATG
CCCTAGGGGGCGGGGGGAAGCTAAGCCAGCTTTTTTTAACATTTAAAATGTTAATTCCATTTTAAATGC
ACAGATGTTTTTATTTCATAAGGGTTTCAATGTGCATGAATGCTGCAATATTCCTGTTACCAAAGCTAG
TATAAATAAAAATAGATAAACGTGGAAATTACTTAGAGTTTCTGTCATTAACGTTTCCTTCCTCAGTTG
ACAACATAAATGCGCTGCTGAGCAAGCCAGTTTGCATCTGTCAGGATCAATTTCCCATTATGCCAGTCA
TATTAATTACTAGTCAATTAGTTGATTTTTATTTTTGACATATACATGTGAATGAAAGACCCCACCTGT
AGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAA
AAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGC
AGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTG
GTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAG
TTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA
CTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTATGCTCCCCGAGCTCAATAAAAGAGCCCA
CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAAC
CCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTA
CCCGTCAGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGA
CCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTG
ATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTG
ACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCC
CGACCTGAGTCCTAAAATCCCGATCGTTTAGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTG
GTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGAC
CGAAGCCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTG
TATTTGTCTGAAAATATGGGCCCGGGCTAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGG
AAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGC

TCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACC
CAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACC
TGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCT
CTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTAT
CCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCC
CTTGTAAACTTCCCTGACCCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAG
GCTCTCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGA
[SEQ ID NO:958]. The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:958 encodes a FcRL-5-targeted CAR (designated as 109 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-1031) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:236, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:235, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 207-1031 of SEQ ID NO: 957 encodes the human scFv. Nucleotides 1041-1253 of SEQ ID NO: 958 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1254-1379 of SEQ ID NO: 958 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1380-1718 of SEQ ID NO: 958 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 958 are shown in Table 237.

Table 237

Portions	Nucleotide Sequence Positions of SEQ ID NO: 958	Number of Nucleotides
anti-FcRL5 scFv 109	207..1031	825
CD8a TM	1041..1253	213
4-1BB	1254..1379	126

CD3zeta	1380..1718	339
LTR	1998..2467	470
M13 fwd	3166..3182	17
AmpR promoter	3657..3761	105
AmpR	3762..4622	861
ori	4793..5381	589
CAP binding site	5669..5690	22
lac promoter	5705..5735	31
lac operator	5743..5759	17
M13 rev	5767..5783	17
LTR	6192..6785	594
MMLV Psi	6848..7205	358
gag (truncated)	7270..7686	417

In certain embodiments, the isolated nucleic acid molecule comprises nucleic acids having the sequence set forth in SEQ ID NO:959 provided below:

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CCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTA
GAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATC
GCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAGACTGCCA
TGGAAACCGATACACTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGATCCACAGGCGATGTTGTGA
TGACTCAGTCTCCACCCTCCCTGTCCGTCACCCCTGGAGAGCCGGCCTCCATCACCTGCAGGTCTAGTC
AGAGCCTCCTGGAAAGAAATGCATACAACTACTTGGATTGGTACCTGCAGAGGCCAGGACAGTCTCCAC
AGCTCCTGATCTACTTGGGTTCTAATCGGGCCGCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAG
GCAGAGATTTTACACTGAAAATCAGCAGAGTGGAGCCTGAGGATGTTGGGGTTTATTACTGCATGCAAG
CTCTACAAGCTCCGTTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTTCTAGAGGTGGTGGTG
GTAGCGGCGGCGGCGGCTCTGGTGGTGGTGGATCCCTCGAGATGGCCGAAGTGCAGCTGGTGCAGTCTG
GGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCA
GCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTA
GTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGA
ACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAATGGG
GCCCGTTTCAGGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGCGGCCGCAC
CCACCACGACGCCAGCGCCGCGACCACCAACCCCGGCGCCCACGATCGCGTCGCAGCCCCTGTCCCTGC
GCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATA
TCTACATCTGGGCGCCCCTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACT
GCAACAAACGGGGCAGAAAGAAGCTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTA
CTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGA
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AGTTCAGCAGGAGCGCAGAGCCCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATC
TAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGC
CGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACA
GTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTA
CAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAACAGCCACTCGAGG
ATCCGGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATA
TCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAA
GGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATG
GAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGG
GCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGA
ATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCC
CCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT
GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGC
TCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGC
CCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGG
AGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCACACATGCAGCATGTATCAAAATT
AATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTACTTAAAGTTACATTGGCTTCCTTG
AAATAAACATGGAGTATTCAGAATGTGTCATAAATATTTCTAATTTTAAGATAGTATCTCCATTGGCTT
TCTACTTTTTCTTTTATTTTTTTTTGTCCTCTGTCTTCCATTTGTTGTTGTTGTTGTTTGTTTGTTTGT
TTGTTGGTTGGTTGGTTAATTTTTTTTTAAAGATCCTACACTATAGTTCAAGCTAGACTATTAGCTACT
CTGTAACCCAGGGTGACCTTGAAGTCATGGGTAGCCTGCTGTTTTAGCCTTCCCACATCTAAGATTACA
GGTATGAGCTATCATTTTTGGTATATTGATTGATTGATTGATTGATGTGTGTGTGTGTGATTGTGTTTG
TGTGTGTGACTGTGAAAATGTGTGTATGGGTGTGTGTGAATGTGTGTATGTATGTGTGTGTGTGAGTGT
GTGTGTGTGTGTGTGCATGTGTGTGTGTGTGACTGTGTCTATGTGTATGACTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGTGAAAAAATATTCTATGGTAGTGAGAGCCAACGCTCCG
GCTCAGGTGTCAGGTTGGTTTTTGAGACAGAGTCTTTCACTTAGCTTGGAATTCACTGGCCGTCGTTTT
ACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGC
CAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGA
ATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCT
CAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCC
CTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTG
TCAGAGGTTTTCACCGTCATCACCGAAACGCGCGATGACGAAAGGGCCTCGTGATACGCCTATTTTTAT
AGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAA
CCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAA
TGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTT
TTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATC
AGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCC
CCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTG
ACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAG
TCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTG

ATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTTGCTCTTAGGAGTTTCCTAATACATCCCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGGGGGCGGGGGGAAGCTAAGCCAGCTTTTTTTAACATTTAAAATGTTAATTCCATTTTAAATGCACAGATGTTTTTATTTCATAAGGGTTTCAATGTGCATGAATGCTGCAATATTCCTGTTACCAAAGCTAGTATAAATAAAAATAGATAAACGTGGAAATTACTTAGAGTTTCTGTCATTAACGTTTCCTTCCTCAGTTGACAACATAAATGCGCTGCTGAGCAAGCCAGTTTGCATCTGTCAGGATCAATTTCCCATTATGCCAGTCATATTAATTACTAGTCAATTAGTTGATTTTTATTTTTGACATATACATGTGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTATGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGATTTTA

TGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCTAAAATCCCGATCGTTTAGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATATGGGCCCGGGCTAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGA [SEQ ID NO:959]. The isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:959 encodes a FcRL-5-targeted CAR (designated as 117 FcRL5-targeted BBz CAR) comprising a fully human scFv (encoded by nucleotides 207-1025 of SEQ ID NO:959) that comprises a heavy chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:268, a light chain variable region comprising amino acids having the sequence set forth in SEQ ID NO:267, and a linker having an amino acid sequence of SEQ ID NO:307 positioned between the heavy chain variable region and the light chain variable region, a transmembrane domain comprising a CD8 polypeptide having 137 to 207 of SEQ ID NO: 960, and an intracellular domain comprising a CD3ξ polypeptide comprising amino acids 52 to 163 of SEQ ID NO: 941, and a co-stimulatory signaling region comprising a 4-1BB polypeptide having amino acids 214-255 of SEQ ID NO: 943. Nucleotides 207-1025 of SEQ ID NO: 959 encodes the human scFv. Nucleotides 1035-1247 of SEQ ID NO: 959 encodes the CD8 polypeptide comprised in the transmembrane domain. Nucleotides 1248-1373 of SEQ ID NO: 959 encodes the 4-1BB polypeptide comprised in the intracellular domain. Nucleotides 1374-1712 of SEQ ID NO: 959 encodes the CD3zeta polypeptide comprised in the intracellular domain. Other portions of SEQ ID NO: 959 are shown in Table 238.

Table 238

Portions	Nucleotide Sequence	Number of Nucleotides

	Positions of SEQ ID NO: 959	
anti-FcRL5 scFv 117	207..1025	819
CD8a TM	1035..1247	213
4-1BB	1248..1373	126
CD3zeta	1374..1712	339
LTR	1992..2461	470
M13 fwd	3160..3176	17
AmpR promoter	3651..3755	105
AmpR	3756..4616	861
ori	4787..5375	589
CAP binding site	5663..5684	22
lac promoter	5699..5729	31
lac operator	5737..5753	17
M13 rev	5761..5777	17
LTR	6186..6779	594
MMLV Psi	6842..7199	358
gag (truncated)	7264..7680	417

In certain embodiments, the isolated nucleic acid molecule encodes a functional portion of a presently disclosed FcRL5-targeted CAR. As used herein, the term “functional portion” refers to any portion, part or fragment of a presently disclosed FcRL5-targeted CAR, which portion, part or fragment retains the biological activity of the FcRL5-targeted CAR (the parent CAR). For example, functional portions encompass the portions, parts or fragments of a presently disclosed FcRL5-targeted CAR that retains the ability to recognize a target cell, to treat a disease, *e.g.*, multiple myeloma, to a similar, same, or even a higher extent as the parent CAR. In certain embodiments, an isolated nucleic acid molecule encoding a functional portion of a presently disclosed FcRL5-targeted CAR can encode a protein comprising, *e.g.*, about 10%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, and 95%, or more of the parent CAR, *e.g.*, of the nucleic acid sequences set forth in SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID

NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958 or SEQ ID NO:959.

III. Immunoresponsive Cells

The presently disclosed subject matter provides immunoresponsive cells expressing a CAR that comprises an extracellular antigen-binding domain, a transmembrane domain and an intracellular domain, where the extracellular antigen-binding domain specifically binds to FcRL5 (*e.g.*, human FcRL5), as described above. In certain embodiments, the extracellular antigen-binding domain specifically binds to domain 7 of FcRL5. In certain embodiments, the extracellular antigen-binding domain specifically binds to domain 8 of FcRL5. In certain embodiments, the extracellular antigen-binding domain specifically binds to domain 9 of FcRL5. The immunoresponsive cells can be transduced with a presently disclosed CAR such that the cells express the CAR. The presently disclosed subject matter also provides methods of using such cells for the treatment of a tumor, *e.g.*, multiple myeloma (MM). The immunoresponsive cells of the presently disclosed subject matter can be cells of the lymphoid lineage. The lymphoid lineage, comprising B, T and natural killer (NK) cells, provides for the production of antibodies, regulation of the cellular immune system, detection of foreign agents in the blood, detection of cells foreign to the host, and the like. Non-limiting examples of immunoresponsive cells of the lymphoid lineage include T cells, Natural Killer (NK) cells, cytotoxic T lymphocytes (CTLs), regulatory T cells, embryonic stem cells, and pluripotent stem cells (*e.g.*, those from which lymphoid cells may be differentiated). T cells can be lymphocytes that mature in the thymus and are chiefly responsible for cell-mediated immunity. T cells are involved in the adaptive immune system. The T cells of the presently disclosed subject matter can be any type of T cells, including, but not limited to, T helper cells, cytotoxic T cells, memory T cells (including central memory T cells, stem-cell-like memory T cells (or stem-like memory T cells), and two types of effector memory T cells: *e.g.*, T_{EM} cells and T_{EMRA} cells), Regulatory T cells (also known as suppressor T cells), Natural killer T cells, Mucosal associated invariant T cells, and $\gamma\delta$ T cells. In certain embodiments, the CAR-expressing T cells express Foxp3 to achieve and maintain a T regulatory phenotype. Natural killer (NK) cells can be lymphocytes that are part of cell-mediated immunity and act during the innate immune response. NK cells do not require prior activation in order to perform their cytotoxic effect on target cells. Cytotoxic T cells (CTL or killer T cells) are a subset of T lymphocytes capable of inducing the death of infected somatic or tumor cells.

The immunoresponsive cells of the presently disclosed subject matter can express an extracellular antigen-binding domain (*e.g.*, an scFV, a Fab that is optionally crosslinked, or a $F(ab)_2$) that specifically binds to FcRL5 (*e.g.*, human FcRL5), for the treatment of multiple myeloma. Such immunoresponsive cells can be administered to a subject (*e.g.*, a human subject) in need thereof for the treatment of multiple myeloma. In certain embodiments, the immunoresponsive cell is a T cell. The T cell can be a $CD4^+$ T cell or a $CD8^+$ T cell. In certain embodiments, the T cell is a $CD4^+$ T cell. In another embodiment, the T cell is a $CD8^+$ T cell.

A presently disclosed immunoresponsive cell can be further transduced with at least one co-stimulatory ligand, such that the immunoresponsive cell co-expresses or is induced to co-express the FcRL5-specific CAR and the at least one co-stimulatory ligand. The interaction between the FcRL5-specific CAR and at least one co-stimulatory ligand provides a non-antigen-specific signal important for full activation of an immunoresponsive cell (*e.g.*, T cell). Co-stimulatory ligands include, but are not limited to, members of the tumor necrosis factor (TNF) superfamily, and immunoglobulin (Ig) superfamily ligands. TNF is a cytokine involved in systemic inflammation and stimulates the acute phase reaction. Its primary role is in the regulation of immune cells. Members of TNF superfamily share a number of common features. The majority of TNF superfamily members are synthesized as type II transmembrane proteins (extracellular C-terminus) containing a short cytoplasmic segment and a relatively long extracellular region. TNF superfamily members include, without limitation, nerve growth factor (NGF), CD40L (CD40L)/CD154, CD137L/4-1BBL, TNF-α, CD134L/OX40L/CD252, CD27L/CD70, Fas ligand (FasL), CD30L/CD153, tumor necrosis factor beta (TNFβ)/lymphotoxin-alpha (LTα), lymphotoxin-beta (LTβ), CD257/B cell-activating factor (BAFF)/Blys/THANK/Tall-1, glucocorticoid-induced TNF Receptor ligand (GITRL), and TNF-related apoptosis-inducing ligand (TRAIL), LIGHT (TNFSF14). The immunoglobulin (Ig) superfamily is a large group of cell surface and soluble proteins that are involved in the recognition, binding, or adhesion processes of cells. These proteins share structural features with immunoglobulins -- they possess an immunoglobulin domain (fold).

Immunoglobulin superfamily ligands include, but are not limited to, CD80 and CD86, both ligands for CD28, PD-L1/(B7-H1) that ligands for PD-1. In certain embodiments, the at least one co-stimulatory ligand is selected from the group consisting of 4-1BBL, CD80, CD86, CD70, OX40L, CD48, TNFRSF14, PD-L1, and combinations thereof. In certain embodiments, the immunoresponsive cell is transduced with one co-stimulatory ligand that is 4-1BBL. In certain embodiments, the immunoresponsive cell is transduced with two co-stimulatory ligands that are 4-1BBL and CD80. CARs transduced with at least one co-stimulatory ligand are described in U.S. Patent No. 8,389,282, which is incorporated by reference in its entirety.

Furthermore, a presently disclosed immunoresponsive cell can be further transduced with at least one cytokine, such that the immunoresponsive cell secretes the at least one cytokine as well as expresses the FcRL5-specific CAR. In certain embodiments, the at least one cytokine is selected from the group consisting of IL-2, IL-3, IL-6, IL-7, IL-11, IL-12, IL-15, IL-17, and IL-21. In certain embodiments, the cytokine is IL-12.

The FcRL5-specific or FcRL5-targeted human lymphocytes that can be used in peripheral donor lymphocytes, *e.g.*, those disclosed in Sadelain, M., *et al.* 2003 *Nat Rev Cancer* 3:35-45 (disclosing peripheral donor lymphocytes genetically modified to express CARs), in Morgan, R.A., *et al.* 2006 *Science* 314:126-129 (disclosing peripheral donor lymphocytes genetically modified to express a full-length tumor antigen-recognizing T cell receptor complex comprising the α and β heterodimer), in Panelli, M.C., *et al.* 2000 *J Immunol* 164:495-504; Panelli, M.C., *et al.* 2000 *J Immunol* 164:4382-4392 (disclosing lymphocyte cultures derived from tumor infiltrating lymphocytes (TILs) in tumor biopsies), and in Dupont, J., *et al.* 2005 *Cancer Res* 65:5417-5427; Papanicolaou, G.A., *et al.* 2003 *Blood* 102:2498-2505 (disclosing selectively *in vitro*-expanded antigen-specific peripheral blood leukocytes employing artificial antigen-presenting cells (AAPCs) or pulsed dendritic cells). The immunoresponsive cells (*e.g.*, T cells) can be autologous, non-autologous (*e.g.*, allogeneic), or derived *in vitro* from engineered progenitor or stem cells.

In certain embodiments, a presently disclosed immunoresponsive cell (*e.g.*, T cell) expresses from about 1 to about 4, from about 2 to about 4, from about 3 to about 4, from about 1 to about 2, from about 1 to about 3, or from about 2 to about 3 vector copy numbers/cell of a presently disclosed FcRL5-specific CAR.

The unpurified source of CTLs may be any known in the art, such as the bone marrow, fetal, neonate or adult or other hematopoietic cell source, *e.g.*, fetal liver, peripheral blood or umbilical cord blood. Various techniques can be employed to separate the cells. For instance, negative selection methods can remove non-CTLs initially. Monoclonal antibodies are particularly useful for identifying markers associated with particular cell lineages and/or stages of differentiation for both positive and negative selections.

A large proportion of terminally differentiated cells can be initially removed by a relatively crude separation. For example, magnetic bead separations can be used initially to remove large numbers of irrelevant cells. Preferably, at least about 80%, usually at least 70% of the total hematopoietic cells will be removed prior to cell isolation.

Procedures for separation include, but are not limited to, density gradient centrifugation; resetting; coupling to particles that modify cell density; magnetic separation with antibody-coated magnetic beads; affinity chromatography; cytotoxic agents joined to or used in conjunction with a mAb, including, but not limited to, complement and cytotoxins; and panning with antibody attached to a solid matrix, *e.g.* plate, chip, elutriation or any other convenient technique.

Techniques for separation and analysis include, but are not limited to, flow cytometry, which can have varying degrees of sophistication, *e.g.*, a plurality of color channels, low angle and obtuse light scattering detecting channels, impedance channels.

The cells can be selected against dead cells, by employing dyes associated with dead cells such as propidium iodide (PI). Preferably, the cells are collected in a medium comprising 2% fetal calf serum (FCS) or 0.2% bovine serum albumin (BSA) or any other suitable, preferably sterile, isotonic medium.

IV. Vectors

Genetic modification of immunoresponsive cells (*e.g.*, T cells, CTL cells, NK cells) can be accomplished by transducing a substantially homogeneous cell composition with a recombinant DNA or RNA construct. The vector can be a retroviral vector (*e.g.*, gamma retroviral), which is employed for the introduction of the DNA or RNA construct into the host cell genome. For example, a polynucleotide encoding the FcRL5-specific CAR can be cloned into a retroviral vector and expression can be driven from its endogenous promoter, from the retroviral long terminal repeat, or from an alternative internal promoter.

Non-viral vectors or RNA may be used as well. Random chromosomal integration, or targeted integration (*e.g.*, using a nuclease, transcription activator-like effector nucleases (TALENs), Zinc-finger nucleases (ZFNs), and/or clustered regularly interspaced short palindromic repeats (CRISPRs), or transgene expression (*e.g.*, using a natural or chemically modified RNA) can be used.

For initial genetic modification of the cells to provide FcRL5-specific CAR expressing cells, a retroviral vector is generally employed for transduction, however any other suitable viral vector or non-viral delivery system can be used. For subsequent genetic modification of the cells to provide cells comprising an antigen presenting complex comprising at least two co-stimulatory ligands, retroviral gene transfer (transduction) likewise proves effective. Combinations of retroviral vector and an appropriate packaging line are also suitable, where the capsid proteins will be functional for infecting human cells. Various amphotropic virus-producing cell lines are known, including, but not limited to, PA12 (Miller, *et al.* (1985) *Mol. Cell. Biol.* 5:431-437); PA317 (Miller, *et al.* (1986) *Mol. Cell. Biol.* 6:2895-2902); and CRIP (Danos, *et al.* (1988) *Proc. Natl. Acad. Sci.* USA 85:6460-6464). Non -amphotropic particles are suitable too, *e.g.*, particles pseudotyped with VSVG, RD114 or GALV envelope and any other known in the art.

Possible methods of transduction also include direct co-culture of the cells with producer cells, *e.g.*, by the method of Bregni, *et al.* (1992) *Blood* 80:1418-1422, or culturing with viral supernatant alone or concentrated vector stocks with or without appropriate growth factors and polycations, *e.g.*, by the method of Xu, *et al.* (1994) *Exp. Hemat.* 22:223-230; and Hughes, *et al.* (1992) *J. Clin. Invest.* 89:1817.

Transducing viral vectors can be used to express a co-stimulatory ligand (*e.g.*, 4-1BBL and IL-12) in an immunoresponsive cell. Preferably, the chosen vector exhibits high efficiency of infection and stable integration and expression (*see, e.g.*, Cayouette et al., Human Gene Therapy 8:423-430, 1997; Kido *et al.*, Current Eye Research 15:833-844, 1996; Bloomer *et al.*, Journal of Virology 71:6641-6649, 1997; Naldini *et al.*, Science 272:263 267, 1996; and Miyoshi *et al.*, Proc. Natl. Acad. Sci. U.S.A. 94:10319, 1997). Other viral vectors that can be used include, for example, adenoviral, lentiviral, and adeno-associated viral vectors, vaccinia virus, a bovine papilloma virus, or a herpes virus, such as Epstein-Barr Virus (also see, for example, the vectors of Miller, Human Gene Therapy 15-14, 1990; Friedman, Science 244:1275-1281, 1989; Eglitis et al., BioTechniques 6:608-614, 1988; Tolstoshev et al., Current Opinion in Biotechnology 1:55-61, 1990; Sharp, The Lancet 337:1277-1278, 1991; Cornetta et al., Nucleic Acid Research and Molecular Biology 36:311-322, 1987; Anderson, Science 226:401-409, 1984; Moen, Blood Cells 17:407-416, 1991; Miller et al., Biotechnology 7:980-990, 1989; Le Gal La Salle et al., Science 259:988-990, 1993; and Johnson, Chest 107:77S- 83S, 1995). Retroviral vectors are particularly well developed and have been used in clinical settings (Rosenberg et al., N. Engl. J. Med 323:370, 1990; Anderson et al., U.S. Pat. No. 5,399,346).

In certain non-limiting embodiments, the vector expressing a presently disclosed FcRL5-targeted CAR is a retroviral vector, *e.g.*, a 293galv9 retroviral vector.

Non-viral approaches can also be employed for the expression of a protein in cell. For example, a nucleic acid molecule can be introduced into a cell by administering the nucleic acid in the presence of lipofection (Feigner et al., Proc. Nat'l. Acad. Sci. U.S.A. 84:7413, 1987; Ono et al., Neuroscience Letters 17:259, 1990; Brigham et al., Am. J. Med. Sci. 298:278, 1989; Staubinger et al., Methods in Enzymology 101:512, 1983), asialoorosomucoid-polylysine conjugation (Wu et al., Journal of Biological Chemistry 263:14621 , 1988; Wu et al., Journal of Biological Chemistry 264:16985, 1989), or by micro-injection under surgical conditions (Wolff et al., Science 247:1465, 1990). Other non-viral means for gene transfer include transfection in vitro using calcium phosphate, DEAE dextran, electroporation, and protoplast fusion. Liposomes can also be potentially beneficial for delivery of DNA into a cell. Transplantation of normal genes into the affected tissues of a subject can also be accomplished by transferring a normal nucleic acid into a cultivatable cell type *ex vivo* (*e.g.*, an autologous or heterologous primary cell or progeny thereof), after which the cell (or its descendants) are injected into a targeted tissue or are injected systemically. Recombinant receptors can also be derived or obtained using transposases or targeted nucleases (*e.g.* Zinc finger nucleases, meganucleases, or TALE nucleases). Transient expression may be obtained by RNA electroporation.

cDNA expression for use in polynucleotide therapy methods can be directed from any suitable promoter (*e.g.*, the human cytomegalovirus (CMV), simian virus 40 (SV40), or metallothionein promoters), and regulated by any appropriate mammalian regulatory element or intron (*e.g.* the elongation factor 1 α enhancer/promoter/intron structure). For example, if desired, enhancers known to preferentially direct gene expression in specific cell types can be used to direct the expression of a nucleic acid. T he enhancers used can include, without limitation, those that are characterized as tissue- or cell-specific enhancers. Alternatively, if a genomic clone is used as a therapeutic construct, regulation can be mediated by the cognate regulatory sequences or, if desired, by regulatory sequences derived from a heterologous source, including any of the promoters or regulatory elements described above.

The resulting cells can be grown under conditions similar to those for unmodified cells, whereby the modified cells can be expanded and used for a variety of purposes.

V. Polypeptides and Analogs and Polynucleotides

Also included in the presently disclosed subject matter are extracellular antigen-binding domains that specifically binds to FcRL5 (*e.g.*, human FcRL5) (*e.g.*, an scFv, such as an scFv derived from antibodies F56 and F119, a Fab, or a $(Fab)_2$), CD3ζ, CD8, CD28, *etc.* polypeptides or fragments thereof, and polynucleotides encoding thereof that are modified in ways that enhance their anti-tumor activity when expressed in an immunoresponsive cell. In certain embodiments, the presently disclosed subject matter further provides extracellular antigen-binding domains that specifically binds to domain 9 FcRL5 (*e.g.*, domain 7, domain 8 or domain 9 of human FcRL5) (*e.g.*, an scFv, a Fab, or a $(Fab)_2$), CD3ζ, CD8, CD28, *etc.* polypeptides or fragments thereof, and polynucleotides encoding thereof that are modified in ways that enhance their anti-tumor activity when expressed in an immunoresponsive cell.

The presently disclosed subject matter provides methods for optimizing an amino acid sequence or a nucleic acid sequence by producing an alteration in the sequence. Such alterations may comprise certain mutations, deletions, insertions, or post-translational modifications. The presently disclosed subject matter further comprises analogs of any naturally-occurring polypeptide of the presently disclosed subject matter. Analogs can differ from a naturally-occurring polypeptide of the presently disclosed subject matter by amino acid sequence differences, by post-translational modifications, or by both. Analogs of the presently disclosed subject matter can generally exhibit at least about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99% or more identity with all or part of a naturally-occurring amino, acid sequence of the presently disclosed subject matter. The length of sequence comparison is at least 5, 10, 15, 20, 25, 50, 75, 100 or more amino acid residues. Again, in an exemplary approach to determining the degree of identity, a BLAST program may be used, with a probability score between e^{-3} and e^{-100} indicating a closely related sequence. Modifications comprise *in vivo* and *in vitro* chemical derivatization of polypeptides, *e.g.*, acetylation, carboxylation, phosphorylation, or glycosylation; such modifications may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. Analogs can also differ from the naturally-occurring polypeptides of the presently disclosed subject matter by alterations in primary sequence. These include genetic variants, both natural and induced (for example, resulting from random mutagenesis by irradiation or exposure to ethanemethylsulfate or by site-specific mutagenesis as described in Sambrook, Fritsch and Maniatis, Molecular Cloning: A Laboratory Manual (2d ed.), CSH Press, 1989, or Ausubel et al., supra). Also included are cyclized peptides, molecules, and analogs which contain residues other than L-amina acids, *e.g.*, D-amino acids or non-naturally occurring or synthetic amino acids, *e.g.*, beta (β) or gamma (γ) amino acids.

In addition to full-length polypeptides, the presently disclosed subject matter also provides fragments of any one of the polypeptides or peptide domains of the presently disclosed subject matter. A fragment can be at least 5, 10, 13, or 15 amino acids. In certain embodiments, a fragment is at least 20 contiguous amino acids, at least 30 contiguous amino acids, or at least 50 contiguous amino acids. In certain embodiments, a fragment is at least 60 to 80, 100, 200, 300 or more contiguous amino acids. Fragments of the presently disclosed subject matter can be generated by methods known to those of ordinary skill in the art or may result from normal protein processing (*e.g.*, removal of amino acids from the nascent polypeptide that are not required for biological activity or removal of amino acids by alternative mRNA splicing or alternative protein processing events).

Non-protein analogs have a chemical structure designed to mimic the functional activity of a protein of the invention. Such analogs are administered according to methods of the presently disclosed subject matter. Such analogs may exceed the physiological activity of the original polypeptide. Methods of analog design are well known in the art, and synthesis of analogs can be carried out according to such methods by modifying the chemical structures such that the resultant analogs increase the anti-neoplastic activity of the original polypeptide when expressed in an immunoresponsive cell. These chemical modifications include, but are not limited to, substituting alternative R groups and varying the degree of saturation at specific carbon atoms of a reference polypeptide. The protein analogs can be relatively resistant to *in vivo* degradation, resulting in a more prolonged therapeutic effect upon administration. Assays for measuring functional activity include, but are not limited to, those described in the Examples below.

In accordance with the presently disclosed subject matter, the polynucleotides encoding an extracellular antigen-binding domain that specifically binds to FcRL5 (*e.g.*, an scFV (*e.g.*, an scFv derived from antibodies F56 and F119), a Fab, Fab' or a $(Fab')_2$), CD3ζ, CD8, CD28) can be modified by codon optimization. Codon optimization can alter both naturally occurring and recombinant gene sequences to achieve the highest possible levels of productivity in any given expression system. Factors that are involved in different stages of protein expression include codon adaptability, mRNA structure, and various *cis*-elements in transcription and translation. Any suitable codon optimization methods or technologies that are known to ones skilled in the art can be used to modify the polynucleotids of the presently disclosed subject matter, including, but not limited to, OPTIMUMGENE™, Encor optimization, and Blue Heron.

VI. Administration

FcRL5-specific CARs and immunoresponsive cells expressing thereof of the presently disclosed subject matter can be provided systemically or directly to a subject for treating or preventing a neoplasia. In certain embodiments, the FcRL5-specific CARs and immunoresponsive cells expressing thereof are directly injected into an organ of interest (*e.g.*, an organ affected by a neoplasia). Alternatively or additionally, the FcRL5-specific CARs and immunoresponsive cells expressing thereof are provided indirectly to the organ of interest, for example, by administration into the circulatory system (*e.g.*, the tumor vasculature). Expansion and differentiation agents can be provided prior to, during or after administration of cells and compositions to increase production of T cells *in vitro or in vivo.*

FcRL5-specific CARs and immunoresponsive cells expressing thereof of the presently disclosed subject matter can be administered in any physiologically acceptable vehicle, normally intravascularly, although they may also be introduced into bone or other convenient site where the cells may find an appropriate site for regeneration and differentiation (*e.g.*, thymus). Usually, at least 1 x 10^5 cells can be administered, eventually reaching 1 x 10^{10} or more. A cell population comprising immunoresponsive cells expressing a FcRL5-specific CAR can comprise a purified population of cells. Those skilled in the art can readily determine the percentage of immunoresponsive cells in a cell population using various well-known methods, such as fluorescence activated cell sorting (FACS). The ranges of purity in cell populations comprising genetically modified immunoresponsive cells expressing a FcRL5-specific CAR can be from about 50% to about 55%, from about 55% to about 60%, from about 65% to about 70%, from about 70% to about 75%, from about 75% to about 80%, from about 80% to about 85%; from about 85% to about 90%, from about 90% to about 95%, or from about 95 to about 100%. Dosages can be readily adjusted by those skilled in the art (*e.g.*, a decrease in purity may require an increase in dosage). The immunoresponsive cells can be introduced by injection, catheter, or the like. If desired, factors can also be included, including, but not limited to, interleukins, *e.g.* IL-2, IL-3, IL 6, IL-11, IL-7, IL-12, IL-15, IL-21, as well as the other interleukins, the colony stimulating factors, such as G-, M- and GM-CSF, interferons, *e.g.*, γ-interferon.

Compositions of the presently disclosed subject matter comprise pharmaceutical compositions comprising immunoresponsive cells expressing a FcRL5-specific CAR and a pharmaceutically acceptable carrier. Administration can be autologous or non-autologous. For example, immunoresponsive cells expressing a FcRL5-specific CAR and compositions comprising thereof can be obtained from one subject, and administered to the same subject or a different, compatible subject. Peripheral blood derived T cells of the presently disclosed subject matter or their progeny (*e.g.*, *in vivo, ex vivo or in vitro* derived) can be administered via localized injection, including catheter administration, systemic injection, localized injection, intravenous injection, or parenteral administration. When administering a pharmaceutical composition of the presently disclosed subject matter (*e.g.*, a pharmaceutical composition comprising immunoresponsive cells expressing a FcRL5-specific CAR), it can be formulated in a unit dosage injectable form (solution, suspension, emulsion).

VII. Formulations

Immunoresponsive cells expressing a generally FcRL5-specific CAR and compositions comprising thereof of the presently disclosed subject matter can be conveniently provided as sterile liquid preparations, *e.g.*, isotonic aqueous solutions, suspensions, emulsions, dispersions, or viscous compositions, which may be buffered to a selected pH. Liquid preparations are normally easier to prepare than gels, other viscous compositions, and solid compositions. Additionally, liquid compositions are somewhat more convenient to administer, especially by injection. Viscous compositions, on the other hand, can be formulated within the appropriate viscosity range to provide longer contact periods with specific tissues. Liquid or viscous compositions can comprise carriers, which can be a solvent or dispersing medium containing, for example, water, saline, phosphate buffered saline, polyol (for example, glycerol, propylene glycol, liquid polyethylene glycol, and the like) and suitable mixtures thereof.

Sterile injectable solutions can be prepared by incorporating the compositions comprising immunoresponsive cells expressing a generally FcRL5-specific CAR of the presently disclosed subject matter in the required amount of the appropriate solvent with various amounts of the other ingredients, as desired. Such compositions may be in admixture with a suitable carrier, diluent, or excipient such as sterile water, physiological saline, glucose, dextrose, or the like. The compositions can also be lyophilized. The compositions can contain auxiliary substances such as wetting, dispersing, or emulsifying agents (*e.g.*, methylcellulose), pH buffering agents, gelling or viscosity enhancing additives, preservatives, flavoring agents, colors, and the like, depending upon the route of administration and the preparation desired. Standard texts, such as “REMINGTON’S PHARMACEUTICAL SCIENCE,” 17th edition, 1985, incorporated herein by reference, may be consulted to prepare suitable preparations, without undue experimentation.

Various additives which enhance the stability and sterility of the compositions, including antimicrobial preservatives, antioxidants, chelating agents, and buffers, can be added. Prevention of the action of microorganisms can be ensured by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, and the like. Prolonged absorption of the injectable pharmaceutical form can be brought about by the use of agents delaying absorption, for example, alum inurn monostearate and gelatin. According to the present invention, however, any vehicle, diluent, or additive used would have to be compatible with the immunoresponsive cells expressing a generally FcRL5-specific CAR of the presently disclosed subject matter.

The compositions can be isotonic, i.e., they can have the same osmotic pressure as blood and lacrimal fluid. T he desired isotonicity of the compositions of the presently disclosed subject matter may be accomplished using sodium chloride, or other pharmaceutically acceptable agents such as dextrose, boric acid, sodium tartrate, propylene glycol or other inorganic or organic solutes. Sodium chloride is preferred particularly for buffers containing sodium ions.

Viscosity of the compositions, if desired, can be maintained at the selected level using a pharmaceutically acceptable thickening agent. Methylcellulose can be used because it is readily and economically available and is easy to work with. Other suitable thickening agents include, for example, xanthan gum, carboxymethyl cellulose, hydroxypropyl cellulose, carbomer, and the like. The concentration of the thickener can depend upon the agent selected. The important point is to use an amount that will achieve the selected viscosity. Obviously, the choice of suitable carriers and other additives will depend on the exact route of administration and the nature of the particular dosage form, *e.g.*, liquid dosage form (*e.g.*, whether the composition is to be formulated into a solution, a suspension, gel or another liquid form, such as a time release form or liquid-filled form).

Those skilled in the art will recognize that the components of the compositions should be selected to be chemically inert and will not affect the viability or efficacy of the immunoresponsive cells as describe in the presently disclosed subject matter. This will present no problem to those skilled in chemical and pharmaceutical principles, or problems can be readily avoided by reference to standard texts or by simple experiments (not involving undue experimentation), from this disclosure and the documents cited herein.

One consideration concerning the therapeutic use of the immunoresponsive cells of the presently disclosed subject matter is the quantity of cells necessary to achieve an optimal effect. The quantity of cells to be administered will vary for the subject being treated. In certain embodiments, from about 10^4 to about 10^{10} , from about 10^5 to about 10^9, or from about 10^6 to about 10^8 immunoresponsive cells of the presently disclosed subject matter are administered to a subject. More effective cells may be administered in even smaller numbers. In certain embodiments, at least about 1×10^8, about 2×10^8, about 3×10^8, about 4×10^8, and about 5×10^8 immunoresponsive cells of the presently disclosed subject matter are administered to a human subject. The precise determination of what would be considered an effective dose may be based on factors individual to each subject, including their size, age, sex, weight, and condition of the particular subject. Dosages can be readily ascertained by those skilled in the art from this disclosure and the knowledge in the art.

The skilled artisan can readily determine the amount of cells and optional additives, vehicles, and/or carrier in compositions and to be administered in methods of the presently disclosed subject matter. Typically, any additives (in addition to the active cell(s) and/or agent(s)) are present in an amount of from about 0.001% to about 50% by weight) solution in phosphate buffered saline, and the active ingredient is present in the order of micrograms to milligrams, such as from about 0.0001 wt% to about 5 wt %, from about 0.0001 wt% to about 1 wt %, from about 0.0001 wt% to about 0.05 wt%, from about 0.001 wt% to about 20 wt %, from about 0.01 wt% to about 10 wt %, or from about 0.05 wt% to about 5 wt %. For any composition to be administered to an animal or human, and for any particular method of administration, toxicity should be determined, such as by determining the lethal dose (LD) and LD50 in a suitable animal model *e.g.*, rodent such as mouse; and, the dosage of the composition(s), concentration of components therein and timing of administering the composition(s), which elicit a suitable response. Such determinations do not require undue experimentation from the knowledge of the skilled artisan, this disclosure and the documents cited herein. And, the time for sequential administrations can be ascertained without undue experimentation.

VIII. Methods of Treatment

Tumor Microenvironment. Tumors have a microenvironment that is hostile to the host immune response involving a series of mechanisms by malignant cells to protect themselves from immune recognition and elimination. This “hostile tumor microenvironment" comprises a variety of immune suppressive factors including infiltrating regulatory CD4$^+$ T cells (Tregs), myeloid derived suppressor cells (MDSCs), tumor associated macrophages (TAMs), immune suppressive cytokines including IL-10 and TGF-β, and expression of ligands targeted to immune suppressive receptors expressed by activated T cells (CTLA-4 and PD-1). These mechanisms of immune suppression play a role in the maintenance of tolerance and suppressing inappropriate immune responses, however within the tumor microenvironment these mechanisms prevent an effective anti-tumor immune response. Collectively these immune suppressive factors can induce either marked anergy or apoptosis of adoptively transferred CAR modified T cells upon encounter with targeted tumor cells.

Challenges in tumor immunology. Effective tumor immunity requires recognition of tumor antigens and unopposed tumor elimination by immune effector cells. Tumor antigens must contain peptide epitopes that are presented by the tumor and can be recognized by specific cytotoxic T lymphocytes (CTLs). The primed CTLs must expand to a sufficient number and migrate to tumor sites, wherein they mature into effectors to perform their functions, which are enhanced by helper T cells and dampened by Tregs and inhibitory macrophages.

Targeted T cell therapy with engineered T lymphocytes. T cell engineering is a groundbreaking strategy to potentially resolve many previously observed shortcomings of earlier immunotherapeutic approaches. Within the past year, researchers have reported dramatic complete remissions in relapsed (Brentjens *et al.*, *Blood* 118, 4817-4828 (2011) and Brentjens *et al.*, *Science translational medicine* 5, 177ra138 (2013)), chemorefractory leukemia and metastatic melanoma (Hunder *et al.*, *N. Engl.J.Med.* 358, 2698-2703 (2008); Rosenberg *et al.*, *Nat. Rev. Cancer* 8, 299-308 (2008); and Dudley *et al.*, *J Clin Oncol* 26, 5233-5239 (2008)), obtained with autologous peripheral blood T cells targeted to a defined antigen (CD19 and NY-ESO-1, respectively).

Rationale for a genetic approach: Cell engineering can be used to redirect T cells toward tumor antigens and to enhance T cell function. One impetus for genetic T cell modification is the potential to enhance T cell survival and expansion and to offset T cell death, anergy, and immune suppression. The genetic targeting of T cells can also be refined to prevent undesired destruction of normal tissues.

Chimeric antigen receptors (CARs): Tumor-specific T cells can be generated by the transfer of genes that encode CARs (Brentjens *et al.*, *Clin.Cancer Res.* 13, 5426-5435 (2007); Gade *et al.*, *Cancer Res.* 65, 9080-9088 (2005); Maher *et al.*, *Nat.Biotechnol.* 20, 70-75 (2002); Kershaw *et al.*, *J Immunol* 173, 2143-2150 (2004); Sadelain *et al.*, *Curr Opin Immunol* (2009); and Hollyman *et al.*, *J Immunother* 32, 169-180 (2009)). Second-generation CARs comprise a tumor antigen-binding domain fused to an intracellular signaling domain capable of activating T cells and a co-stimulatory domain designed to augment T cell potency and persistence (Sadelain *et al.*, *Cancer discovery* 3, 388-398 (2013)). CAR design can therefore reconcile antigen recognition with signal transduction, two functions that are physiologically borne by two separate complexes, the TCR heterodimer and the CD3 complex. The CAR's extracellular antigen-binding domain is usually derived from a murine monoclonal antibody (mAb) or from receptors or their ligands. Antigen recognition is therefore not MHC-restricted (Riviere *et al.*, *Curr Hematol Rep* 3, 290-297 (2004); and Stephan *et al.*, *Nat. Med.* 13, 1440-1449 (2007)) and is therefore applicable to any patient expressing the target antigen, using the same CAR. Antigen binding by the CARs triggers phosphorylation of immunoreceptor tyrosine-based activation motifs (ITAMs) in the intracellular domain, initiating a signaling cascade required for cytolysis induction, cytokine secretion, and proliferation. Because MHC restriction of antigen recognition is bypassed, the function of CAR-targeted T cells is not affected by HLA downregulation or defects in the antigen-processing machinery.

T cell requirements for expansion and survival: Proliferation of tumor-specific T cells is needed *ex vivo* and is arguably desirable *in vivo*. T cell proliferation must be accompanied by T cell survival to permit absolute T cell expansion and persistence. To proliferate in response to antigen, T cells must receive two signals. One is provided by TCR recognition of antigenic peptide/MHC complexes displayed on the surface of antigen-presenting cells (APCs) (Sadelain *et al.*, *Curr Opin Immunol* (2009)). The other is provided by a T cell co-stimulatory receptor, such as the CD28 or 4-1BB receptors. Whereas the cytolytic activity of T cells does not require concomitant co-stimulation, there is a critical need for the provision of co-stimulatory signals to sustain the antitumor functions of adoptively transferred T cells, as previously demonstrated (Maher *et al.*, *Nat.Biotechnol.* 20, 70-75 (2002); Sadelain *et al.*, *Cancer discovery* 3, 388-398 (2013); Krause *et al.*, *J Exp Med* 188, 619-626

(1998);Gong *et al.*, *Neoplasia.* 1, 123-127 (1999); and Lyddane *et al.*, *J.Immunol.* 176, 3306-3310 (2006)).

Immune monitoring: Lymphocytes are multifunctional "drugs" that exhibit dynamically evolving effects after infusion. Upon antigen encounter, tumor-specific T cells activate and/or release a variety of proteins that can trigger tumor killing, T cell proliferation, and recruitment or immunomodulation of other immune cells. Thus, measuring which proteins are secreted from which cells, in what quantity, and at what time point yields profound insights into why a particular patient is or is not responding and provides critical feedback for designing more-effective trials. These assay systems will permit direct and meaningful comparisons of clinical approaches and thus help design rational, next-generation therapeutic strategies.

For treatment, the amount administered is an amount effective in producing the desired effect. An effective amount can be provided in one or a series of administrations. An effective amount can be provided in a bolus or by continuous perfusion.

An "effective amount" (or, "therapeutically effective amount") is an amount sufficient to affect a beneficial or desired clinical result upon treatment. An effective amount can be administered to a subject in one or more doses. In terms of treatment, an effective amount is an amount that is sufficient to palliate, ameliorate, stabilize, reverse or slow the progression of the disease, or otherwise reduce the pathological consequences of the disease. The effective amount is generally determined by the physician on a case-by-case basis and is within the skill of one in the art. Several factors are typically taken into account when determining an appropriate dosage to achieve an effective amount. These factors include age, sex and weight of the subject, the condition being treated, the severity of the condition and the form and effective concentration of the immunoresponsive cells administered.

For adoptive immunotherapy using antigen-specific T cells, cell doses in the range of about 10^6 to about 10^{10} (*e.g.*, about 10^9) are typically infused. Upon administration of the immunoresponsive cells into the subject and subsequent differentiation, the immunoresponsive cells are induced that are specifically directed against one specific antigen (*e.g.*, FcRL5). "Induction" of T cells can include inactivation of antigen-specific T cells such as by deletion or anergy. Inactivation is particularly useful to establish or reestablish tolerance such as in autoimmune disorders. The immunoresponsive cells of the presently disclosed subject matter can be administered by any methods known in the art, including, but not limited to, pleural administration, intravenous administration, subcutaneous administration, intranodal administration, intratumoral administration, intrathecal administration, intrapleural administration, intraperitoneal administration, and direct administration to the thymus. In certain embodiments, the immunoresponsive cells and the compositions comprising thereof are intravenously administered to the subject in need.

The presently disclosed subject matter provides various methods of using the immunoresponsive cells (*e.g.*, T cells) expressing a FcRL5-specific CAR. For example, the presently disclosed subject matter provides methods of reducing tumor burden in a subject. In one non-limiting example, the method of reducing tumor burden comprises administering an effective amount of the presently disclosed immunoresponsive cell to the subject, thereby inducing tumor cell death in the subject. The presently disclosed immunoresponsive cell can reduce the number of tumor cells, reduce tumor size, and/or eradicate the tumor in the subject. Non-limiting examples of suitable tumors include multiple myeloma, Non-Hodgkin Lymphoma (especially Mantle Cell), Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burketts Lymphoma, and Waldenstrom's Macroglobulinemia.

The presently disclosed subject matter also provides methods of increasing or lengthening survival of a subject having a neoplasia. In one non-limiting example, the method of increasing or lengthening survival of a subject having neoplasia comprises administering an effective amount of the presently disclosed immunoresponsive cell to the subject, thereby increasing or lengthening survival of the subject. The method can reduce or eradicate tumor burden in the subject. The presently disclosed subject matter further provides methods for treating or preventing a neoplasia in a subject, comprising administering the presently disclosed immunoresponsive cell to the subject.

As used herein, the term "neoplasia" refers to a disease characterized by the pathological proliferation of a cell or tissue and its subsequent migration to or invasion of other tissues or organs. Neoplasia growth is typically uncontrolled and progressive, and occurs under conditions that would not elicit, or would cause cessation of, multiplication of normal cells. Neoplasias can affect a variety of cell types, tissues, or organs, including but not limited to an organ selected from the group consisting of bladder, colon, bone, brain, breast, cartilage, glia, esophagus, fallopian tube, gallbladder, heart, intestines, kidney, liver, lung, lymph node, nervous tissue, ovaries, pleura, pancreas, prostate, skeletal muscle, skin, spinal cord, spleen, stomach, testes, thymus, thyroid, trachea, urogenital tract, ureter, urethra, uterus, and vagina, or a tissue or cell type thereof. Neoplasias include cancers, such as sarcomas, carcinomas, or plasmacytomas (malignant tumor of the plasma cells).

Cancers whose growth may be inhibited using the immunoresponsive cells of the presently disclosed subject matter comprise cancers typically responsive to immunotherapy. Non-limiting examples of cancers for treatment include multiple myeloma, Non-Hodgkin Lymphoma (especially Mantle Cell), Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burketts Lymphoma, and Waldenstrom’s Macroglobulinemia. In certain embodiments, the cancer is multiple myeloma.

Additionally, the presently disclosed subject matter provides methods of increasing immune-activating cytokine production in response to a cancer cell in a subject. In one non-limiting example, the method comprises administering the presently disclosed immunoresponsive cell to the subject. The immune-activating cytokine can be granulocyte macrophage colony stimulating factor (GM-CSF), IFN-α, IFN-β, IFN-γ, TNF-α, IL-2, IL-3, IL-6, IL-11, IL-7, IL-12, IL-15, IL-21, interferon regulatory factor 7 (IRF7), and combinations thereof. In certain embodiments, the immunoresponsive cells including an FcRL5-specific CAR of the presently disclosed subject matter increase the production of GM-CSF, IFN-γ, and/or TNF-α.

Suitable human subjects for therapy typically comprise two treatment groups that can be distinguished by clinical criteria. Subjects with “advanced disease” or “high tumor burden” are those who bear a clinically measurable tumor (*e.g.*, multiple myeloma). A clinically measurable tumor is one that can be detected on the basis of tumor mass (*e.g.*, by palpation, CAT scan, sonogram, mammogram or X-ray; positive biochemical or histopathologic markers on their own are insufficient to identify this population). A pharmaceutical composition embodied in the presently disclosed subject matter is administered to these subjects to elicit an anti-tumor response, with the objective of palliating their condition. Ideally, reduction in tumor mass occurs as a result, but any clinical improvement constitutes a benefit. Clinical improvement comprises decreased risk or rate of progression or reduction in pathological consequences of the tumor (*e.g.*, multiple myeloma).

A second group of suitable subjects is known in the art as the "adjuvant group." These are individuals who have had a history of neoplasia (*e.g.*, multiple myeloma), but have been responsive to another mode of therapy. The prior therapy can have included, but is not restricted to, surgical resection, radiotherapy, and traditional chemotherapy. As a result, these individuals have no clinically measurable tumor. However, they are suspected of being at risk for progression of the disease, either near the original tumor site, or by metastases. This group can be further subdivided into high-risk and low-risk individuals. The subdivision is made on the basis of features observed before or after the initial treatment. These features are known in the clinical arts, and are suitably defined for each different neoplasia. Features typical of high-risk subgroups are those in which the tumor (*e.g.*, multiple myeloma) has invaded neighboring tissues, or who show involvement of lymph nodes. Another group has a genetic predisposition to neoplasia (*e.g.*, multiple myeloma) but has not yet evidenced clinical signs of neoplasia (*e.g.*, multiple myeloma). For instance, women testing positive for a genetic mutation associated with breast cancer, but still of childbearing age, can wish to receive one or more of the antigen-binding fragments described herein in treatment prophylactically to prevent the occurrence of neoplasia until it is suitable to perform preventive surgery.

The subjects can have an advanced form of disease (*e.g.*, multiple myeloma), in which case the treatment objective can include mitigation or reversal of disease progression, and /or amelioration of side effects. The subjects can have a history of the condition, for which they have already been treated, in which case the therapeutic objective will typically include a decrease or delay in the risk of recurrence.

Further modification can be introduced to the FcRL5-specific CAR-expressing immunoresponsive cells (*e.g.*, T cells) to avert or minimize the risks of immunological complications (known as "malignant T-cell transformation"), *e.g.*, graft versus-host disease (GvHD), or when healthy tissues express the same target antigens as the tumor cells, leading to outcomes similar to GvHD. A potential solution to this problem is engineering a suicide gene into the CAR-expressing T cells. Suitable suicide genes include, but are not limited to, Herpes simplex virus thymidine kinase (hsv-tk), inducible Caspase 9 Suicide gene (iCasp-9), and a truncated human epidermal growth factor receptor (EGFRt) polypeptide. In certain embodiments, the suicide gene is an EGFRt polypeptide. The EGFRt polypeptide can enable T cell elimination by administering anti-EGFR monoclonal antibody (*e.g.*, cetuximab). EGFRt can be covalently joined to the 3' terminus of the intracellular domain of the FcRL5-specific CAR. The suicide gene can be included within the vector comprising nucleic acids encoding the presently disclosed FcRL5-specific CARs. In this way, administration of a prodrug designed to activate the suicide gene (*e.g.*, a prodrug (*e.g.*, AP1903 that can activates iCasp-9) during malignant T-cell transformation (*e.g.*, GVHD) triggers apoptosis in the suicide gene-activated CAR-expressing T cells.

IX. Kits

The presently disclosed subject matter provides kits for the treatment or prevention of a neoplasia (*e.g.*, multiple myeloma). In certain embodiments, the kit comprises a therapeutic or prophylactic composition containing an effective amount of an immunoresponsive cell comprising a FcRL5-specific CAR in unit dosage form. In particular embodiments, the cells further expresses at least one co-stimulatory ligand. In certain embodiments, the kit comprises a sterile container which contains a therapeutic or prophylactic vaccine; such containers can be boxes, ampules, bottles, vials, tubes, bags, pouches, blister-packs, or other suitable container forms known in the art. Such containers can be made of plastic, glass, laminated paper, metal foil, or other materials suitable for holding medicaments.

If desired, the immunoresponsive cell is provided together with instructions for administering the cell to a subject having or at risk of developing a neoplasia (*e.g.*, multiple myeloma). The instructions will generally include information about the use of the composition for the treatment or prevention of a neoplasia (*e.g.*, multiple myeloma). In other embodiments, the instructions include at least one of the following: description of the therapeutic agent; dosage schedule and administration for treatment or prevention of a neoplasia (*e.g.*, multiple myeloma) or symptoms thereof; precautions; warnings; indications; counter-indications; overdosage information; adverse reactions; animal pharmacology; clinical studies; and/or references. The instructions may be printed directly on the container (when present), or as a label applied to the container, or as a separate sheet, pamphlet, card, or folder supplied in or with the container.

X. Exemplary extracellular antigen-binding domains (e.g., scFvs)

Table 1

ET200-001
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) Cagtctgtgttgacgcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 1] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtgtatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcgaaggtccgtacgacggtttcgattcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 2] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLG [SEQ ID NO: 3] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGPYDGFDSWGQGTLVTVSS** [SEQ ID NO: 4] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 2

ET200-002
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) Aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattctgtggtattcggcggagggaccaagctgaccgtcctaggt [SEQ ID No. 5] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtacagtctggcactgaggtgaagaagcctggggcctcagtgagggtcgcctgcaaggcttctggttacccctttaacaaatatgacatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggaggcatcatccctatctttcgtacaacaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtatattactgtgcgcgcgaatggttctactgggatatctggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 6] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNSVVFGGGTKLTVLG [SEQ ID NO: 7] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGTEVKKPGASVRVACKASGYPFNKYDINWVRQAPGQGLEWMGGIIPIFRTTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREWFYWDIWGQGTLVTVSS** [SEQ ID NO: 8] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 3

ET200-003
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgactcagccaccctcagtgtccgtgtccccaggacagacagccagcatctcctgctctggaaataaattgggggactaagtatgtttactggtatcagaagaggccaggccagtcccctgtgttggtcatgtatgaagataatcagcggccctcagggatcccggagcggttctctggctccaactctgggaacacagccactctgaccatcagagggacccagactgtggatgaggctgactattactgtcaggcgtgggactccgacactttcgtggtcttcggcggagggaccaaggtcaccgtcctaggt [SEQ ID NO: 9] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagaccgggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatggcatgcactgggtccgccaggctccaggcaaggggctggagtgggtggcagttatatcacatgatggaagtaataaatactacgcagactccgtgaagggccgattcaccatctccagagacaattccaaggacacgctgtatctgcaaatgaacagcctgagaggtgaggacacggccgtatattactgtgcgcgctctaaccagtggtctggttacttctctttcgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 10] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSVSPGQTASISCSGNKLGTKYVYWYQKRPGQSPVLVMYEDNQRPSGIPERFSGSNSGNTATLTIRGTQTVDEADYYCQAWDSDTFVVFGGGTKVTVLG [SEQ ID NO: 11] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVETGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISHDGSNKYYADSVKGRFTISRDNSKDTLYLQMNSLRGEDTAVYYCARSNQWSGYFSFDYWGQGTLVTVSS** [SEQ ID NO: 12] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 4

ET200-006
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtggtggtcatccattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 13] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccacctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaacacttacaatggtcacacaaactatgcacagaagctccagggcagagccacaatgaccgcagacacatccacgaacacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgcgttatctacggttctggtgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 14] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVVVIHYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLG [SEQ ID NO: 15] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINTYNGHTNYAQKLQGRATMTADTSTNTAYMELRSLRSDDTAVYYCARVIYGSGDYWGQGTLVTVSS** [SEQ ID NO: 16] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 5

ET200-007
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccactctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaactgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatcgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 17] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctgcaggagtcgggcccaggactggtgaagccttcggagaccctgtccctcacctgcaatgtctctggttactccatcagcagtggttacttttggggctggatccggcagcccccagggaaggggctggagtggattgggagtatctatcatagtaggagcacctactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgaactctgtgaccgccgcagacacggccgtgtattactgtgcgcgcggttacggttacttcgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 18] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPLSVSVAPGKTARITCGGNNIGSKTVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHRVFGGGTKLTVLG [SEQ ID NO: 19] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQESGPGLVKPSETLSLTCNVSGYSISSGYFWGWIRQPPGKGLEWIGSIYHSRSTYYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAVYYCARGYGYFDYWGQGTLVTVSS** [SEQ ID NO: 20] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 6

ET200-008
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caatctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacaacacccaggcaaagcccccaaactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacttcgaaggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 21] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggaggtgtggtacggcctggggggtccctgagactctcctgtgcagcctctggattcacctttggtgattatggcatgagctgggtccgccaagctccagggaaggggctggagtgggtctctggtattaattggaatggtggtagcacaggttatgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagccgaggacacggccgtatattactgtgcgcgctctaaatacaacttccatgtttactacgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 22] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTSKVFGGGTKLTVLG [SEQ ID NO: 23] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGGVVRPGGSLRLSCAASGFTFGDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSKYNFHVYYDYWGQGTLVTVSS** [SEQ ID NO: 24] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 7

ET200-009
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccaccctcagcgtctgggacccccgggcagacagtcaccatctcttgttctggaagcaactccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcctcatctataggaataatcagcggccctcaggggtccctgaccgattctcaggctccaagtctggcacctcagcctccctggccatcagtgggctccgctccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtgcttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 25] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgctcttctggtaacatggtttcttggaaagatatgtggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 26] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSASGTPGQTVTISCSGSNSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAYVFGTGTKVTVLG [SEQ ID NO: 27] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSSGNMVSWKDMWGQGTLVTVSS** [SEQ ID NO: 28] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 8

ET200-010
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caatctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactctgtctcctggtaccaacaacacccaggcaaagcccccagactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacccctttagtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 29] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcggtgctgttgcttaccatgattggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 30] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPRLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTPLVFGTGTKVTVLG [SEQ ID NO: 31] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGAVAYHDWGQGTLVTVSS** [SEQ ID NO: 32] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 9

ET200-011
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagagggtcaccatctcctgctctggaagcagctccaacatttcgatttatgatgtatcctggtatcagcagctcccaggaacagcccccaaactcctcatttatggcaataataagcgaccctcggggattgctgaccgattctctggctccacgtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatgacagtctgagtgggggggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 33] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **cagatgcagctggtgcaatctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcgaggcttctggaggcaccctcagcagctatgctatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatgtttggtacagcacactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgaaaacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtgttcattacgcttctttcgatcattggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 34] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSAAPGQRVTISCSGSSSNISIYDVSWYQQLPGTAPKLLIYGNNKRPSGIADRFSGSTSGTSATLGITGLQTGDEADYYCGTWDDSLSGGVFGGGTKLTVLG [SEQ ID NO: 35] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QMQLVQSGAEVKKPGSSVKVSCEASGGTLSSYAINWVRQAPGQGLEWMGGIIPMFGTAHYAQKFQGRVTITADESTKTAYMELSSLRSEDTAVYYCARGVHYASFDHWGQGTLVTVSS** [SEQ ID NO: 36] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 10

ET200-012
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctgcggccgcaggacagaaggtcaccatctcctgctctggaagcgactccaacattgggaataattatgtgtcctggtatcaacacctcccagggacagcccccaaactcctcatttatgacgttaaaaatcgaccctcagggattcctgaccggttctccggctccaagtctggctcgtcagccaccctaggcatcgccggactccagcctggggacgaggccgattattactgcggaacatgggacagtcggctggatgcctatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 37] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **cagatgcagctggtgcaatctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagacttctggtttcccctttaatatctttggaatcacctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcggttacaacggtaacacagactacccacagaagttccagggcagagtcaccatgtccacagacacatccacgagtacagcctacatggagctgaggaacctgaaatctgacgacacggccgtgtattactgtgcgcgcggtgcttacggtggtatggatacttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 38] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSAAAGQKVTISCSGSDSNIGNNYVSWYQHLPGTAPKLLIYDVKNRPSGIPDRFSGSKSGSSATLGIAGLQPGDEADYYCGTWDSRLDAYVFGTGTKVTVLG [SEQ ID NO: 39] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QMQLVQSGAEVKKPGASVKVSCKTSGFPFNIFGITWVRQAPGQGLEWMGWISGYNGNTDYPQKFQGRVTMSTDTSTSTAYMELRNLKSDDTAVYYCARGAYGGMDTWGQGTLVTVSS** [SEQ ID NO: 40] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 11

ET200-013
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcacctccaacatcggggcaggttatgatgtacactggtatcagcagcttccaggaacagcccccaaactcctcatctatactaacaactttcggccctcaggggtccctgaccgattctctgcctccaagtctggcacttcagcttccctggccatcactggtctccaggctgaggatgaggctgattattactgcggaacatgggatagcagcctgagtgccgttgtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 41] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctggaactgaggtgaagaagcctggggcctcagtgaaagtctcctgcaaggcttctggttacatgtttaccagttatggtctcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgctaacaatggtaagacaaattatgctaagaaattccaggacagagtcaccatgaccagagacacttccacgagcacaggctacatggaactgaggagcctgagatctgacgacacggccgtatattactgtgcgcgccatatcggtggttcttacttcgatcgttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 42] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSGAPGQRVTISCTGSTSNIGAGYDVHWYQQLPGTAPKLLIYTNNFRPSGVPDRFSASKSGTSASLAITGLQAEDEADYYCGTWDSSLSAVVFGGGTKLTVLG [SEQ ID NO: 43] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGTEVKKPGASVKVSCKASGYMFTSYGLNWVRQAPGQGLEWMGWISANNGKTNYAKKFQDRVTMTRDTSTSTGYMELRSLRSDDTAVYYCARHIGGSYFDRWGQGTLVTVSS** [SEQ ID NO: 44] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 12

ET200-014
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcattatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 45] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagactgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtgatggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagacgaggacacggccgtatattactgtgcgcgctctcatgaagctaacctggttggtgattggtggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 46] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLG [SEQ ID NO: 47] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSDGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRDEDTAVYYCARSHEANLVGDWWGQGTLVTVSS** [SEQ ID NO: 48] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 13

ET200-015
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtggtgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatgtggtattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 49] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctacggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgctggggtggtttcggtgctgttgatcattggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 50] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDVVFGGGTKLTVLG [SEQ ID NO: 51] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARWGGFGAVDHWGQGTLVTVSS** [SEQ ID NO: 52] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 14

ET200-016
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcttctgagctgactcaggaccctgctgtgtctgtggccttgggacagacagtcaagatcacgtgccaaggagacagcctcacagactaccatgcaacctggtaccagcagaagccaggacaggcccctgtcgctgtcatctatgctacaaacaaccggcccactgggatcccagaccgattctctggttccagttccggaaacacagcttctttgaccatcactggggctcaggcggaagatgaggctgactattactgtaattcccgggacagcggcacggacgaagtgttattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 53] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagactgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtagtagttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgcgcggtcagggttacgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 54] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SSELTQDPAVSVALGQTVKITCQGDSLTDYHATWYQQKPGQAPVAVIYATNNRPTGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGTDEVLFGGGTKLTVLG [SEQ ID NO: 55] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVETGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGQGYDYWGQGTLVTVSS** [SEQ ID NO: 56] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 15

ET200-017
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcgtctatgatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgagcatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatactgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 57] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgctactacccgggtatggatatgtggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 58] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLSISRVEAGDEADYYCQVWDSSSDHTVFGTGTKVTVLG [SEQ ID NO: 59] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYPGMDMWGQGTLVTVSS** [SEQ ID NO: 60] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 16

ET200-018
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccgccctcaacgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcgggagaaatggtgtaaactggtaccagcagctcccaggagcggcccccaaagtcctcatctataatgataatcagcgaccctcaggggtccctgaccgagtctctggctcccagtctggctcctcaggcaccctggccatcgatgggcttcggtctgaggatgaggctgattattactgtgcggcatgggatgacagcctgcatggtgtggtattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 61] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcaatgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtggttacggtgattcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 62] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSTSGTPGQRVTISCSGSSSNIGRNGVNWYQQLPGAAPKVLIYNDNQRPSGVPDRVSGSQSGSSGTLAIDGLRSEDEADYYCAAWDDSLHGVVFGGGTKLTVLG [SEQ ID NO: 63] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKVSGYTLNELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARGGYGDSWGQGTLVTVSS** [SEQ ID NO: 64] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 17

ET200-019
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattcttgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 65] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcaatctggggctgaggtgaagaggcctgggtcctcggtgaaggtctcctgcacggcttctggaggcaccttcagcagcgatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggaggaatcatccctatgtttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcgaaggttactactacccgtctgcttacctgggttctgttctgaacgacatctcttctgtttacgatgaatggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 66] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNSWVFGGGTKLTVLG [SEQ ID NO: 67] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKRPGSSVKVSCTASGGTFSSDAISWVRQAPGQGLEWMGGIIPMFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREGYYYPSAYLGSVLNDISSVYDEWGQGTLVTVSS** [SEQ ID NO: 68] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 18

ET200-020
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcacctccaacattggaaataatgatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcgtgagtgcttcttgggtcttcggcagagggaccaagctgaccgtcctaggt [SEQ ID NO: 69] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatccacagaagctccagggcagagtcaccatgaccacagacccatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgctctatgacttctttcgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 70] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSAAPGQKVTISCSGSTSNIGNNDVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSVSASWVFGRGTKLTVLG [SEQ ID NO: 71] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYPQKLQGRVTMTTDPSTSTAYMELRSLRSDDTAVYYCARSMTSFDYWGQGTLVTVSS** [SEQ ID NO: 72] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 19

ET200-021
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcaactccaacattgggaataattatgtatcctggtatcagcaactcccagggacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaggtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatggaataccactgtgactcctggctatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 73] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaagtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacaccgccatgtattactgtgcgcgctctgtttacgacctggatacttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 74] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSAAPGQKVTISCSGSNSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSRSGTSATLGITGLQTGDEADYYCGTWNTTVTPGYVFGTGTKVTVLG [SEQ ID NO: 75] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAMYYCARSVYDLDTWGQGTLVTVSS** [SEQ ID NO: 76] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 20

ET200-022
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgggggccccttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 77] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtcttggggaggctcggaacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagcggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaattccctgtatctgcaaatgaacagtctgagagctgaggacaccgccatgtattactgtgcgcgctaccgtcaggttggttctgcttacgattcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 78] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLGAPYVFGTGTKVTVLG [SEQ ID NO: 79] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSWGGSEQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAMYYCARYRQVGSAYDSWGQGTLVTVSS** [SEQ ID NO: 80] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 21

ET200-023
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) ctgcctgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtatcagcagaagccaggccaggcccctgtgctggtcgtctatgctgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagttatcataattatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 81] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgagcagcctgagatctgaggacaccgccatgtattactgtgcgcgctactggggtttcggtgtttctgatcgttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 82] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) LPVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYADSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSYHNYVFGTGTKVTVLG [SEQ ID NO: 83] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELSSLRSEDTAMYYCARYWGFGVSDRWGQGTLVTVSS** [SEQ ID NO: 84] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 22

ET200-024
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccccgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgacagcagcaatctttgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 85] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **cagatgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctacaactactactactacgattcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 86] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNLWVFGGGTKLTVLG [SEQ ID NO: 87] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARYNYYYYDSWGQGTLVTVSS** [SEQ ID NO: 88] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 23

ET200-025
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacagagtcaccatcacttgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatcaaggttcagtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagattttgcaacttactactgtcaacagagttacagtaccccattcactttcggccctgggaccaaagtggatatcaaacgt [SEQ ID NO: 89] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacaccgccatgtattactgtgcgcgctactggggttacgactcttacgatgaatggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 90] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTKVDIKR [SEQ ID NO: 91] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAMYYCARYWGYDSYDEWGQGTLVTVSS** [SEQ ID NO: 92] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 24

ET200-026
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 93] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcaacaaccattactacaacgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 94] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWVFGGGTKLTVLG [SEQ ID NO: 95] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARNNHYYNDYWGQGTLVTVSS** [SEQ ID NO: 96] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 25

ET200-027
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagggggtcaccatcccctgcactgggagcagctccaacatcggggcaggttatgatgtacactggtaccagcagcttccagggacagcccccaaactcctcatctatggtaacaacaatcggccctcaggggtccctgaccgcttctctggctccaggtctggctcctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtgatgtggtattcggcggagggaccaaggtcaccgtcctaggt [SEQ ID NO: 97] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaagaagcctggggctacagtgaaaatctcctgcaaggtttctggatacaccttcaccgactactacatgcactgggtgcaacaggcccctggaaaagggcttgagtggatgggacttgttgatcctgaagatggtgaaacaatatacgcagagaagttccagggcagagtcaccataaccgcggacacgtctacagacacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgctactggtcttactctttcgactacctgtacatgccggaaggtaacgattggtggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 98] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSGAPGQGVTIPCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGSSASLAITGLQAEDEADYYCQSYDSSLSDVVFGGGTKVTVLG [SEQ ID NO: 99] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGLVDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCARYWSYSFDYLYMPEGNDWWGQGTLVTVSS** [SEQ ID NO: 100] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 26

ET200-028
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgactcagccacccgcagcgtctgggacccccggacagagagtcaccatctcttgttctgggggcgtctccaacatcgggagtggtgctctaaattggtaccagcaactcccaggaacggcccccaaactcctcatctatagttacaatcagcggccctcaggggtctctgaccgattctctggctccaggtctgccacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcaacctgggatgatagtgtgaatggttgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 101] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtacagtctggagctgaggtgaagaagcctggggattcagtgaaggtctcctgcaagccttctggttacaattttctcaactatggtatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggattagcacttacaccggtaacacaaactatgcacagaagctgcagggcagagtcaccttcaccacagacacatccacgagcacagcctacatggagatgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcgacctgtactactacgaaggtgttgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 102] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPAASGTPGQRVTISCSGGVSNIGSGALNWYQQLPGTAPKLLIYSYNQRPSGVSDRFSGSRSATSASLAISGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLG [SEQ ID NO: 103] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] QVQLVQSGAEVKKPGDSVKVSCKPSGYNFLNYGINWVRQAPGQGLEWMGWISTYTGNTNYAQKLQGRVTFTTDTSTSTAYMEMRSLRSDDTAVYYCARDLYYYEGVDYWGQGTLVTVSS [SEQ ID NO: 104] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 27

ET200-029
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccagggttacctgtgggggaaacaacattggaagtgaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgttggtcatctattatgataccgaccggccctcagggatccctgagcgattctctggctcccactctgggaccacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagggatcatgtggtattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 105] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctgggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcggcctctggattcaccttcagtagctatgctatgcactgggtccgccaggctccaggcaagggactggagtgggtggcagttatatcatatgatggaagcaataaatactacgcagactccgtgaagggcctattcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagctgaggacacggccgtgtattactgtgcgcgctcttacttcacttctggtttctacgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 106] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSVSVAPGKTARVTCGGNNIGSESVHWYQQKPGQAPVLVIYYDTDRPSGIPERFSGSHSGTTATLTISRVEAGDEADYYCQVWDSSRDHVVFGGGTKLTVLG [SEQ ID NO: 107] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGLFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSYFTSGFYDYWGQGTLVTVSS** [SEQ ID NO: 108] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 28

ET200-030
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagttccaacatcggggcaggttatgatgtaaattggtatcagcagtttccaggaacagcccccaaactcctcatctatggtaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggctcttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 109] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **cagatgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcatgtcttctatgtactacgattggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 110] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGSYVFGTGTKVTVLG [SEQ ID NO: 111] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QMQLVQSGAEVKKPGASVKVSCKASGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARMSSMYYDWGQGTLVTVSS** [SEQ ID NO: 112] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 29

ET200-031
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgattatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 113] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagactgggggaggcttggtcaagcctggagggtccctgagactctcctgtgcagcctctggattcaccgtcagtgactactacatgagctggatccgccaggctccagggaagggcctggagtggatttcatacattagtggtagtggtaatagcatatactacgcagactctgtgaagggccgattcaccatctccagggacaacgccaagaactcactggatctgcaaatgaccagcctgagagccgaggacacggccgtatattactgtgcgcgctctactaaattcgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 114] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDYVFGTGTKVTVLG [SEQ ID NO: 115] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVETGGGLVKPGGSLRLSCAASGFTVSDYYMSWIRQAPGKGLEWISYISGSGNSIYYADSVKGRFTISRDNAKNSLDLQMTSLRAEDTAVYYCARSTKFDYWGQGTLVTVSS** [SEQ ID NO: 116] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 30

ET200-032
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) ctgcctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacgtcggaagttacactgtaaactggtaccggcaactcccaggaacggcccccacactcctcatctataataataatcagcggccctcaggggtccctgaccgattctctgactccaagtctggcacctcggcctccctgaccattagtgggctccagcctgaggatgaggctgattattattgtgcagcatgggatgacaggctgggtggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 117] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtctggagcagaggtgaaaaagccgggggagtctctgaagatctcctgtaagggttctggatacagctttaccaactactggatcggctgggtgcgccagatgcccgggaaaggcctggagtggatggggatcatctatcctggtgactctgataccagatacagcccgtccttccaaggccaggtcaccatctcagccgacaagtccatcagcaccgcctacctacagtggagcagcctgaaggcctcggacaccgccatgtattactgtgcgcgctctactggttcttctcatatgtctgatgaatggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 118] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) LPVLTQPPSASGTPGQRVTISCSGSSSNVGSYTVNWYRQLPGTAPTLLIYNNNQRPSGVPDRFSDSKSGTSASLTISGLQPEDEADYYCAAWDDRLGGYVFGTGTKVTVLG [SEQ ID NO: 119] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARSTGSSHMSDEWGQGTLVTVSS** [SEQ ID NO: 120] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 31

ET200-033
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaatcattgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 121] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caagtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggagatcactcatagtggaaggtccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgctcttctatcatgtctgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 122] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNHWVFGGGTKLTVLG [SEQ ID NO: 123] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEITHSGRSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSSIMSDYWGQGTLVTVSS** [SEQ ID NO: 124] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 32

ET200-034
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcacctccaacatcggggcaggttatgatgtacactggtaccagcagcttccaggaacagcccccaaactcctcatcaacaataacaggaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatggcagcctgactggtgcagtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 125] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcatgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcggttctgctctggaccattacgatcgttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 126] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSGAPGQRVTISCTGSTSNIGAGYDVHWYQQLPGTAPKLLINNNRNRPSGVPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDGSLTGAVFGGGTKLTVLG [SEQ ID NO: 127] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGSALDHYDRWGQGTLVTVSS** [SEQ ID NO: 128] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 33

ET200-035
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcaccaattgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 129] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctacaactactacttcaacgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 130] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTNWVFGGGTKLTVLG [SEQ ID NO: 131] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARYNYYFNDYWGQGTLVTVSS** [SEQ ID NO: 132] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 34

ET200-037
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 133] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **cagatgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgctctatgttcggtgctcatgattcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 134] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLG [SEQ ID NO: 135] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSMFGAHDSWGQGTLVTVSS** [SEQ ID NO: 136] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 35

ET200-038
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaacatcggggcaggttttgatgtacactggtaccagctacttccaggaacagcccccaaactcctcatctatgctaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctcctggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggtgtggtattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 137] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcaatctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtgcttctttcgaccgtcatgataactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 138] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGFDVHWYQLLPGTAPKLLIYANSNRPSGVPDRFSGSKSGTSASLAITGLLAEDEADYYCQSYDSSLSGVVFGGGTKLTVLG [SEQ ID NO: 139] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGASFDRHDNWGQGTLVTVSS** [SEQ ID NO: 140] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 36

ET200-039
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagttcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 141] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgctctaactactactacaacgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 142] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWVFGGGTKLTVLG [SEQ ID NO: 143] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSNYYYNDYWGQGTLVTVSS** [SEQ ID NO: 144] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 37

ET200-040
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaacatcggggcaggttatgatgtacactggtaccagcagcttccaggaacagcccccaaactcctcatctatggtaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 145] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctactctggtgtttactacgattggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 146] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGYVFGTGTKVTVLG [SEQ ID NO: 147] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARYSGVYYDWGQGTLVTVSS** [SEQ ID NO: 148] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 38

ET200-041
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggggtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccgacaactttgtgcagtggtaccagcagcgcccgggcggtgtccccaccactgtgatctttaatgatgacgaaagaccctctggcgtccctgatcggttctctggctccatcgacacctcctccaattctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgataataataatcgaggggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 149] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatgaaccctaacagtggtaacacaggctatgcacagaagttccagggcagagtcaccatgaccaggaacacctccataagcacagcctacatggagctgagcaacctgagatctgaggacacggccgtgtattactgtgcgcgctactactcttacggttacgattggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 150] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSGSPGKTVTISCTGSSGSIADNFVQWYQQRPGGVPTTVIFNDDERPSGVPDRFSGSIDTSSNSASLTISGLKTEDEADYYCQSYDNNNRGVFGGGTKLTVLG [SEQ ID NO: 151] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSNLRSEDTAVYYCARYYSYGYDWGQGTLVTVSS** [SEQ ID NO: 152] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 39

ET200-042
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagacggtcaccatctcctgcactgggggcagctccaacatcgggacaggttattttgtaaattggtaccagcaggttccaggaaaagcccccaaactcctcatcctgggtaacaataatcggccctcgggggtccctgaccgactctccggctccacgtccggcacctcagcctccctggccatcactgggctccaggctgaggatgagggtacttattactgccagtcctatgacagcagcctgagtggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 153] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtacagctgcagcagtcaggtccaggactggtgaagccctcgcagaccctctcactcacctgtggcatctccggggacagtgtctctaccaacagtgttgcttggcactggatcaggcagtccccatcgagaggccttgagtggctgggaaggacatactacaggtccaagtggtctaatgactatggagtatctgtgaaaagtcgaatcaccatcatcccagacacatccaagaaccagttctccctgcagctgaactctgtgactcccgaggacacggctgtgtattactgtgcgcgctcttcttcttggtaccagatcttcgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 154] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSGAPGQTVTISCTGGSSNIGTGYFVNWYQQVPGKAPKLLILGNNNRPSGVPDRLSGSTSGTSASLAITGLQAEDEGTYYCQSYDSSLSGYVFGTGTKVTVLG [SEQ ID NO: 155] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQSGPGLVKPSQTLSLTCGISGDSVSTNSVAWHWIRQSPSRGLEWLGRTYYRSKWSNDYGVSVKSRITIIPDTSKNQFSLQLNSVTPEDTAVYYCARSSSWYQIFDYWGQGTLVTVSS** [SEQ ID NO: 156] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 40

ET200-043
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagcgacagcatagccaacaactatgttcagtggtaccagcagcgcccgggcagtgcccccaccaatgtgatctacgaagatgtccaaagaccctctggggtccctgatcggttctctgggtccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgtctactattgtcagtcttatcatagcgacaatcgttgggtgttcggcggcgggaccaagctgaccgtcctaggt [SEQ ID NO: 157] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacacggccgtatattactgtgcgcgctctggtgcttactgggactactctgtttacgatgaatggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 158] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTGSSDSIANNYVQWYQQRPGSAPTNVIYEDVQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEAVYYCQSYHSDNRWVFGGGTKLTVLG [SEQ ID NO: 159] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSGAYWDYSVYDEWGQGTLVTVSS** [SEQ ID NO: 160] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 41

ET200-044
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgactcagccaccctcagtgtccgtgtccccaggacagacagccaccatcgcctgttctggacataaattggggataaatatgcttcctggtatcagcagaagtcgggccagtcccctgtgttgatcatctatcaggataataagcggccctcagggattcctgagcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctctggatgaggctgactattattgtcaggcgtgggacagtagtacttatgtggcattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 161] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctgcaggagtccggcccaggactggtgaagccttcggagaccctgtccctcacctgcgttgtctctggtggctccatcagcagtagtaactggtggagctgggtccgccagcccccagggaaggggctggagtggattggggaaatctatcatagtgggagccccaactacaacccatccctcaagagtcgagtcaccatatcagtagacaagtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcatgactactcatactttcggttacgatgcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 162] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSVSPGQTATIACSGHKLGDKYASWYQQKSGQSPVLIIYQDNKRPSGIPERFSGSNSGNTATLTISGTQALDEADYYCQAWDSSTYVAFGGGTKLTVLG [SEQ ID NO: 163] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQESGPGLVKPSETLSLTCVVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSPNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARMTTHTFGYDAWGQGTLVTVSS** [SEQ ID NO: 164] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 42

ET200-045
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagcctgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccacgattacttgtgggggaaacaacattggaagtgaaagtgtgcactggtaccaccagaagccaggccaggcccctgtgttggtcatctatgatgatgccggccggccctcagggatccctgagcgattcactggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggacagaaatagtgctcagtttgtcttcggacctgggaccaaggtcaccgtcctaggt [SEQ ID NO: 165] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcggtgttcatctggattggtggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 166] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QPVLTQPPSVSVAPGKTATITCGGNNIGSESVHWYHQKPGQAPVLVIYDDAGRPSGIPERFTGSNSGNTATLTISRVEAGDEADYYCQVWDRNSAQFVFGPGTKVTVLG [SEQ ID NO: 167] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGVHLDWWGQGTLVTVSS** [SEQ ID NO: 168] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 43

ET200-069
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtggttatgtcttcggaactgggaccaagctgaccgtcctaggt [SEQ ID NO: 169] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcctgtacgaaggtggttaccatggttggggttcttggctgtcttctgattcttggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 170] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYVFGTGTKLTVLG [SEQ ID NO: 171] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLYEGGYHGWGSWLSSDSWGQGTLVTVSS** [SEQ ID NO: 172] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 44

ET200-078
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttattgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 173] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgcgcgaaggggcatttgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 174] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYWVFGGGTKLTVLG [SEQ ID NO: 175] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGAFDAFDIWGQGTMVTVS [SEQ ID NO: 176] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 45

ET200-079
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgagctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcttcatctataggaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtggttatctcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 177] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaatggcgactccaactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 178] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYELTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLFIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYLFGTGTKVTVLG [SEQ ID NO: 179] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCANGDSNYYYGMDVWGQGTTVTVSS** [SEQ ID NO: 180] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 46

ET200-081
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgccctgactcagcctgcctccgtgtccgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacattggtggttataactatgtctcctggtaccaacaacacccaggcaaagcccccaaactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcatctcatatacacgcacctggaacccctatgtcttcgggagtgggaccaaggtcaccgtcctaggt [SEQ ID NO: 181] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtctgggggaggcgtggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccgtcaagctccagggaagggtctggagtgggtctctcttattagtggggatggtggtagcacatactatgcagactctgtgaagggccgattcaccatctccagagacaacagcaaaaactccctgtatctgcaaatgaacagtctgagaactgaggacaccgccttgtattactgtgcaaaagatcgggcagcagctggctactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 182] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSALTQPASVSGSPGQSITISCTGTSSDIGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCISYTRTWNPYVFGSGTKVTVLG [SEQ ID NO: 183] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGGGVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLISGDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRTEDTALYYCAKDRAAAGYYYYGMDVWGQGTTVTVSS** [SEQ ID NO: 184] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 47

ET200-097
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) ctgcctgtgctgactcagccaccctcagtgtccgtgtccccaggacagacagccatcatcacctgctctggagataaattgggggaaaaatatgtttcctggtatcagcagaagccaggccagtcccctgtactggtcatcgatcaagataccaggaggccctcagggatccctgagcgattctctggctccaactctgggaccacagccactctgaccatcagcgggacccaggctatggatgaggctgactattactgtcaggcgtgggacaggggtgtggtattcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 185] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggagacttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttaatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggagtggtaataacataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagatagtatacggtatggcatcacctggggaggttttgactactggggccagggaaccctggtcaccgtctcctca** [SEQ ID NO: 186] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) LPVLTQPPSVSVSPGQTAIITCSGDKLGEKYVSWYQQKPGQSPVLVIDQDTRRPSGIPERFSGSNSGTTATLTISGTQAMDEADYYCQAWDRGVVFGGGTKLTVLG [SEQ ID NO: 187] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGDLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWSGNNIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDSIRYGITWGGFDYWGQGTLVTVSS** [SEQ ID NO: 188] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 48

ET200-098
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagcctgtgctgactcagccaccctcggtgtccaagggcttgagacagaccgccacactcacctgcactgggaacagcaacaatgttggcaacctaggagtagcttggctgcagcagcaccagggccaccctcccaaactcctatcctacaggaataacaaccggccctcagggatctcagagagattatctgcatccaggtcaggaaacacagcctccctgaccattactggactccagcctgaggacgaggctgactattactgctcagcatgggacagtagcctcagtgcttgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 189] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggagtcgtggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccgtcaagctccggggaagggtctggagtgggtctctcttattaattgggatggtggtagcacctactatgcagactctgtgaagggtcgattcaccatctccagagacaacagcaaaaactccctgtatctgcaaatgaacagtctgagagctgaggacaccgccttgtattactgtgcaaaagggatgggcctgagggcgtttgactactggggccagggaaccctggtcaccgtctcctca** [SEQ ID NO: 190] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QPVLTQPPSVSKGLRQTATLTCTGNSNNVGNLGVAWLQQHQGHPPKLLSYRNNNRPSGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLSAWVFGGGTKLTVLG [SEQ ID NO: 191] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLINWDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGMGLRAFDYWGQGTLVTVSS** [SEQ ID NO: 192] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 49

ET200-099
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtccggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcttcatgggatgacagcctgaatggccgttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 193] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtacagtctggggctgaggtgaggaagcctggggcctcagtgaaggtttcctgcaagacttctggatacaccttcagttggtatgctatacattgggtgcgccaggcccccggacaaaggcttgagtggatgggatggatcaacgctggcaatggaaacacaaaatattcacagaaatttcagggcagagtcagtcttaccagggacacatccgcgagcacagcctacatggagctgagcagcctgagatctgatgacacggctgtgtattactgtgcgagacccgataattatggttcgggtggggatgtttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 194] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCASWDDSLNGRYVFGTGTKVTVLG [SEQ ID NO: 195] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVRKPGASVKVSCKTSGYTFSWYAIHWVRQAPGQRLEWMGWINAGNGNTKYSQKFQGRVSLTRDTSASTAYMELSSLRSDDTAVYYCARPDNYGSGGDVFDIWGQGTMVTVSS** [SEQ ID NO: 196] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 50

ET200-100
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactttgtgcagtggtaccagcagcgcccgggcagtgcccccacccctatgatctatgaggataacaacagacccccctggggtccctgatcggttctctgcctccgtcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgataccagcaatgtggtattcggcgggggggaccaagctgaccgtcctaggt [SEQ ID NO: 197] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggaggcttggtacagcctggagggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatgaaatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtggtagtaccatatactacgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggctgtttattactgtgcacgctgggactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 198] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTRSSGSIASNFVQWYQQRPGSAPTPMIYEDNNRPPGVPDRFSASVDSSSNSASLTISGLKTEDEADYYCQSYDTSNVVFGGGTKLTVLG [SEQ ID NO: 199] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARWDYGMDVWGQGTTVTVSS** [SEQ ID NO: 200] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 51

ET200-101
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccaccctcagcgtctgggcccccgggcagagggtcaccgtctcttgttctggaagcaactccaacatcggaagtaactacgttaactggtaccagcagttcccaggaacggcccccaaactcctcatgtatagtagtagtcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccactctgaggatgaggctgattattactgtgctacatgggatgacagcctgaatgcttgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 201] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaggaagcctggggcctcagtgaaggtttcctgcaagacttctggatacaccttcacttggtatgctatacattgggtgcgccaggcccccggacaaaggcttgagtggatgggatggatcaacgctggcagtggaaacacaaaatattcacagaaatttcagggcagagtcacccttaccagggacacatccgcgagcacagcgtacatggagctgagcagcctgagatctgatgacacggctgtgtattactgtgcgagacccaataactatggttcgggtggggatgtttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 202] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSASGAPGQRVTVSCSGSNSNIGSNYVNWYQQFPGTAPKLLMYSSSQRPSGVPDRFSGSKSGTSASLAISGLHSEDEADYYCATWDDSLNAWVFGGGTKLTVLG [SEQ ID NO: 203] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVRKPGASVKVSCKTSGYTFTWYAIHWVRQAPGQRLEWMGWINAGSGNTKYSQKFQGRVTLTRDTSASTAYMELSSLRSDDTAVYYCARPNNYGSGGDVFDIWGQGTMVTVSS** [SEQ ID NO: 204] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 52

ET200-102
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgagtgcttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 205] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaagtttcctgcaaggcttctggatacaccttcacgaactatgctctgcattgggtgcgccaggcccccggacaagggcttgagtggatggcatggatcaacggtggcaatggtaacacaaaatattcacagaacttccagggcagagtcaccattaccagggacacatccgcgagcacagcctatatggagctgagcagcctgagatctgaagacacggctgtgtattactgtgcgaaaccggaggaaacagctggaacaatccactttgactactggggccagggaaccccggtcaccgtctcctca** [SEQ ID NO: 206] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAYVFGTGTKVTVLG [SEQ ID NO: 207] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYALHWVRQAPGQGLEWMAWINGGNGNTKYSQNFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAKPEETAGTIHFDYWGQGTPVTVSS** [SEQ ID NO: 208] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 53

ET200-103
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcaccatcacggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 209] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtacagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgggggagggttactatgatagtagtggttattccaacggtgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 210] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTITVFGGGTKLTVLG [SEQ ID NO: 211] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAGEGYYDSSGYSNGDAFDIWGQGTMVTVSS** [SEQ ID NO: 212] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 54

ET200-104
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaatgtggtattcggcggagggaccaaggtcaccgtcctaggt [SEQ ID NO: 213] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggaggcttggtacagcctggagggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatgaaatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtggtagtaccatatactacgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggctgtttattactgtgcacgctgggactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 214] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNVVFGGGTKVTVLG [SEQ ID NO: 215] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARWDYGMDVWGQGTTVTVSS** [SEQ ID NO: 216] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 55

ET200-105
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcagtgtccgtgtccccaggacagacagccagcatcacctgctctggagatagattgacgaataaatatgtttcctggtatcaacagaagccaggccagtcccctgtgttggtcatctatgaggatgccaagcggccctcagggatccctgcgcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctatggatgagtctgaatattactgtcaggcgtgggacagcagtgtggtggtttttggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 217] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggatttacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagtataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagatgaggacacggccttgtattactgtgcaaaagaccgaggggggggagttatcgttaaggatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 218] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVSPGQTASITCSGDRLTNKYVSWYQQKPGQSPVLVIYEDAKRPSGIPARFSGSNSGNTATLTISGTQAMDESEYYCQAWDSSVVVFGGGTKLTVLG [SEQ ID NO: 219] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTALYYCAKDRGGGVIVKDAFDIWGQGTMVTVSS** [SEQ ID NO: 220] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 56

ET200-106
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgagctgactcagccacccgcagcgtctgggacccccggacagagagtcaccatctcttgttctgggggcgtctccaacatcgggagtggtgctctaaattggtaccagcaactcccaggaacggcccccaaactcctcatctatagttacaatcagcggccctcaggggtctctgaccgattctctggctccaggtctgccacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcaacctgggatgatagtgtgaatggttgggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 221] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctggagctgaggtgaagaagcctggggattcagtgaaggtctcctgcaagccttctggttacaattttctcaactatggtatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggattagcacttacaccggtaacacaaactatgcacagaagctgcagggcagagtcaccttcaccacagacacatccacgagcacagcctacatggagatgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgccagcagggtggtggttggtacgatgtttggggtcaaggtactctggtcaccgtctcctca** [SEQ ID NO: 222] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYELTQPPAASGTPGQRVTISCSGGVSNIGSGALNWYQQLPGTAPKLLIYSYNQRPSGVSDRFSGSRSATSASLAISGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLG [SEQ ID NO: 223] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGAEVKKPGDSVKVSCKPSGYNFLNYGINWVRQAPGQGLEWMGWISTYTGNTNYAQKLQGRVTFTTDTSTSTAYMEMRSLRSDDTAVYYCARQQGGGWYDVWGQGTLVTVSS** [SEQ ID NO: 224] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 57

ET200-107
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggagagaaggtcaccatctcctgctctggaagcaacttcaatgttggaaataatgatgtatcctggtatcagcaactcccaggtgcagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctggacatcaccgggctccacagtgacgacgaggccgattattactgcggaacatgggatagcagcctgaatactggggggtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 225] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatactatcagctgggtacgacaggcccctggacaagggcttgagtggatgggatggatcagcacttacaatggtctcacaaactatgcacagaacctccagggcagagtcaccatgactacagacacattcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattactgtgtgagagaggggtccccgactacggtgacttcgcgtcctttgactactggggccagggaaccctggtcaccgtctcctca** [SEQ ID NO: 226] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSAAPGEKVTISCSGSNFNVGNNDVSWYQQLPGAAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLDITGLHSDDEADYYCGTWDSSLNTGGVFGTGTKVTVLG [SEQ ID NO: 227] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYTISWVRQAPGQGLEWMGWISTYNGLTNYAQNLQGRVTMTTDTFTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFASFDYWGQGTLVTVSS** [SEQ ID NO: 228] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 58

ET200-108

DNA Sequence

(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag)

cagtctgtgttgacgcagccgccctcagtgtctgcgcccccgggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagttcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggatttctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcgccggactccagactggggacgaggccgattattactgcggaacatgggataccagcctgagtggtttttatgtcttcggaagtgggaccaaggtcaccgtcctaggt [SEQ ID NO: 229]

tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305]

gaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatactatcagctgggtacgacaggcccctggacaagggcttgagtggatgggatggatcagcacttacaatggtctcacaaactatgcacagaacctccagggcagagtcaccatgactacagacacattcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattactgtgtgagagaggggtccccCgactacggtgacttcgcgtcctttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 230]

ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]

Amino Acid Sequence

(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag)

QSVLTQPPSVSAPPGQKVTISCSGSSSNIGNNYVSWYQQFPGTAPKLLIYDNNKRPSGISDRFSGSKSGTSATLGIAGLQTGDEADYYCGTWDTSLSGFYVFGSGTKVTVLG [SEQ ID NO: 231]

SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307]

EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYTISWVRQAPGQGLEWMGWISTYNGLTNYAQNLQGRVTMTTDTFTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFASFDYWGQGTLVTVSS [SEQ ID NO: 232]

TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 59

ET200-109
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) ctgcctgtgctgactcagccaccctcagcgtctgcgacccccgggcagagggtcaccatctcttgttctggaaccacctccaacatcggaagtaatactgtacactggtaccagcagctcccagggacggcccccaaactcctcatctataataataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctacatattcctgtgcaacatgggatgacagcctgagtggtgtggtcttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 233] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagatcccgcctacggtgactacgagtatgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 234] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) LPVLTQPPSASATPGQRVTISCSGTTSNIGSNTVHWYQQLPGTAPKLLIYNNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEATYSCATWDDSLSGVVFGGGTKLTVLG [SEQ ID NO: 235] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPAYGDYEYDAFDIWGQGTMVTVSS** [SEQ ID NO: 236] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 60

ET200-110
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaactaatggtgtaaactggttccagcagttcccaggaacggcccccaaactcctcatctatactaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgcggatgaggctgattattactgtgcagtgtgggaccacagcctgaatggtccggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 237] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagggggccggttttgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 238] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSASGTPGQRVTISCSGSSSNIGTNGVNWFQQFPGTAPKLLIYTNDQRPSGVPDRFSGSKSGTSASLAISGLQSADEADYYCAVWDHSLNGPVFGGGTKLTVLG [SEQ ID NO: 239] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGAGFDAFDIWGQGTMVTVSS** [SEQ ID NO: 240] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 61

ET200-111
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgagactgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 241] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagaggggctagatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 242] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDETDYYCAAWDDSLNGYVFGTGTKVTVLG [SEQ ID NO: 243] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLDAFDIWGQGTMVTVSS** [SEQ ID NO: 244] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 62

ET200-112
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatgtatagtaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattattgtgcagcatgggatgacagcctgaatggttatgtcttcgcagctgggacccagctcaccgttttaagt [SEQ ID NO: 245] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagaggggctagatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 246] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLMYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFAAGTQLTVLS [SEQ ID NO: 247] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLDAFDIWGQGTMVTVSS** [SEQ ID NO: 248] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 63

ET200-113
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcactggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgagtgctgcttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 249] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacagctttaccagctatactatcagctgggttcgacaggcccctggacaaggccttgagtggatgggatgggtcagcacttacaatggtctcagaaactatgcacagaacctccagggcagagtcaccatgactacagacacactcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattattgtgtgagagaggggtccccgactacggtgacttcgcggcctttgactactggggccagggcaccctggtcaccgtctcctca** [SEQ ID NO: 250] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAAYVFGTGTKVTVLG [SEQ ID NO: 251] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYTISWVRQAPGQGLEWMGWVSTYNGLRNYAQNLQGRVTMTTDTLTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFAAFDYWGQGTLVTVSS** [SEQ ID NO: 252] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 64

ET200-114
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccaccctcagcgtctgagacccccgggcagagggtcaccatctcttgttctggaagcaggtccaacatcggaactaatattgtacactggtaccagcagcgcccaggaatggcccccaaactcctcacttatggtagtcggcggccctcaggggtcccggaccgattctctggctccaagtttggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattattgtgcagcatgggatgacagtctgaatggtccggctttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 253] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagacggtgggggctactttgactactggggccagggaaccctggtcaccgtctcctca** [SEQ ID NO: 254] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSASETPGQRVTISCSGSRSNIGTNIVHWYQQRPGMAPKLLTYGSRRPSGVPDRFSGSKFGTSASLAISGLQSEDEADYYCAAWDDSLNGPAFGGGTKLTVLG [SEQ ID NO: 255] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGYFDYWGQGTLVTVSS** [SEQ ID NO: 256] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 65

ET200-115
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaatatcggggcacgttatgatgtacactggtaccagcaactcccaggaacagcccccgactcctcatctctgctaactacgatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagtgtgagtgcttgggtgttcggcggagggaccaaggtcaccgtcctaggt [SEQ ID NO: 257] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaagtgcagctggtgcagtctggggctgaagtgaaggagcctggggcctcagtgaggatctcctgccaggcatctggatacaacttcatcagttattatatgcactgggtgcggcaggcccctgggcaaggtcttgagtggatgggcaccatcaacccaggcagtggtgagacagactactcacagaagttgcagggcagagtcaccatgaccagggacccgtccacgggtacattcgacatggggctgagcagcctgacatctggggacacggccgtctattattgtgcgacaggtctcatcagaggagctagcgatgcttttaatatctggggccgggggacaatggtcaccgtctcttca** [SEQ ID NO: 258] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSGAPGQRVTISCTGSSSNIGARYDVHWYQQLPGTAPRLLISANYDRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSVSAWVFGGGTKVTVLG [SEQ ID NO: 259] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKEPGASVRISCQASGYNFISYYMHWVRQAPGQGLEWMGTINPGSGETDYSQKLQGRVTMTRDPSTGTFDMGLSSLTSGDTAVYYCATGLIRGASDAFNIWGRGTMVTVSS** [SEQ ID NO: 260] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 66

ET200-116
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagcctgtgctgactcagccaccctcagtgtccgtgtccccaggacagacggccgccatcccctgttctggagataagttggggataaatttgcttcctggtatcagcagaagccaggccagtcccctgtgctggtcatctatcaagatactaagcggccctcagggatccctgagcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctatggatgaggctgactattactgtcagacgtgggccagcggcattgtggtgttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 261] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtacagctgcagcagtcaggtccaggactggtgaagccctcgcagaccctctcactcacctgtgccatctccggggacagtgtctctagcaacagtgctgcttggaactggatcaggcagtccccatcgagaggccttgagtggctgggaaggacatactacaggtccaagtggtataatgattatgcagtatctgtgaaaagtcgaataaccatcaacccagacacatccaagaaccagttctccctgcagctgaactctgtgactcccgaggacacggctgtgtattactgtgcaagagagcgcagtggctggaagggatttgactactggggccagggaaccctggtcaccgtctcctca** [SEQ ID NO: 262] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QPVLTQPPSVSVSPGQTAAIPCSGDKLGDKFASWYQQKPGQSPVLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQTWASGIVVFGGGTKLTVLG [SEQ ID NO: 263] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARERSGWKGFDYWGQGTLVTVSS** [SEQ ID NO: 264] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 67

ET200-117
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) gatgttgtgatgactcagtctccaccctccctgtccgtcacccctggagagccggcctccatcacctgcaggtctagtcagagcctcctggaaagaaatgcatacaactacttggattggtacctgcagaggccaggacagtctccacagctcctgatctacttgggttctaatcgggccgccggggtccctgacaggttcagtggcagtggatcaggcagagattttacactgaaaatcagcagagtggagcctgaggatgttggggtttattactgcatgcaagctctacaagctccgttcactttcggcggagggaccaaggtggagatcaaacgt [SEQ ID NO: 265] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaagtgcagctggtgcagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacacggccgtatattactgtgcgaaatggggcccgtttcaggatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 266] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) DVVMTQSPPSLSVTPGEPASITCRSSQSLLERNAYNYLDWYLQRPGQSPQLLIYLGSNRAAGVPDRFSGSGSGRDFTLKISRVEPEDVGVYYCMQALQAPFTFGGGTKVEIKR [SEQ ID NO: 267] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKWGPFQDAFDIWGQGTMVTVSS** [SEQ ID NO: 268] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 68

ET200-118
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacagcacccgggcaaagcccccaaactcatgatttatgaggtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacccccttatgtcttcggagcagggaccaaggtcaccgtcctaggt [SEQ ID NO: 269] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagccaggtggacagcagtggcatcagaccaccactttgactactggggccagggaacgctggtcaccgtctcctca** [SEQ ID NO: 270] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTPYVFGAGTKVTVLG [SEQ ID NO: 271] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKARWTAVASDHHFDYWGQGTLVTVSS** [SEQ ID NO: 272] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 69

ET200-119
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgcttactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaagctgaccgtcctaggt [SEQ ID NO: 273] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagattgggactacatggacgtctggggcaaagggaccacggtcaccgtctcctca** [SEQ ID NO: 274] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKLTVLG [SEQ ID NO: 275] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDWDYMDVWGKGTTVTVSS** [SEQ ID NO: 276] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 70

ET200-120
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgagctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 277] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtgcagctggtggagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagacctatctcggggagctaacccgcattactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 278] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYELTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLG [SEQ ID NO: 279] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLSRGANPHYYYYYGMDVWGQGTTVTVSS** [SEQ ID NO: 280] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 71

ET200-121
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccgtctcctgcactgggagcagatccaacatcggggcaggatatgatgtacactggtaccagcaacttccaggaacagcccccaaactcctcatctatggaaatagtaatcggcctccaggggtccctgaccgattctctgggtctaagtctggcacctcagcctccctggtcatcactgggctccaggctgaggatgccgctgattattactgccagtcctatgacaacactgtgcgtgaatcaccttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 281] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcaacagagagtaatttagtgtcccggcactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 282] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QSVLTQPPSVSGAPGQRVTVSCTGSRSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPPGVPDRFSGSKSGTSASLVITGLQAEDAADYYCQSYDNTVRESPYVFGTGTKVTVLG [SEQ ID NO: 283] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATESNLVSRHYYYYGMDVWGQGTTVTVSS** [SEQ ID NO: 284] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 72

ET200-122
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) ctgcctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaaccagctccaacatcggaagtaattctgtagactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgaatctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 285] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaagtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaaccctaacagtggtggcacaaactatgcacagaagtttcagggcagggtcaccatgaccagggacacgtccatcagcacagcctacatggagctgagcaggctgagatctgacgacacggccgtgtattactgtgcgagagattacggatactatggttcggggagttattcgagcggcccccttttactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 286] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) LPVLTQPPSASGTPGQRVTISCSGTSSNIGSNSVDWYQQLPGTAPKLLIYSNNQRPSGVPDRISGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLG [SEQ ID NO: 287] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDYGYYGSGSYSSGPLYYYYGMDVWGQGTTVTVSS** [SEQ ID NO: 288] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 73

ET200-123
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatgtataataatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctcaatggttatgtcttcggacctgggaccaaggtcaccgtcctaggt [SEQ ID NO: 289] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtggagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagacctatctcggggagctaacccgcattactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca** [SEQ ID NO: 290] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLMYNNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGPGTKVTVLG [SEQ ID NO: 291] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLSRGANPHYYYYYGMDVWGQGTTVTVSS** [SEQ ID NO: 292] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 74

ET200-125
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) aattttatgctgactcagccccacgctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagtattgccagcaactatgtgcagtggtaccagcagcgcccgggcagttcccccgcactgtgatttatgaggataatcaaagaccctctggggtccctggtcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgattccaccagtgtgcttttcggcggagggaccaagctgaccgtcctaggt [SEQ ID NO: 293] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **gaggtccagctggtgcagtctggggctgaggtgaagaagccagggtcctcggtgaaggtctcctgcaaggcctcgggaggcaccttcagcagcaattctctcagctgggtgcgacaggcccctggacaagggcttgagtggatgggaaggatcttccctatcctgggtataacaaactatgcacagaagttccagggcagagtcacgattaccgcggacaaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtctattactgtgcgagaggaaactaccaatggtatgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 294] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) NFMLTQPHAVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPRTVIYEDNQRPSGVPGRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTSVLFGGGTKLTVLG [SEQ ID NO: 295] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSNSLSWVRQAPGQGLEWMGRIFPILGITNYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGNYQWYDAFDIWGQGTMVTVSS** [SEQ ID NO: 296] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 75

ET200-005
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) cagcctgtgctgactcagccaccctcagtgtcagtggtcccaggaaagacggccaggattacctgtgggggaaaaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtggtggtcatccattatgatagtgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 297] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccaactatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacataagctccagggcagagtcaccatgaccacagacacatccacgagcacagccaacatggagctgaggagcctgagacctgacgacactgccgtgtattactgtgcgcgctcttacttcggttctcatgattactggggtcaaggtactctggtgaccgtctcctca** [SEQ ID NO: 298] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) QPVLTQPPSVSVVPGKTARITCGGKNIGSKSVHWYQQKPGQAPVVVIHYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLG [SEQ ID NO: 299] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQAPGQGLEWMGWISAYNGNTNYAHKLQGRVTMTTDTSTSTANMELRSLRPDDTAVYYCARSYFGSHDYWGQGTLVTVSS** [SEQ ID NO: 300] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

Table 76

ET200-124
DNA Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) tcctatgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggatttcctgtgggggaaacgacattggaagtaaaagtgttttctggtatcagcagaggccaggccaggcccctgtgttggtcgtctatgatgatagcgaccggccctcagggctccctgagcgattctctggcttcaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaagtgtgggatagtagtagtgatcattatgtcttcggaactgggaccaaggtcaccgtcctaggt [SEQ ID NO: 301] tctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcc [SEQ ID NO: 305] **caggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagatataacctatggttcggggagttatggtgcttttgatatctggggccaagggacaatggtcaccgtctcttca** [SEQ ID NO: 302] ACTAGTGGCCAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCT [SEQ ID NO: 306]
Amino Acid Sequence
(light chain variable region scFv linker **heavy chain variable region** His tag + HA tag) SYVLTQPPSVSVAPGKTARISCGGNDIGSKSVFWYQQRPGQAPVLVVYDDSDRPSGLPERFSGFNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLG [SEQ ID NO: 303] SRGGGGSGGGGSGGGGSLEMA [SEQ ID NO: 307] **QVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDITYGSGSYGAFDIWGQGTMVTVSS** [SEQ ID NO: 304] TSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 308]

XI. Exemplary extracellular antigen-binding domains (e.g., scFvs) comprising a heavy chain variable region, a light chain variable region and a linker peptide

Table 77

ET200-001
DNA Sequence
Cagtctgtgttgacgcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtgtatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcgaaggtccgtacgacggtttcgattcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 593]
Amino Acid Sequence
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGPYDGFDSWGQGTLVTVSS [SEQ ID NO: 594]

Table 78

ET200-002
DNA Sequence
Aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattctgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggcactgaggtgaagaagcctggggcctcagtgagggtcgcctgcaaggcttctggttacccctttaacaaatatgacatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggaggcatcatccctatctttcgtacaacaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggag

ctgagcagcctgagatctgaggacacggccgtatattactgtgcgcgcgaatggttctactgggatatctggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 595]
<u>Amino Acid Sequence</u>
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNSVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGTEVKKPGASVRVACKASGYPFNKYDINWVRQAPGQGLEWMGGIIPIFRTTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREWFYWDIWGQGTLVTVSS [SEQ ID NO: 596]

Table 79

ET200-003
<u>DNA Sequence</u>
Cagtctgtgttgactcagccaccctcagtgtccgtgtccccaggacagacagccagcatctcctgctctggaaataaattggggactaagtatgtttactggtatcagaagaggccaggccagtcccctgtgttggtcatgtatgaagataatcagcggccctcagggatcccggagcggttctctggctccaactctgggaacacagccactctgaccatcagagggacccagactgtggatgaggctgactattactgtcaggcgtgggactccgacactttcgtggtcttcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagaccgggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatggcatgcactgggtccgccaggctccaggcaaggggctggagtgggtggcagttatatcacatgatggaagtaataaatactacgcagactccgtgaagggccgattcaccatctccagagacaattccaaggacacgctgtatctgcaaatgaacagcctgagaggtgaggacacggccgtatattactgtgcgcgctctaaccagtggtctggttacttctctttcgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 597]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSVSPGQTASISCSGNKLGTKYVYWYQKRPGQSPVLVMYEDNQRPSGIPERFSGSNSGNTATLTIRGTQTVDEADYYCQAWDSDTFVVFGGGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISHDGSNKYYADSVKGRFTISRDNSKDTLYLQMNSLRGEDTAVYYCARSNQWSGYFSFDYWGQGTLVTVSS [SEQ ID NO: 598]

Table 80

ET200-006
<u>DNA Sequence</u>
Tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacat

tggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtggtggtcatccattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccacctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaacacttacaatggtcacacaaactatgcacagaagctccagggcagagccacaatgaccgcagacacatccacgaacacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgcgttatctacggttctggtgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 599]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVVVIHYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINTYNGHTNYAQKLQGRATMTADTSTNTAYMELRSLRSDDTAVYYCARVIYGSGDYWGQGTLVTVSS [SEQ ID NO: 600]

Table 81

ET200-007
DNA Sequence
Tcctatgtgctgactcagccactctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaactgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatcgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctgcaggagtcgggcccaggactggtgaagccttcggagaccctgtccctcacctgcaatgtctctggttactccatcagcagtggttacttttggggctggatccggcagcccccagggaaggggctggagtggattgggagtatctatcatagtaggagcacctactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgaactctgtgaccgccgcagacacggccgtgtattactgtgcgcgcggttacggttacttcgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 601]
Amino Acid Sequence
SYVLTQPLSVSVAPGKTARITCGGNNIGSKTVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHRVFGGGTKL

TVLGSRGGGGSGGGGSGGGGSLEMAQVQLQESGPGLVKPSETLSLTCNVSGYSISSGYFWGWIRQPPGKGLEWIGSIYHSRSTYYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAVYYCARGYGYFDYWGQGTLVTVSS [SEQ ID NO: 602]

Table 82

ET200-008
DNA Sequence
Caatctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacaacacccaggcaaagcccccaaactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacttcgaaggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggtgtggtacggcctggggggtccctgagactctcctgtgcagcctctggattcacctttggtgattatggcatgagctgggtccgccaagctccagggaaggggctggagtgggtctctggtattaattggaatggtggtagcacaggttatgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagccgaggacacggccgtatattactgtgcgcgctctaaatacaacttccatgtttactacgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 603]
Amino Acid Sequence
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTSKVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGVVRPGGSLRLSCAASGFTFGDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSKYNFHVYYDYWGQGTLVTVSS [SEQ ID NO: 604]

Table 83

ET200-009
DNA Sequence
Cagtctgtgttgacgcagccaccctcagcgtctgggacccccgggcagacagtcaccatctcttgttctggaagcaactccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcctcatctataggaataatcagcggccctcaggggtccctgaccgattctcaggctccaagtctggcacctcagcctccctggccatcagtgggctccgctccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtgcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttacca

gctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgctcttctggtaacatggtttcttggaaagatatgtggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 605]
<u>Amino Acid Sequence</u>
QSVLTQPPSASGTPGQTVTISCSGSNSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSSGNMVSWKDMWGQGTLVTVSS [SEQ ID NO: 606]

Table 84

ET200-010
<u>DNA Sequence</u>
Caatctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactctgtctcctggtaccaacaacacccaggcaaagcccccagactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacccctttagtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcggtgctgttgcttaccatgattggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 607]
<u>Amino Acid Sequence</u>
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPRLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTPLVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGAVAYHDWGQGTLVTVSS [SEQ ID NO: 608]

Table 85

ET200-011
DNA Sequence
Cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagagggtcaccatctcctgctctggaagcagctccaacatttcgatttatgatgtatcctggtatcagcagctcccaggaacagcccccaaactcctcatttatggcaataataagcgaccctcggggattgctgaccgattctctggctccacgtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatgacagtctgagtgggggggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcaatctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcgaggcttctggaggcaccctcagcagctatgctatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatgtttggtacagcacactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgaaaacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtgttcattacgcttctttcgatcattggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 609]
Amino Acid Sequence
QSVVTQPPSVSAAPGQRVTISCSGSSSNISIYDVSWYQQLPGTAPKLLIYGNNKRPSGIADRFSGSTSGTSATLGITGLQTGDEADYYCGTWDDSLSGGVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGSSVKVSCEASGGTLSSYAINWVRQAPGQGLEWMGGIIPMFGTAHYAQKFQGRVTITADESTKTAYMELSSLRSEDTAVYYCARGVHYASFDHWGQGTLVTVSS [SEQ ID NO: 610]

Table 86

ET200-012
DNA Sequence
Cagtctgtgttgacgcagccgccctcagtgtctgcggccgcaggacagaaggtcaccatctcctgctctggaagcgactccaacattgggaataattatgtgtcctggtatcaacacctcccagggacagcccccaaactcctcatttatgacgttaaaaatcgaccctcagggattcctgaccggttctccggctccaagtctggctcgtcagccaccctaggcatcgccggactccagcctggggacgaggccgattattactgcggaacatgggacagtcggctggatgcctatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcaatctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagacttctggtttcccctttaatatctttggaatcacctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcggttacaacggtaacacagactacccacagaagttccagggcagagtcaccatgtccacagacacatccacgagtacagcctacatggagctgaggaacctgaaatctgacgacacggccgtgtattactgtgcgcgcggtgcttacggtggtatggatacttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 611]

Amino Acid Sequence
QSVLTQPPSVSAAAGQKVTISCSGSDSNIGNNYVSWYQHLPGTAPKLLIYDVKNRPSGIPDRFSGSKSGSSATLGIAGLQPGDEADYYCGTWDSRLDAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGASVKVSCKTSGFPFNIFGITWVRQAPGQGLEWMGWISGYNGNTDYPQKFQGRVTMSTDTSTSTAYMELRNLKSDDTAVYYCARGAYGGMDTWGQGTLVTVSS [SEQ ID NO: 612]

Table 87

ET200-013
DNA Sequence
Cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcacctccaacatcggggcaggttatgatgtacactggtatcagcagcttccaggaacagcccccaaactcctcatctatactaacaactttcggccctcaggggtccctgaccgattctctgcctccaagtctggcacttcagcttccctggccatcactggtctccaggctgaggatgaggctgattattactgcggaacatgggatagcagcctgagtgccgttgtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctggaactgaggtgaagaagcctggggcctcagtgaaagtctcctgcaaggcttctggttacatgtttaccagttatggtctcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgctaacaatggtaagacaaattatgctaagaaattccaggacagagtcaccatgaccagagacacttccacgagcacaggctacatggaactgaggagcctgagatctgacgacacggccgtatattactgtgcgcgccatatcggtggttcttacttcgatcgttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 613]
Amino Acid Sequence
QSVVTQPPSVSGAPGQRVTISCTGSTSNIGAGYDVHWYQQLPGTAPKLLIYTNNFRPSGVPDRFSASKSGTSASLAITGLQAEDEADYYCGTWDSSLSAVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGTEVKKPGASVKVSCKASGYMFTSYGLNWVRQAPGQGLEWMGWISANNGKTNYAKKFQDRVTMTRDTSTSTGYMELRSLRSDDTAVYYCARHIGGSYFDRWGQGTLVTVSS [SEQ ID NO: 614]

Table 88

ET200-014
DNA Sequence
Tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggc

cctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagactgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtgatggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagacgaggacacggccgtatattactgtgcgcgctctcatgaagctaacctggttggtgattggtggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 615]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSDGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRDEDTAVYYCARSHEANLVGDWWGQGTLVTVSS [SEQ ID NO: 616]

Table 89

ET200-015
DNA Sequence
Cagtctgtggtgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggcccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctacggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgctggggtggtttcggtgctgttgatcattggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 617]
Amino Acid Sequence
QSVVTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASG

YTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARWGGFGAVDHWGQGTLVTVSS [SEQ ID NO: 618]

Table 90

ET200-016
DNA Sequence
Tcttctgagctgactcaggaccctgctgtgtctgtggccttgggacagacagtcaagatcacgtgccaaggagacagcctcacagactaccatgcaacctggtaccagcagaagccaggacaggcccctgtcgctgtcatctatgctacaaacaaccggcccactgggatcccagaccgattctctggttccagttccggaaacacagcttctttgaccatcactggggctcaggcggaagatgaggctgactattactgtaattcccgggacagcggcacggacgaagtgttattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagactgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtagtagttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgcgcggtcagggttacgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 619]
Amino Acid Sequence
SSELTQDPAVSVALGQTVKITCQGDSLTDYHATWYQQKPGQAPVAVIYATNNRPTGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGTDEVLFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGQGYDYWGQGTLVTVSS [SEQ ID NO: 620]

Table 91

ET200-017
DNA Sequence
Tcctatgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcgtctatgatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgagcatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatactgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcac

caactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgctactacccgggtatggatatgtggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 621]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLSISRVEAGDEADYYCQVWDSSSDHTVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYPGMDMWGQGTLVTVSS [SEQ ID NO: 622]

Table 92

ET200-018
DNA Sequence
Caggctgtgctgactcagccgccctcaacgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcgggagaaatggtgtaaactggtaccagcagctcccaggagcggcccccaaagtcctcatctataatgataatcagcgaccctcaggggtccctgaccgagtctctggctcccagtctggctcctcaggcaccctggccatcgatgggcttcggtctgaggatgaggctgattattactgtgcggcatgggatgacagcctgcatggtgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcaatgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtggttacggtgattcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 623]
Amino Acid Sequence
QAVLTQPPSTSGTPGQRVTISCSGSSSNIGRNGVNWYQQLPGAAPKVLIYNDNQRPSGVPDRVSGSQSGSSGTLAIDGLRSEDEADYYCAAWDDSLHGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKVSGYTLNELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARGGYGDSWGQGTLVTVSS [SEQ ID NO: 624]

Table 93

ET200-019
DNA Sequence

Aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattcttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcaatctggggctgaggtgaagaggcctgggtcctcggtgaaggtctcctgcacggcttctggaggcaccttcagcagcgatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggaggaatcatccctatgtttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcgaaggttactactacccgtctgcttacctgggttctgttctgaacgacatctcttctgtttacgatgaatggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 625]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNSWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKRPGSSVKVSCTASGGTFSSDAISWVRQAPGQGLEWMGGIIPMFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREGYYYPSAYLGSVLNDISSVYDEWGQGTLVTVSS [SEQ ID NO: 626]

Table 94

ET200-020
DNA Sequence
Cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcacctccaacattggaaataatgatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcgtgagtgcttcttgggtcttcggcagagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatccacagaagctccagggcagagtcaccatgaccacagacccatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgctctatgacttctttcgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 627]
Amino Acid Sequence

QSVVTQPPSVSAAPGQKVTISCSGSTSNIGNNDVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSVSASWVFGRGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYPQKLQGRVTMTTDPSTSTAYMELRSLRSDDTAVYYCARSMTSFDYWGQGTLVTVSS [SEQ ID NO: 628]

Table 95

ET200-021
DNA Sequence
Cagtctgtgttgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcaactccaacattgggaataattatgtatcctggtatcagcaactcccagggacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaggtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatggaataccactgtgactcctggctatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacaccgccatgtattactgtgcgcgctctgtttacgacctggatacttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 629]
Amino Acid Sequence
QSVLTQPPSVSAAPGQKVTISCSGSNSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSRSGTSATLGITGLQTGDEADYYCGTWNTTVTPGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAMYYCARSVYDLDTWGQGTLVTVSS [SEQ ID NO: 630]

Table 96

ET200-022
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactg

gggacgaggccgattattactgcggaacatgggatagcagcctgggggccccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtcttggggaggctcggaacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagcggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaattccctgtatctgcaaatgaacagtctgagagctgaggacaccgccatgtattactgtgcgcgctaccgtcaggttggttctgcttacgattcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 631]
<u>Amino Acid Sequence</u>
QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLGAPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSWGGSEQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAMYYCARYRQVGSAYDSWGQGTLVTVSS [SEQ ID NO: 632]

Table 97

ET200-023
<u>DNA Sequence</u>
ctgcctgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtatcagcagaagccaggccaggcccctgtgctggtcgtctatgctgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagttatcataattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgaggacaccgccatgtattactgtgcgcgctactggggtttcggtgtttctgatcgttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 633]
<u>Amino Acid Sequence</u>
LPVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYADSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSYHNYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTS

TSTAYMELSSLRSEDTAMYYCARYWGFGVSDRWGQGTLVTVSS [SEQ ID NO: 634]

Table 98

ET200-024
<u>DNA Sequence</u>
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccccgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgacagcagcaatctttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctacaactactactactacgattcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 635]
<u>Amino Acid Sequence</u>
NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNLWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARYNYYYYDSWGQGTLVTVSS [SEQ ID NO: 636]

Table 99

ET200-025
<u>DNA Sequence</u>
gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacagagtcaccatcacttgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatcaaggttcagtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagattttgcaacttactactgtcaacagagttacagtaccccattcactttcggccctgggaccaaagtggatatcaaacgttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcac

agaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacaccgccatgtattactgtgcgcgctactggggttacgactcttacgatgaatggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 637]
Amino Acid Sequence
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTKVDIKRSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAMYYCARYWGYDSYDEWGQGTLVTVSS [SEQ ID NO: 638]

Table 100

ET200-026
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcaacaaccattactacaacgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 639]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARNNHYYNDYWGQGTLVTVSS [SEQ ID NO: 640]

Table 101

ET200-027
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagggggtcaccatcccctgcactgggagcagct

ccaacatcggggcaggttatgatgtacactggtaccagcagcttccagggacagcccccaaactcctcatctatggtaacaacaatcggccctcaggggtccctgaccgcttctctggctccaggtctggctcctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtgatgtggtattcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctggggctacagtgaaaatctcctgcaaggtttctggatacaccttcaccgactactacatgcactgggtgcaacaggcccctggaaaagggcttgagtggatgggacttgttgatcctgaagatggtgaaacaatatacgcagagaagttccagggcagagtcaccataaccgcggacacgtctacagacacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgctactggtcttactctttcgactacctgtacatgccggaaggtaacgattggtggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 641]
Amino Acid Sequence
QSVLTQPPSVSGAPGQGVTIPCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGSSASLAITGLQAEDEADYYCQSYDSSLSDVVFGGGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGLVDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCARYWSYSFDYLYMPEGNDWWGQGTLVTVSS [SEQ ID NO: 642]

Table 102

ET200-028
DNA Sequence
cagtctgtgttgactcagccacccgcagcgtctgggacccccggacagagagtcaccatctcttgttctgggggcgtctccaacatcgggagtggtgctctaaattggtaccagcaactcccaggaacggcccccaaactcctcatctatagttacaatcagcggccctcaggggtctctgaccgattctctggctccaggtctgccacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcaacctgggatgatagtgtgaatggttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggagctgaggtgaagaagcctggggattcagtgaaggtctcctgcaagccttctggttacaattttctcaactatggtatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggattagcacttacaccggtaacacaaactatgcacagaagctgcagggcagagtcaccttcaccacagacacatccacgagcacagcctacatggagatgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcgacctgtactactacgaaggtgttgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 643]
Amino Acid Sequence
QSVLTQPPAASGTPGQRVTISCSGGVSNIGSGALNWYQQLPGTAPKLLIYSYNQRPSGVSDRFSGSRSATSASLAISGLQSEDEADYYCATWDDSVNGWVFGGGT

KLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGDSVKVSCKPSGYNFLNYGINWVRQAPGQGLEWMGWISTYTGNTNYAQKLQGRVTFTTDTSTSTAYMEMRSLRSDDTAVYYCARDLYYYEGVDYWGQGTLVTVSS [SEQ ID NO: 644]

Table 103

ET200-029
DNA Sequence
caggctgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccagggttacctgtgggggaaacaacattggaagtgaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgttggtcatctattatgataccgaccggccctcagggatccctgagcgattctctggctcccactctgggaccacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagggatcatgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctgggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcggcctctggattcaccttcagtagctatgctatgcactgggtccgccaggctccaggcaagggactggagtgggtggcagttatatcatatgatggaagcaataaatactacgcagactccgtgaagggcctattcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagctgaggacacggccgtgtattactgtgcgcgctcttacttcacttctggtttctacgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 645]
Amino Acid Sequence
QAVLTQPPSVSVAPGKTARVTCGGNNIGSESVHWYQQKPGQAPVLVIYYDTDRPSGIPERFSGSHSGTTATLTISRVEAGDEADYYCQVWDSSRDHVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGLFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSYFTSGFYDYWGQGTLVTVSS [SEQ ID NO: 646]

Table 104

ET200-030
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagttccaacatcggggcaggttatgatgtaaattggtatcagcagtttccaggaacagcccccaaactcctcatctatggtaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggctcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaga

tgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcatgtcttctatgtactacgattggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 647]
<u>Amino Acid Sequence</u>
QSVVTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGSYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGASVKVSCKASGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARMSSMYYDWGQGTLVTVSS [SEQ ID NO: 648]

Table 105

ET200-031
<u>DNA Sequence</u>
tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagactgggggaggcttggtcaagcctggagggtccctgagactctcctgtgcagcctctggattcaccgtcagtgactactacatgagctggatccgccaggctccagggaagggcctggagtggatttcatacattagtggtagtggtaatagcatatactacgcagactctgtgaagggccgattcaccatctccagggacaacgccaagaactcactggatctgcaaatgaccagcctgagagccgaggacacggccgtatattactgtgcgcgctctactaaattcgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 649]
<u>Amino Acid Sequence</u>
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVKPGGSLRLSCAASGFTVSDYYMSWIRQAPGKGLEWISYISGSGNSIYYADSVKGRFTISRDNAKNSLDLQMTSLRAEDTAVYYCARSTKFDYWGQGTLVTVSS [SEQ ID NO: 650]

Table 106

ET200-032
DNA Sequence
ctgcctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacgtcggaagttacactgtaaactggtaccggcaactcccaggaacggcccccacactcctcatctataataataatcagcggccctcaggggtccctgaccgattctctgactccaagtctggcacctcggcctccctgaccattagtgggctccagcctgaggatgaggctgattattattgtgcagcatgggatgacaggctgggtggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggagcagaggtgaaaaagccgggggagtctctgaagatctcctgtaagggttctggatacagctttaccaactactggatcggctgggtgcgccagatgcccgggaaaggcctggagtggatggggatcatctatcctggtgactctgataccagatacagcccgtccttccaaggccaggtcaccatctcagccgacaagtccatcagcaccgcctacctacagtggagcagcctgaaggcctcggacaccgccatgtattactgtgcgcgctctactggttcttctcatatgtctgatgaatggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 651]
Amino Acid Sequence
LPVLTQPPSASGTPGQRVTISCSGSSSNVGSYTVNWYRQLPGTAPTLLIYNNNQRPSGVPDRFSDSKSGTSASLTISGLQPEDEADYYCAAWDDRLGGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARSTGSSHMSDEWGQGTLVTVSS [SEQ ID NO: 652]

Table 107

ET200-033
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaatcattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaagtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggagatcactcatagtggaaggtccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgctcttctatcatgtctgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 653]

<u>Amino Acid Sequence</u>
NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNHWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEITHSGRSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSSIMSDYWGQGTLVTVSS [SEQ ID NO: 654]

Table 108

ET200-034
<u>DNA Sequence</u>
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcacctccaacatcggggcaggttatgatgtacactggtaccagcagcttccaggaacagcccccaaactcctcatcaacaataacaggaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatggcagcctgactggtgcagtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcatgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcggttctgctctggaccattacgatcgttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 655]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSGAPGQRVTISCTGSTSNIGAGYDVHWYQQLPGTAPKLLINNNRNRPSGVPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDGSLTGAVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGSALDHYDRWGQGTLVTVSS [SEQ ID NO: 656]

Table 109

ET200-035
<u>DNA Sequence</u>
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaa

gactgaggacgaggctgactactactgtcagtcttatgatagcaccaattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctacaactactacttcaacgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 657]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTNWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARYNYYFNDYWGQGTLVTVSS [SEQ ID NO: 658]

Table 110

ET200-037
DNA Sequence
tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgctctatgttcggtgctcatgattcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 659]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSMFGAHDSWGQGTLVTVSS [SEQ ID

NO: 660]

Table 111

ET200-038
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaacatcggggcaggttttgatgtacactggtaccagctacttccaggaacagcccccaaactcctcatctatgctaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctcctggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggtgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcaatctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtgcttctttcgaccgtcatgataactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 661]
Amino Acid Sequence
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGFDVHWYQLLPGTAPKLLIYANSNRPSGVPDRFSGSKSGTSASLAITGLLAEDEADYYCQSYDSSLSGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGASFDRHDNWGQGTLVTVSS [SEQ ID NO: 662]

Table 112

ET200-039
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagttcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgag

cagcctgagatctgaggacacggccgtgtattactgtgcgcgctctaactactactacaacgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 663]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSNYYYNDYWGQGTLVTVSS [SEQ ID NO: 664]

Table 113

ET200-040
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaacatcggggcaggttatgatgtacactggtaccagcagcttccaggaacagcccccaaactcctcatctatggtaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctactctggtgtttactacgattggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 665]
Amino Acid Sequence
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARYSGVYYDWGQGTLVTVSS [SEQ ID NO: 666]

Table 114

ET200-041
DNA Sequence
aattttatgctgactcagccccactctgtgtcggggtctccggggaagacggtaaccatctcctgcaccggcagcagtggc

agcattgccgacaactttgtgcagtggtaccagcagcgcccgggcggtgtccccaccactgtgatctttaatgatgacgaaagaccctctggcgtccctgatcggttctctggctccatcgacacctcctccaattctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgataataataatcgaggggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatgaaccctaacagtggtaacacaggctatgcacagaagttccagggcagagtcaccatgaccaggaacacctccataagcacagcctacatggagctgagcaacctgagatctgaggacacggccgtgtattactgtgcgcgctactactcttacggttacgattggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 667]
Amino Acid Sequence
NFMLTQPHSVSGSPGKTVTISCTGSSGSIADNFVQWYQQRPGGVPTTVIFNDDERPSGVPDRFSGSIDTSSNSASLTISGLKTEDEADYYCQSYDNNNRGVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSNLRSEDTAVYYCARYYSYGYDWGQGTLVTVSS [SEQ ID NO: 668]

Table 115

ET200-042
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagacggtcaccatctcctgcactgggggcagctccaacatcgggacaggttattttgtaaattggtaccagcaggttccaggaaaagcccccaaactcctcatcctgggtaacaataatcggccctcgggggtccctgaccgactctccggctccacgtccggcacctcagcctccctggccatcactgggctccaggctgaggatgagggtacttattactgccagtcctatgacagcagcctgagtggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtacagctgcagcagtcaggtccaggactggtgaagccctcgcagaccctctcactcacctgtggcatctccggggacagtgtctctaccaacagtgttgcttggcactggatcaggcagtccccatcgagaggccttgagtggctgggaaggacatactacaggtccaagtggtctaatgactatggagtatctgtgaaaagtcgaatcaccatcatcccagacacatccaagaaccagttctccctgcagctgaactctgtgactcccgaggacacggctgtgtattactgtgcgcgctcttcttcttggtaccagatcttcgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 669]
Amino Acid Sequence
QSVVTQPPSVSGAPGQTVTISCTGGSSNIGTGYFVNWYQQVPGKAPKLLILGNNNRPSGVPDRLSGSTSGTSASLAITGLQAEDEGTYYCQSYDSSLSGYVFGTGT

KVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQSGPGLVKPSQTLSLTCGISGDSVSTNSVAWHWIRQSPSRGLEWLGRTYYRSKWSNDYGVSVKSRITIIPDTSKNQFSLQLNSVTPEDTAVYYCARSSSWYQIFDYWGQGTLVTVSS [SEQ ID NO: 670]

Table 116

ET200-043
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagcgacagcatagccaacaactatgttcagtggtaccagcagcgcccgggcagtgcccccaccaatgtgatctacgaagatgtccaaagaccctctggggtccctgatcggttctctgggtccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgtctactattgtcagtcttatcatagcgacaatcgttgggtgttcggcggcgggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacacggccgtatattactgtgcgcgctctggtgcttactgggactactctgtttacgatgaatggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 671]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTGSSDSIANNYVQWYQQRPGSAPTNVIYEDVQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEAVYYCQSYHSDNRWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSGAYWDYSVYDEWGQGTLVTVSS [SEQ ID NO: 672]

Table 117

ET200-044
DNA Sequence
cagtctgtgttgactcagccaccctcagtgtccgtgtccccaggacagacagccaccatcgcctgttctggacataaattggggataaatatgcttcctggtatcagcagaagtcgggccagtcccctgtgttgatcatctatcaggataataagcggccctcagggattcctgagcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctctggatgaggctgactattattgtcaggcgtgggacagtagtacttatgtggcattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctgcaggagt

ccggcccaggactggtgaagccttcggagaccctgtccctcacctgcgttgtctctggtggctccatcagcagtagtaactggtggagctgggtccgccagcccccagggaaggggctggagtggattggggaaatctatcatagtgggagccccaactacaacccatccctcaagagtcgagtcaccatatcagtagacaagtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcatgactactcatactttcggttacgatgcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 673]
Amino Acid Sequence
QSVLTQPPSVSVSPGQTATIACSGHKLGDKYASWYQQKSGQSPVLIIYQDNKRPSGIPERFSGSNSGNTATLTISGTQALDEADYYCQAWDSSTYVAFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQESGPGLVKPSETLSLTCVVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSPNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARMTTHTFGYDAWGQGTLVTVSS [SEQ ID NO: 674]

Table 118

ET200-045
DNA Sequence
cagcctgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccacgattacttgtgggggaaacaacattggaagtgaaagtgtgcactggtaccaccagaagccaggccaggcccctgtgttggtcatctatgatgatgccggccggccctcagggatccctgagcgattcactggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggacagaaatagtgctcagtttgtcttcggacctgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcggtgttcatctggattggtggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 675]
Amino Acid Sequence
QPVLTQPPSVSVAPGKTATITCGGNNIGSESVHWYHQKPGQAPVLVIYDDAGRPSGIPERFTGSNSGNTATLTISRVEAGDEADYYCQVWDRNSAQFVFGPGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGVHLDWWGQGTLVTVSS [SEQ ID NO: 676]

Table 119

ET200-069

DNA Sequence
cagtctgtcgtgacgcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtggttatgtcttcggaactgggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcctgtacgaaggtggttaccatggttggggttcttggctgtcttctgattcttggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 677]
Amino Acid Sequence
QSVVTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYVFGTGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLYEGGYHGWGSWLSSDSWGQGTLVTVSS [SEQ ID NO: 678]

Table 120

ET200-078
DNA Sequence
cagtctgtgttgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgcgcgaaggggcatttgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 679]
Amino Acid Sequence

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGAFDAFDIWGQGTMVTVSS [SEQ ID NO: 680]

Table 121

ET200-079
DNA Sequence
tcctatgagctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcttcatctataggaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtggttatctcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaatggcgactccaactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 681]
Amino Acid Sequence
SYELTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLFIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYLFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCANGDSNYYYGMDVWGQGTTVTVSS [SEQ ID NO: 682]

Table 122

ET200-081
DNA Sequence
cagtctgccctgactcagcctgcctccgtgtccgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacattggtggttataactatgtctcctggtaccaacaacacccaggcaaagcccccaaactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcatctcatatacacgcacctggaacccctatgtcttcgggagtgggaccaaggtcaccgtc

ctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctgggggaggcgtggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccgtcaagctccagggaagggtctggagtgggtctctcttattagtggggatggtggtagcacatactatgcagactctgtgaagggccgattcaccatctccagagacaacagcaaaaactccctgtatctgcaaatgaacagtctgagaactgaggacaccgccttgtattactgtgcaaaagatcgggcagcagctggctactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 683]
Amino Acid Sequence
QSALTQPASVSGSPGQSITISCTGTSSDIGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCISYTRTWNPYVFGSGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGGGVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLISGDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRTEDTALYYCAKDRAAAGYYYYGMDVWGQGTTVTVSS [SEQ ID NO: 684]

Table 123

ET200-097
DNA Sequence
ctgcctgtgctgactcagccaccctcagtgtccgtgtccccaggacagacagccatcatcacctgctctggagataaattggggaaaaatatgtttcctggtatcagcagaagccaggccagtcccctgtactggtcatcgatcaagataccaggaggccctcagggatccctgagcgattctctggctccaactctgggaccacagccactctgaccatcagcgggacccaggctatggatgaggctgactattactgtcaggcgtgggacaggggtgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggagacttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttaatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggagtggtaataacataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagatagtatacggtatggcatcacctggggaggttttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 685]
Amino Acid Sequence
LPVLTQPPSVSVSPGQTAIITCSGDKLGEKYVSWYQQKPGQSPVLVIDQDTRRPSGIPERFSGSNSGTTATLTISGTQAMDEADYYCQAWDRGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGDLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWSGNNIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDSIRYGITWGGFDYWGQGTLVTVSS [SEQ ID

NO: 686]

Table 124

ET200-098
DNA Sequence
cagcctgtgctgactcagccaccctcggtgtccaagggcttgagacagaccgccacactcacctgcactgggaacagcaacaatgttggcaacctaggagtagcttggctgcagcagcaccagggccaccctcccaaactcctatcctacaggaataacaaccggccctcagggatctcagagagattatctgcatccaggtcaggaaacacagcctccctgaccattactggactccagcctgaggacgaggctgactattactgctcagcatgggacagtagcctcagtgcttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggagtcgtggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccgtcaagctccggggaagggtctggagtgggtctctcttattaattgggatggtggtagcacctactatgcagactctgtgaagggtcgattcaccatctccagagacaacagcaaaaactccctgtatctgcaaatgaacagtctgagagctgaggacaccgccttgtattactgtgcaaaagggatgggcctgagggcgtttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 687]
Amino Acid Sequence
QPVLTQPPSVSKGLRQTATLTCTGNSNNVGNLGVAWLQQHQGHPPKLLSYRNNNRPSGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLSAWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGVVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLINWDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGMGLRAFDYWGQGTLVTVSS [SEQ ID NO: 688]

Table 125

ET200-099
DNA Sequence
cagtctgtgttgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtccggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcttcatgggatgacagcctgaatggccgttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggggctgaggtgaggaagcctggggcctcagtgaaggtttcctgcaagacttctggatacaccttcagttggtatgctatacattgggtgcgccaggcccccggacaaaggcttgagtggatgggatggatcaacgctggcaatggaaacacaaaatattcacagaaatttcagggcagagtcagtcttaccagggacacatccgcgagcacagcctacatggagctg

agcagcctgagatctgatgacacggctgtgtattactgtgcgagacccgataattatggttcgggtggggatgtttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 689]
Amino Acid Sequence
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCASWDDSLNGRYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVRKPGASVKVSCKTSGYTFSWYAIHWVRQAPGQRLEWMGWINAGNGNTKYSQKFQGRVSLTRDTSASTAYMELSSLRSDDTAVYYCARPDNYGSGGDVFDIWGQGTMVTVSS [SEQ ID NO: 690]

Table 126

ET200-100
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactttgtgcagtggtaccagcagcgcccgggcagtgcccccacccctatgatctatgaggataacaacagaccccctggggtccctgatcggttctctgcctccgtcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgataccagcaatgtggtattcggcgggggggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggagggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatgaaatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtggtagtaccatatactacgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggctgtttattactgtgcacgctgggactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 691]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNFVQWYQQRPGSAPTPMIYEDNNRPPGVPDRFSASVDSSSNSASLTISGLKTEDEADYYCQSYDTSNVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARWDYGMDVWGQGTTVTVSS [SEQ ID NO: 692]

Table 127

ET200-101
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggcccccgggcagagggtcaccgtctcttgttctggaagcaactc

caacatcggaagtaactacgttaactggtaccagcagttcccaggaacggcccccaaactcctcatgtatagtagtagtcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccactctgaggatgaggctgattattactgtgctacatgggatgacagcctgaatgcttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaggaagcctggggcctcagtgaaggtttcctgcaagacttctggatacaccttcacttggtatgctatacattgggtgcgccaggcccccggacaaaggcttgagtggatgggatggatcaacgctggcagtggaaacacaaaatattcacagaaatttcagggcagagtcacccttaccagggacacatccgcgagcacagcgtacatggagctgagcagcctgagatctgatgacacggctgtgtattactgtgcgagacccaataactatggttcgggtggggatgtttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 693]
Amino Acid Sequence
QAVLTQPPSASGAPGQRVTVSCSGSNSNIGSNYVNWYQQFPGTAPKLLMYSSSQRPSGVPDRFSGSKSGTSASLAISGLHSEDEADYYCATWDDSLNAWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVRKPGASVKVSCKTSGYTFTWYAIHWVRQAPGQRLEWMGWINAGSGNTKYSQKFQGRVTLTRDTSASTAYMELSSLRSDDTAVYYCARPNNYGSGGDVFDIWGQGTMVTVSS [SEQ ID NO: 694]

Table 128

ET200-102
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactgggacgaggccgattattactgcggaacatgggatagcagcctgagtgcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaagtttcctgcaaggcttctggatacaccttcacgaactatgctctgcattgggtgcgccaggcccccggacaagggcttgagtggatggcatggatcaacggtggcaatggtaacacaaaatattcacagaacttccagggcagagtcaccattaccagggacacatccgcgagcacagcctatatggagctgagcagcctgagatctgaagacacggctgtgtattactgtgcgaaaccggaggaaacagctggaacaatccactttgactactggggccagggaaccccggtcaccgtctcctca [SEQ ID NO: 695]
Amino Acid Sequence
QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAYVFGTGTK

VTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTNYALHWVRQAPGQGLEWMAWINGGNGNTKYSQNFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAKPEETAGTIHFDYWGQGTPVTVSS [SEQ ID NO: 696]

Table 129

ET200-103
DNA Sequence
caggctgtgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcaccatcacggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgggggagggttactatgatagtagtggttattccaacggtgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 697]
Amino Acid Sequence
QAVLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTITVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAGEGYYDSSGYSNGDAFDIWGQGTMVTVSS [SEQ ID NO: 698]

Table 130

ET200-104
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaatgtggtattcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcag

ctggtggagtctgggggaggcttggtacagcctggagggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatgaaatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtggtagtaccatatactacgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggctgtttattactgtgcacgctgggactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 699]
<u>Amino Acid Sequence</u>
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNVVFGGGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARWDYGMDVWGQGTTVTVSS [SEQ ID NO: 700]

Table 131

ET200-105
<u>DNA Sequence</u>
tcctatgtgctgactcagccaccctcagtgtccgtgtccccaggacagacagccagcatcacctgctctggagatagattgacgaataaatatgtttcctggtatcaacagaagccaggccagtcccctgtgttggtcatctatgaggatgccaagcggccctcagggatccctgcgcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctatggatgagtctgaatattactgtcaggcgtgggacagcagtgtggtggtttttggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggatttacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagtataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagatgaggacacggccttgtattactgtgcaaaagaccgaggggggggagttatcgttaaggatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 701]
<u>Amino Acid Sequence</u>
SYVLTQPPSVSVSPGQTASITCSGDRLTNKYVSWYQQKPGQSPVLVIYEDAKRPSGIPARFSGSNSGNTATLTISGTQAMDESEYYCQAWDSSVVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTALYYCAKDRGGGVIVKDAFDIWGQGTMVTVSS [SEQ ID NO: 702]

Table 132

ET200-106
DNA Sequence
tcctatgagctgactcagccacccgcagcgtctgggacccccggacagagagtcaccatctcttgttctgggggcgtctccaacatcgggagtggtgctctaaattggtaccagcaactcccaggaacggcccccaaactcctcatctatagttacaatcagcggccctcaggggtctctgaccgattctctggctccaggtctgccacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcaacctgggatgatagtgtgaatggttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctggagctgaggtgaagaagcctggggattcagtgaaggtctcctgcaagccttctggttacaattttctcaactatggtatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggattagcacttacaccggtaacacaaactatgcacagaagctgcagggcagagtcaccttcaccacagacacatccacgagcacagcctacatggagatgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgccagcagggtggtggttggtacgatgtttggggtcaaggtactctggtcaccgtctcctca [SEQ ID NO: 703]
Amino Acid Sequence
SYELTQPPAASGTPGQRVTISCSGGVSNIGSGALNWYQQLPGTAPKLLIYSYNQRPSGVSDRFSGSRSATSASLAISGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGAEVKKPGDSVKVSCKPSGYNFLNYGINWVRQAPGQGLEWMGWISTYTGNTNYAQKLQGRVTFTTDTSTSTAYMEMRSLRSDDTAVYYCARQQGGGWYDVWGQGTLVTVSS [SEQ ID NO: 704]

Table 133

ET200-107
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggagagaaggtcaccatctcctgctctggaagcaacttcaatgttggaaataatgatgtatcctggtatcagcaactcccaggtgcagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctggacatcaccgggctccacagtgacgacgaggccgattattactgcggaacatgggatagcagcctgaatactgggggggtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatactatcagctgggtacgacaggcccctggacaagggcttgagtggatgggatggatcagcacttacaatggtctcacaaactatgcacagaacctccagggcagagtcaccatgactacagacacattcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattactgtgtgagagaggggtcccccgactacggtgacttcgcgtcctttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 705]

Amino Acid Sequence
QSVVTQPPSVSAAPGEKVTISCSGSNFNVGNNDVSWYQQLPGAAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLDITGLHSDDEADYYCGTWDSSLNTGGVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYTISWVRQAPGQGLEWMGWISTYNGLTNYAQNLQGRVTMTTDTFTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFASFDYWGQGTLVTVSS [SEQ ID NO: 706]

Table 134

ET200-108
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctgcgcccccgggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagttcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggatttctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcgccggactccagactggggacgaggccgattattactgcggaacatgggataccagcctgagtggtttttatgtcttcggaagtgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatactatcagctgggtacgacaggcccctggacaagggcttgagtggatgggatggatcagcacttacaatggtctcacaaactatgcacagaacctccagggcagagtcaccatgactacagacacattcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattactgtgtgagagaggggtcccccgactacggtgacttcgcgtcctttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 707]
Amino Acid Sequence
QSVLTQPPSVSAPPGQKVTISCSGSSSNIGNNYVSWYQQFPGTAPKLLIYDNNKRPSGISDRFSGSKSGTSATLGIAGLQTGDEADYYCGTWDTSLSGFYVFGSGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYTISWVRQAPGQGLEWMGWISTYNGLTNYAQNLQGRVTMTTDTFTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFASFDYWGQGTLVTVSS [SEQ ID NO: 708]

Table 135

ET200-109
DNA Sequence
ctgcctgtgctgactcagccaccctcagcgtctgcgacccccgggcagagggtcaccatctcttgttctggaaccacctccaacatcggaagtaatactgtacactggtaccagcagctcccagggacggcccccaaactcctcatctataataataatcagc

ggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctacatattcctgtgcaacatgggatgacagcctgagtggtgtggtcttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagatcccgcctacggtgactacgagtatgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 709]
<u>Amino Acid Sequence</u>
LPVLTQPPSASATPGQRVTISCSGTTSNIGSNTVHWYQQLPGTAPKLLIYNNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEATYSCATWDDSLSGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPAYGDYEYDAFDIWGQGTMVTVSS [SEQ ID NO: 710]

Table 136

ET200-110
<u>DNA Sequence</u>
cagtctgtgttgacgcagccgccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaactaatggtgtaaactggttccagcagttcccaggaacggcccccaaactcctcatctatactaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgcggatgaggctgattattactgtgcagtgtgggaccacagcctgaatggtccggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagaggggccggttttgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 711]
<u>Amino Acid Sequence</u>
QSVLTQPPSASGTPGQRVTISCSGSSSNIGTNGVNWFQQFPGTAPKLLIYTNDQRPSGVPDRFSGSKSGTSASLAISGLQSADEADYYCAVWDHSLNGPVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKAS

GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGAGFDAFDIWGQGTMVTVSS [SEQ ID NO: 712]

Table 137

ET200-111
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgagactgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagaggggctagatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 713]
Amino Acid Sequence
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDETDYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLDAFDIWGQGTMVTVSS [SEQ ID NO: 714]

Table 138

ET200-112
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatgtatagtaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattattgtgcagcatgggatgacagcctgaatggttatgtcttcgcagctgggacccagctcaccgttttaagttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcacc

aactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagaggggctagatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 715]
<u>Amino Acid Sequence</u>
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLMYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFAAGTQLTVLSSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLDAFDIWGQGTMVTVSS [SEQ ID NO: 716]

Table 139

ET200-113
<u>DNA Sequence</u>
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcactggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgagtgctgcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacagctttaccagctatactatcagctgggttcgacaggcccctggacaaggccttgagtggatgggatgggtcagcacttacaatggtctcagaaactatgcacagaacctccagggcagagtcaccatgactacagacacactcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattattgtgtgagagaggggtcccccgactacggtgacttcgcggcctttgactactggggccagggcaccctggtcaccgtctcctca [SEQ ID NO: 717]
<u>Amino Acid Sequence</u>
QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYSFTSYTISWVRQAPGQGLEWMGWVSTYNGLRNYAQNLQGRVTMTTDTLTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFAAFDYWGQGTLVTVSS [SEQ ID NO: 718]

Table 140

ET200-114
<u>DNA Sequence</u>

caggctgtgctgactcagccaccctcagcgtctgagacccccgggcagagggtcaccatctcttgttctggaagcaggtccaacatcggaactaatattgtacactggtaccagcagcgcccaggaatggcccccaaactcctcacttatggtagtcggcggccctcaggggtcccggaccgattctctggctccaagtttggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattattgtgcagcatgggatgacagtctgaatggtccggctttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagacggtgggggctactttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 719]
<u>Amino Acid Sequence</u>
QAVLTQPPSASETPGQRVTISCSGSRSNIGTNIVHWYQQRPGMAPKLLTYGSRRPSGVPDRFSGSKFGTSASLAISGLQSEDEADYYCAAWDDSLNGPAFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGYFDYWGQGTLVTVSS [SEQ ID NO: 720]

Table 141

ET200-115
<u>DNA Sequence</u>
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaatatcggggcacgttatgatgtacactggtaccagcaactcccaggaacagcccccgactcctcatctctgctaactacgatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagtgtgagtgcttgggtgttcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctggggctgaagtgaaggagcctggggcctcagtgaggatctcctgccaggcatctggatacaacttcatcagttattatatgcactgggtgcggcaggcccctgggcaaggtcttgagtggatgggcaccatcaacccaggcagtggtgagacagactactcacagaagttgcagggcagagtcaccatgaccagggacccgtccacgggtacattcgacatggggctgagcagcctgacatctggggacacggccgtctattattgtgcgacaggtctcatcagaggagctagcgatgcttttaatatctggggccgggggacaatggtcaccgtctcttca [SEQ ID NO: 721]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGARYDVHWYQQLPGTAPRLLISANYDRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSVSAWVFGGG

TKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKEPGASVRISCQASGYNFISYYMHWVRQAPGQGLEWMGTINPGSGETDYSQKLQGRVTMTRDPSTGTFDMGLSSLTSGDTAVYYCATGLIRGASDAFNIWGRGTMVTVSS [SEQ ID NO: 722]

Table 142

ET200-116
DNA Sequence
cagcctgtgctgactcagccaccctcagtgtccgtgtccccaggacagacggccgccatcccctgttctggagataagttggggataaatttgcttcctggtatcagcagaagccaggccagtcccctgtgctggtcatctatcaagatactaagcggccctcagggatccctgagcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctatggatgaggctgactattactgtcagacgtgggccagcggcattgtggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtacagctgcagcagtcaggtccaggactggtgaagccctcgcagaccctctcactcacctgtgccatctccggggacagtgtctctagcaacagtgctgcttggaactggatcaggcagtccccatcgagaggccttgagtggctgggaaggacatactacaggtccaagtggtataatgattatgcagtatctgtgaaaagtcgaataaccatcaacccagacacatccaagaaccagttctccctgcagctgaactctgtgactcccgaggacacggctgtgtattactgtgcaagagagcgcagtggctggaagggatttgactactggggccagggaaccctggtcaccgtctcctca [SEQ ID NO: 723]
Amino Acid Sequence
QPVLTQPPSVSVSPGQTAAIPCSGDKLGDKFASWYQQKPGQSPVLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQTWASGIVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARERSGWKGFDYWGQGTLVTVSS [SEQ ID NO: 724]

Table 143

ET200-117
DNA Sequence
gatgttgtgatgactcagtctccaccctccctgtccgtcacccctggagagccggcctccatcacctgcaggtctagtcagagcctcctggaaagaaatgcatacaactacttggattggtacctgcagaggccaggacagtctccacagctcctgatctacttgggttctaatcgggccgccggggtccctgacaggttcagtggcagtggatcaggcagagattttacactgaaaatcagcagagtggagcctgaggatgttggggtttattactgcatgcaagctctacaagctccgttcactttcggcggagggaccaaggtggagatcaaacgttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaa

gtgcagctggtgcagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacacggccgtatattactgtgcgaaatggggcccgtttcaggatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 725]
<u>Amino Acid Sequence</u>
DVVMTQSPPSLSVTPGEPASITCRSSQSLLERNAYNYLDWYLQRPGQSPQLLIYLGSNRAAGVPDRFSGSGSGRDFTLKISRVEPEDVGVYYCMQALQAPFTFGGGTKVEIKRSRGGGGSGGGGSGGGGSLEMAEVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKWGPFQDAFDIWGQGTMVTVSS [SEQ ID NO: 726]

Table 144

ET200-118
<u>DNA Sequence</u>
caggctgtgctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacagcacccgggcaaagcccccaaactcatgatttatgaggtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcaccccttatgtcttcggagcagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagccaggtggacagcagtggcatcagaccaccactttgactactggggccagggaacgctggtcaccgtctcctca [SEQ ID NO: 727]
<u>Amino Acid Sequence</u>
QAVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTPYVFGAGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKARWTAVASDHHFDYWGQGTLVTVSS [SEQ ID NO: 728]

Table 145

ET200-119
DNA Sequence
caggctgtgcttactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagattgggactacatggacgtctggggcaaagggaccacggtcaccgtctcctca [SEQ ID NO: 729]
Amino Acid Sequence
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDWDYMDVWGKGTTVTVSS [SEQ ID NO: 730]

Table 146

ET200-120
DNA Sequence
tcctatgagctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagacctatctcggggagctaacccgcattactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 731]

<u>Amino Acid Sequence</u>
SYELTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLSRGANPHYYYYYGMDVWGQGTTVTVSS [SEQ ID NO: 732]

Table 147

ET200-121
<u>DNA Sequence</u>
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccgtctcctgcactgggagcagatccaacatcggggcaggatatgatgtacactggtaccagcaacttccaggaacagcccccaaactcctcatctatggaaatagtaatcggcctccaggggtccctgaccgattctctgggtctaagtctggcacctcagcctccctggtcatcactgggctccaggctgaggatgccgctgattattactgccagtcctatgacaacactgtgcgtgaatcaccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcaacagagagtaatttagtgtcccggcactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 733]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSGAPGQRVTVSCTGSRSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPPGVPDRFSGSKSGTSASLVITGLQAEDAADYYCQSYDNTVRESPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATESNLVSRHYYYYGMDVWGQGTTVTVSS [SEQ ID NO: 734]

Table 148

ET200-122
<u>DNA Sequence</u>
ctgcctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaaccagctccaacatcggaagtaattctgtagactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagc

ggccctcaggggtccctgaccgaatctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaaccctaacagtggtggcacaaactatgcacagaagtttcagggcagggtcaccatgaccagggacacgtccatcagcacagcctacatggagctgagcaggctgagatctgacgacacggccgtgtattactgtgcgagagattacggatactatggttcggggagttattcgagcggcccccttttactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 735]
Amino Acid Sequence
LPVLTQPPSASGTPGQRVTISCSGTSSNIGSNSVDWYQQLPGTAPKLLIYSNNQRPSGVPDRISGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDYGYYGSGSYSSGPLYYYYGMDVWGQGTTVTVSS [SEQ ID NO: 736]

Table 149

ET200-123
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatgtataataatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctcaatggttatgtcttcggacctgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtggagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagacctatctcggggagctaacccgcattactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctca [SEQ ID NO: 737]
Amino Acid Sequence
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLMYNNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGPGT

KVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLSRGANPHYYYYYGMDVWGQGTTVTVSS [SEQ ID NO: 738]

Table 150

ET200-125
<u>DNA Sequence</u>
aattttatgctgactcagccccacgctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagtattgccagcaactatgtgcagtggtaccagcagcgcccgggcagttcccccgcactgtgatttatgaggataatcaaagaccctctggggtccctggtcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgattccaccagtgtgcttttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagccagggtcctcggtgaaggtctcctgcaaggcctcgggaggcaccttcagcagcaattctctcagctgggtgcgacaggcccctggacaagggcttgagtggatgggaaggatcttccctatcctgggtataacaaactatgcacagaagttccagggcagagtcacgattaccgcggacaaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtctattactgtgcgagaggaaactaccaatggtatgatgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 739]
<u>Amino Acid Sequence</u>
NFMLTQPHAVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPRTVIYEDNQRPSGVPGRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTSVLFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSNSLSWVRQAPGQGLEWMGRIFPILGITNYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGNYQWYDAFDIWGQGTMVTVSS [SEQ ID NO: 740]

Table 151

ET200-005
<u>DNA Sequence</u>
cagcctgtgctgactcagccaccctcagtgtcagtggtcccaggaaagacggccaggattacctgtgggggaaaaaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtggtggtcatccattatgatagtgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgca

gctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccaactatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacataagctccagggcagagtcaccatgaccacagacacatccacgagcacagccaacatggagctgaggagcctgagacctgacgacactgccgtgtattactgtgcgcgctcttacttcggttctcatgattactggggtcaaggtactctggtgaccgtctcctca [SEQ ID NO: 741]
<u>Amino Acid Sequence</u>
QPVLTQPPSVSVVPGKTARITCGGKNIGSKSVHWYQQKPGQAPVVVIHYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQAPGQGLEWMGWISAYNGNTNYAHKLQGRVTMTTDTSTSTANMELRSLRPDDTAVYYCARSYFGSHDYWGQGTLVTVSS [SEQ ID NO: 742]

Table 152

ET200-124
<u>DNA Sequence</u>
tcctatgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggatttcctgtgggggaaacgacattggaagtaaaagtgttttctggtatcagcagaggccaggccaggcccctgtgttggtcgtctatgatgatagcgaccggccctcagggctccctgagcgattctctggcttcaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaagtgtgggatagtagtagtgatcattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagatataacctatggttcggggagttatggtgcttttgatatctggggccaagggacaatggtcaccgtctcttca [SEQ ID NO: 743]
<u>Amino Acid Sequence</u>
SYVLTQPPSVSVAPGKTARISCGGNDIGSKSVFWYQQRPGQAPVLVVYDDSDRPSGLPERFSGFNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDITYGSGSYGAFDIWGQGTMVTVSS [SEQ ID NO: 744]

XII. Exemplary extracellular antigen-binding domains (e.g., scFvs) comprising a heavy chain variable region, a light chain variable region, a linker peptide and a His-tag and HA-tag

Table 153

ET200-001
DNA Sequence
cagtctgtgttgacgcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtgtatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcgaaggtccgtacgacggtttcgattcttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 745]
Amino Acid Sequence
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGPYDGFDSWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 746]

Table 154

ET200-002
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattctgtggtattcggcggagggaccaagctgac

cgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggcactgaggtgaagaagcctggggcctcagtgagggtcgcctgcaaggcttctggttaccccttaacaaatatgacatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggaggcatcatccctatctttcgtacaacaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtatattactgtgcgcgcgaatggttctactgggatatctggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 747]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNSVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGTEVKKPGASVRVACKASGYPFNKYDINWVRQAPGQGLEWMGGIIPIFRTTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREWFYWDIWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 748]

Table 155

ET200-003
DNA Sequence
cagtctgtgttgactcagccaccctcagtgtccgtgtccccaggacagacagccagcatctcctgctctggaaataaattgggactaagtatgtttactggtatcagaagaggccaggccagtcccctgtgttggtcatgtatgaagataatcagcggccctcagggatcccggagcggttctctggctccaactctgggaacacagccactctgaccatcagagggacccagactgtggatgaggctgactattactgtcaggcgtgggactccgacactttcgtggtcttcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagaccggggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatggcatgcactgggtccgccaggctccaggcaaggggctggagtgggtggcagttatatcacatgatggaagtaataaatactacgcagactccgtgaagggccgattcaccatctccagagacaattccaaggacacgctgtatctgcaaatgaacagcctgagaggtgaggacacggccgtatattactgtgcgcgctctaaccagtggtctggttacttctctttcgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 749]
Amino Acid Sequence
QSVLTQPPSVSVSPGQTASISCSGNKLGTKYVYWYQKRPGQSPVLVMYEDNQRPSGIPERFSGSNSGNTATLTIRGTQTVDEADYYCQAWDSDTFVVFGGGTKVT

VLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISHDGSNKYYADSVKGRFTISRDNSKDTLYLQMNSLRGEDTAVYYCARSNQWSGYFSDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 750]

Table 156

ET200-006
DNA Sequence
tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtggtggtcatccattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccacctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaacacttacaatggtcacacaaactatgcacagaagctccagggcagagccacaatgaccgcagacacatccacgaacacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgcgttatctacggttctggtgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 751]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVVVIHYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINTYNGHTNYAQKLQGRATMTADTSTNTAYMELRSLRSDDTAVYYCARVIYGSGDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 752]

Table 157

ET200-007
DNA Sequence
tcctatgtgctgactcagccactctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaactgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggcc

ctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatcgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctgcaggagtcgggcccaggactggtgaagccttcggagaccctgtccctcacctgcaatgtctctggttactccatcagcagtggttacttttggggctggatccggcagcccccagggaaggggctggagtggattgggagtatctatcatagtaggagcacctactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgaactctgtgaccgccgcagacacggccgtgtattactgtgcgcgcggttacggttacttcgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 753]
Amino Acid Sequence
SYVLTQPLSVSVAPGKTARITCGGNNIGSKTVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHRVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQESGPGLVKPSETLSLTCNVSGYSISSGYFWGWIRQPPGKGLEWIGSIYHSRSTYYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAVYYCARGYGYFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 754]

Table 158

ET200-008
DNA Sequence
caatctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacaacacccaggcaaagcccccaaactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacttcgaaggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggtgtggtacggcctggggggtccctgagactctcctgtgcagcctctggattcacctttggtgattatggcatgagctgggtccgccaagctccagggaaggggctggagtgggtctctggtattaattggaatggtggtagcacaggttatgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagccgaggacacggccgtatattactgtgcgcgctctaaatacaacttccatgtttactacgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 755]
Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTSKVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGVVRPGGSLRLSCAASGFTFGDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSKYNFHVYYDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 756]

Table 159

ET200-009
DNA Sequence
cagtctgtgttgacgcagccaccctcagcgtctgggacccccgggcagacagtcaccatctcttgttctggaagcaactccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcctcatctataggaataatcagcggccctcaggggtccctgaccgattctcaggctccaagtctggcacctcagcctccctggccatcagtgggctccgctccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtgcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgctcttctggtaacatggtttcttggaaagatatgtggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 757]
Amino Acid Sequence
QSVLTQPPSASGTPGQTVTISCSGSNSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSSGNMVSWKDMWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 758]

Table 160

ET200-010
DNA Sequence

caatctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactctgtctcctggtaccaacaacacccaggcaaagcccccagactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacccctttagtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcggtgctgttgcttaccatgattggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 759]
<u>Amino Acid Sequence</u>
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPRLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTPLVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGAVAYHDWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 760]

Table 161

ET200-011
<u>DNA Sequence</u>
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagagggtcaccatctcctgctctggaagcagctccaacatttcgatttatgatgtatcctggtatcagcagctcccaggaacagcccccaaactcctcatttatggcaataataagcgaccctcggggattgctgaccgattctctggctccacgtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatgacagtctgagtgggggggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcaatctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcgaggcttctggaggcaccctcagcagctatgctatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatgtttggtacagcacactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgaaaacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtgttcattacgcttctttcgatcattggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgac

gttccggactacgcttct [SEQ ID NO: 761]
Amino Acid Sequence
QSVVTQPPSVSAAPGQRVTISCSGSSSNISIYDVSWYQQLPGTAPKLLIYGNNKRPSGIADRFSGSTSGTSATLGITGLQTGDEADYYCGTWDDSLSGGVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGSSVKVSCEASGGTLSSYAINWVRQAPGQGLEWMGGIIPMFGTAHYAQKFQGRVTITADESTKTAYMELSSLRSEDTAVYYCARGVHYASFDHWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 762]

Table 162

ET200-012
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctgcggccgcaggacagaaggtcaccatctcctgctctggaagcgactccaacattgggaataattatgtgtcctggtatcaacacctcccagggacagcccccaaactcctcatttatgacgttaaaaatcgaccctcagggattcctgaccggttctccggctccaagtctggctcgtcagccaccctaggcatcgccggactccagcctggggacgaggccgattattactgcggaacatgggacagtcggctggatgcctatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcaatctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagacttctggtttcccctttaatatctttggaatcacctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcggttacaacggtaacacagactacccacagaagttccagggcagagtcaccatgtccacagacacatccacgagtacagcctacatggagctgaggaacctgaaatctgacgacacggccgtgtattactgtgcgcgcggtgcttacggtggtatggatacttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 763]
Amino Acid Sequence
QSVLTQPPSVSAAAGQKVTISCSGSDSNIGNNYVSWYQHLPGTAPKLLIYDVKNRPSGIPDRFSGSKSGSSATLGIAGLQPGDEADYYCGTWDSRLDAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGASVKVSCKTSGFPFNIFGITWVRQAPGQGLEWMGWISGYNGNTDYPQKFQGRVTMSTDTSTSTAYMELRNLKSDDTAVYYCARGAYGGMDTWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 764]

Table 163

ET200-013
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcacctccaacatcggggcaggttatgatgtacactggtatcagcagcttccaggaacagcccccaaactcctcatctatactaacaactttcggccctcaggggtccctgaccgattctctgcctccaagtctggcacttcagcttccctggccatcactggtctccaggctgaggatgaggctgattattactgcggaacatgggatagcagcctgagtgccgttgtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctggaactgaggtgaagaagcctggggcctcagtgaaagtctcctgcaaggcttctggttacatgtttaccagttatggtctcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgctaacaatggtaagacaaattatgctaagaaattccaggacagagtcaccatgaccagagacacttccacgagcacaggctacatggaactgaggagcctgagatctgacgacacggccgtatattactgtgcgcgccatatcggtggttcttacttcgatcgttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 765]
Amino Acid Sequence
QSVVTQPPSVSGAPGQRVTISCTGSTSNIGAGYDVHWYQQLPGTAPKLLIYTNNFRPSGVPDRFSASKSGTSASLAITGLQAEDEADYYCGTWDSSLSAVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGTEVKKPGASVKVSCKASGYMFTSYGLNWVRQAPGQGLEWMGWISANNGKTNYAKKFQDRVTMTRDTSTSTGYMELRSLRSDDTAVYYCARHIGGSYFDRWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 766]

Table 164

ET200-014
DNA Sequence
tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagactgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtgatggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacag

cctgagagacgaggacacggccgtatattactgtgcgcgctctcatgaagctaacctggttggtgattggtggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 767]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSDGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRDEDTAVYYCARSHEANLVGDWWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 768]

Table 165

ET200-015
DNA Sequence
cagtctgtggtgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctacggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgctggggtggtttcggtgctgttgatcattggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 769]
Amino Acid Sequence
QSVVTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARWGGFGAVDHWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 770]

Table 166

ET200-016
DNA Sequence
tcttctgagctgactcaggaccctgctgtgtctgtggccttgggacagacagtcaagatcacgtgccaaggagacagcctcacagactaccatgcaacctggtaccagcagaagccaggacaggcccctgtcgctgtcatctatgctacaaacaaccggcccactgggatcccagaccgattctctggttccagttccggaaacacagcttctttgaccatcactggggctcaggcggaagatgaggctgactattactgtaattcccgggacagcggcacggacgaagtgttattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagactgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtagtagttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgcgcggtcagggttacgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 771]
Amino Acid Sequence
SSELTQDPAVSVALGQTVKITCQGDSLTDYHATWYQQKPGQAPVAVIYATNNRPTGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGTDEVLFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGQGYDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 772]

Table 167

ET200-017
DNA Sequence
Tcctatgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcgtctatgatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgagcatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatactgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtg

gttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgctactacccgggtatggatatgtggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 773]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLSISRVEAGDEADYYCQVWDSSSDHTVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYPGMDMWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 774]

Table 168

ET200-018
DNA Sequence
Caggctgtgctgactcagccgccctcaacgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcgggagaaatggtgtaaactggtaccagcagctcccaggagcggcccccaaagtcctcatctataatgataatcagcgaccctcaggggtccctgaccgagtctctggctcccagtctggctcctcaggcaccctggccatcgatgggcttcggtctgaggatgaggctgattattactgtgcggcatgggatgacagcctgcatggtgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcaatgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtggttacggtgattcttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 775]
Amino Acid Sequence
QAVLTQPPSTSGTPGQRVTISCSGSSSNIGRNGVNWYQQLPGAAPKVLIYNDNQRPSGVPDRVSGSQSGSSGTLAIDGLRSEDEADYYCAAWDDSLHGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKVSGYTLNELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMED

TSTDTAYMELSSLRSEDTAVYYCARGGYGDSWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 776]

Table 169

ET200-019
DNA Sequence
Aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattcttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcaatctggggctgaggtgaagaggcctgggtcctcggtgaaggtctcctgcacggcttctggaggcaccttcagcagcgatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggaggaatcatccctatgtttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcgaaggttactactacccgtctgcttacctgggttctgttctgaacgacatctcttctgtttacgatgaatggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 777]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNSWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKRPGSSVKVSCTASGGTFSSDAISWVRQAPGQGLEWMGGIIPMFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREGYYYPSAYLGSVLNDISSVYDEWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 778]

Table 170

ET200-020
DNA Sequence
Cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcacctccaacattggaaataatgatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcgtgagtgcttcttgggtcttcggcagagggaccaagctg

accgtcctaggttctagaggtggtggtggtagcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatccacagaagctccagggcagagtcaccatgaccacagacccatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgctctatgacttctttcgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 779]
<u>Amino Acid Sequence</u>
QSVVTQPPSVSAAPGQKVTISCSGSTSNIGNNDVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSVSASWVFGRGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYPQKLQGRVTMTTDPSTSTAYMELRSLRSDDTAVYYCARSMTSFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 780]

Table 171

ET200-021
<u>DNA Sequence</u>
Cagtctgtgttgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcaactccaacattgggaataattatgtatcctggtatcagcaactcccagggacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaggtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatggaataccactgtgactcctggctatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacaccgccatgtattactgtgcgcgctctgtttacgacctggatacttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 781]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSAAPGQKVTISCSGSNSNIGNNYVSWYQQLPGTAPKLLIYDNN

KRPSGIPDRFSGSRSGTSATLGITGLQTGDEADYYCGTWNTTVTPGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAMYYCARSVYDLDTWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 782]

Table 172

ET200-022
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgggggccccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtcttggggaggctcggaacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagcggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaattccctgtatctgcaaatgaacagtctgagagctgaggacaccgccatgtattactgtgcgcgctaccgtcaggttggttctgcttacgattcttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 783]
Amino Acid Sequence
QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLGAPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSWGGSEQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAMYYCARYRQVGSAYDSWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 784]

Table 173

ET200-023
DNA Sequence
ctgcctgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacat

tggaagtaaaagtgtgcactggtatcagcagaagccaggccaggcccctgtgctggtcgtctatgctgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagttatcataattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgagcagcctgagatctgaggacaccgccatgtattactgtgcgcgctactggggtttcggtgtttctgatcgttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 785]
Amino Acid Sequence
LPVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYADSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSYHNYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELSSLRSEDTAMYYCARYWGFGVSDRWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 786]

Table 174

ET200-024
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccccgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgacagcagcaatctttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctacaactactactactacgattcttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 787]

Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNLWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARYNYYYYDSWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 788]

Table 175

ET200-025
DNA Sequence
gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacagagtcaccatcacttgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatcaaggttcagtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagattttgcaacttactactgtcaacagagttacagtaccccattcactttcggccctgggaccaaagtggatatcaaacgttctagaggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacaccgccatgtattactgtgcgcgctactggggttacgactcttacgatgaatggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 789]
Amino Acid Sequence
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTKVDIKRSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAMYYCARYWGYDSYDEWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 790]

Table 176

ET200-026

<u>DNA Sequence</u>
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcaacaaccattactacaacgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 791]
<u>Amino Acid Sequence</u>
NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARNNHYYNDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 792]

Table 177

ET200-027
<u>DNA Sequence</u>
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagggggtcaccatcccctgcactgggagcagctccaacatcggggcaggttatgatgtacactggtaccagcagcttccagggacagcccccaaactcctcatctatggtaacaacaatcggccctcaggggtccctgaccgcttctctggctccaggtctggctcctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtgatgtggtattcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctggggctacagtgaaaatctcctgcaaggtttctggatacaccttcaccgactactacatgcactgggtgcaacaggcccctggaaaagggcttgagtggatgggacttgttgatcctgaagatggtgaaacaatatacgcagagaagttccagggcagagtcaccataaccgcggacacgtctacagacacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgctactggtcttactctttcgactacctgtacatg

ccggaaggtaacgattggtggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 793]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSGAPGQGVTIPCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGSSASLAITGLQAEDEADYYCQSYDSSLSDVVFGGGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGLVDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCARYWSYSFDYLYMPEGNDWWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 794]

Table 178

ET200-028
<u>DNA Sequence</u>
cagtctgtgttgactcagccacccgcagcgtctgggacccccggacagagagtcaccatctcttgttctgggggcgtctccaacatcgggagtggtgctctaaattggtaccagcaactcccaggaacggcccccaaactcctcatctatagttacaatcagcggccctcaggggtctctgaccgattctctggctccaggtctgccacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcaacctgggatgatagtgtgaatggttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggagctgaggtgaagaagcctggggattcagtgaaggtctcctgcaagccttctggttacaattttctcaactatggtatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggattagcacttacaccggtaacacaaactatgcacagaagctgcagggcagagtcaccttcaccacagacacatccacgagcacagcctacatggagatgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcgacctgtactactacgaaggtgttgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 795]
<u>Amino Acid Sequence</u>
QSVLTQPPAASGTPGQRVTISCSGGVSNIGSGALNWYQQLPGTAPKLLIYSYNQRPSGVSDRFSGSRSATSASLAISGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGDSVKVSCKPSGYNFLNYGINWVRQAPGQGLEWMGWISTYTGNTNYAQKLQGRVTFTTDTSTSTAYMEMRSLRSDDTAVYYCARDLYYYEGVDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 796]

Table 179

ET200-029
DNA Sequence
caggctgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccagggttacctgtgggggaaacaacattggaagtgaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgttggtcatctattatgataccgaccggccctcagggatccctgagcgattctctggctcccactctgggaccacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagggatcatgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctgggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcggcctctggattcaccttcagtagctatgctatgcactgggtccgccaggctccaggcaagggactggagtgggtggcagttatatcatatgatggaagcaataaatactacgcagactccgtgaagggcctattcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagctgaggacacggccgtgtattactgtgcgcgctcttacttcacttctggtttctacgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 797]
Amino Acid Sequence
QAVLTQPPSVSVAPGKTARVTCGGNNIGSESVHWYQQKPGQAPVLVIYYDTDRPSGIPERFSGSHSGTTATLTISRVEAGDEADYYCQVWDSSRDHVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGLFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSYFTSGFYDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 798]

Table 180

ET200-030
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagttccaacatcggggcaggttatgatgtaaattggtatcagcagtttccaggaacagcccccaaactcctcatctatggtaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggctcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatg

gtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcatgtcttctatgtactacgattggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 799]
Amino Acid Sequence
QSVVTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGSYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGASVKVSCKASGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARMSSMYYDWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 800]

Table 181

ET200-031
DNA Sequence
tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagactgggggaggcttggtcaagcctggagggtccctgagactctcctgtgcagcctctggattcaccgtcagtgactactacatgagctggatccgccaggctccagggaagggcctggagtggatttcatacattagtggtagtggtaatagcatatactacgcagactctgtgaagggccgattcaccatctccagggacaacgccaagaactcactggatctgcaaatgaccagcctgagagccgaggacacggccgtatattactgtgcgcgctctactaaattcgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 801]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVKPGGSLRLSCAASGFTVSDYYMSWIRQAPGKGLEWISYISGSGNSIYYADSVKGRFTISRDNAKNSLDLQMTSLRAEDTAVYYCARSTKFDYWGQGTLVTVSSTSGQAGQHHHHHHGA

YPYDVPDYAS [SEQ ID NO: 802]

Table 182

ET200-032
DNA Sequence
ctgcctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacgtcggaagttacactgtaaactggtaccggcaactcccaggaacggcccccacactcctcatctataataataatcagcggccctcaggggtccctgaccgattctctgactccaagtctggcacctcggcctccctgaccattagtgggctccagcctgaggatgaggctgattattattgtgcagcatgggatgacaggctgggtggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggagcagaggtgaaaaagccgggggagtctctgaagatctcctgtaagggttctggatacagctttaccaactactggatcggctgggtgcgccagatgcccgggaaaggcctggagtggatggggatcatctatcctggtgactctgataccagatacagcccgtccttccaaggccaggtcaccatctcagccgacaagtccatcagcaccgcctacctacagtggagcagcctgaaggcctcggacaccgccatgtattactgtgcgcgctctactggttcttctcatatgtctgatgaatggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 803]
Amino Acid Sequence
LPVLTQPPSASGTPGQRVTISCSGSSSNVGSYTVNWYRQLPGTAPTLLIYNNNQRPSGVPDRFSDSKSGTSASLTISGLQPEDEADYYCAAWDDRLGGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARSTGSSHMSDEWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 804]

Table 183

ET200-033
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaatcattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaagtg

cagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggagatcactcatagtggaaggtccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgctcttctatcatgtctgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 805]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNHWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEITHSGRSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSSIMSDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 806]

Table 184

ET200-034
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcacctccaacatcggggcaggttatgatgtacactggtaccagcagcttccaggaacagcccccaaactcctcatcaacaataacaggaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatggcagcctgactggtgcagtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcatgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgcggttctgctctggaccattacgatcgttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 807]
Amino Acid Sequence
QSVLTQPPSVSGAPGQRVTISCTGSTSNIGAGYDVHWYQQLPGTAPKLLINNNRNRPSGVPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDGSLTGAVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCK

ASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGSALDHYDRWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 808]

Table 185

ET200-035
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcaccaattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctacaactactacttcaacgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 809]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTNWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARYNYYFNDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 810]

Table 186

ET200-037
DNA Sequence
tcctatgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccaggattacctgtgggggaaacaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtgctggtcatctattatgatagcgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggg

gatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccagatgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacactgccgtgtattactgtgcgcgctctatgttcggtgctcatgattcttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 811]
Amino Acid Sequence
SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSMFGAHDSWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 812]

Table 187

ET200-038
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaacatcggggcaggttttgatgtacactggtaccagctacttccaggaacagcccccaaactcctcatctatgctaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctcctggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggtgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcaatctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgcggtgcttctttcgaccgtcatgataactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 813]
Amino Acid Sequence
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGFDVHWYQLLPGTAPKLLIYANS

NRPSGVPDRFSGSKSGTSASLAITGLLAEDEADYYCQSYDSSLSGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGASFDRHDNWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 814]

Table 188

ET200-039
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagttcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgcgctctaactactactacaacgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 815]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSNYYYNDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 816]

Table 189

ET200-040
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctc

caacatcggggcaggttatgatgtacactggtaccagcagcttccaggaacagcccccaaactcctcatctatggtaacagcaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagcctgagtggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacactgccgtgtattactgtgcgcgctactctggtgtttactacgattggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 817]
<u>Amino Acid Sequence</u>
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCARYSGVYYDWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 818]

Table 190

ET200-041
<u>DNA Sequence</u>
aattttatgctgactcagccccactctgtgtcggggtctccggggaagacggtaaccatctcctgcaccggcagcagtggcagcattgccgacaactttgtgcagtggtaccagcagcgcccgggcggtgtccccaccactgtgatctttaatgatgacgaaagaccctctggcgtccctgatcggttctctggctccatcgacacctcctccaattctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgataataataatcgaggggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatgaaccctaacagtggtaacacaggctatgcacagaagttccagggcagagtcaccatgaccaggaacacctccataagcacagcctacatggagctgagcaacctgagatctgaggacacggccgtgtattactgtgcgcgctactactcttacggttacgattggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 819]

Amino Acid Sequence
NFMLTQPHSVSGSPGKTVTISCTGSSGSIADNFVQWYQQRPGGVPTTVIFNDDERPSGVPDRFSGSIDTSSNSASLTISGLKTEDEADYYCQSYDNNNRGVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSNLRSEDTAVYYCARYYSYGYDWGQGTLVTVSSTSGQAGQHHHHHGAYPYDVPDYAS [SEQ ID NO: 820]

Table 191

ET200-042
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctggggccccagggcagacggtcaccatctcctgcactgggggcagctccaacatcgggacaggttattttgtaaattggtaccagcaggttccaggaaaagcccccaaactcctcatcctgggtaacaataatcggccctcgggggtccctgaccgactctccggctccacgtccggcacctcagcctccctggccatcactgggctccaggctgaggatgagggtacttattactgccagtcctatgacagcagcctgagtggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtacagctgcagcagtcaggtccaggactggtgaagccctcgcagaccctctcactcacctgtggcatctccggggacagtgtctctaccaacagtgttgcttggcactggatcaggcagtccccatcgagaggccttgagtggctgggaaggacatactacaggtccaagtggtctaatgactatggagtatctgtgaaaagtcgaatcaccatcatcccagacacatccaagaaccagttctccctgcagctgaactctgtgactcccgaggacacggctgtgtattactgtgcgcgctcttcttcttggtaccagatcttcgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 821]
Amino Acid Sequence
QSVVTQPPSVSGAPGQTVTISCTGGSSNIGTGYFVNWYQQVPGKAPKLLILGNNNRPSGVPDRLSGSTSGTSASLAITGLQAEDEGTYYCQSYDSSLSGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQSGPGLVKPSQTLSLTCGISGDSVSTNSVAWHWIRQSPSRGLEWLGRTYYRSKWSNDYGVSVKSRITIIPDTSKNQFSLQLNSVTPEDTAVYYCARSSSWYQIFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 822]

Table 192

ET200-043

DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcaccggcagcagcgacagcatagccaacaactatgttcagtggtaccagcagcgcccgggcagtgcccccaccaatgtgatctacgaagatgtccaaagaccctctggggtccctgatcggttctctgggtccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgtctactattgtcagtcttatcatagcgacaatcgttgggtgttcggcggcgggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacacggccgtatattactgtgcgcgctctggtgcttactgggactactctgtttacgatgaatggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 823]
Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTGSSDSIANNYVQWYQQRPGSAPTNVIYEDVQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEAVYYCQSYHSDNRWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSGAYWDYSVYDEWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 824]

Table 193

ET200-044
DNA Sequence
cagtctgtgttgactcagccaccctcagtgtccgtgtccccaggacagacagccaccatcgcctgttctggacataaattgggggataaatatgcttcctggtatcagcagaagtcgggccagtcccctgtgttgatcatctatcaggataataagcggccctcagggattcctgagcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctctggatgaggctgactattattgtcaggcgtgggacagtagtacttatgtggcattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctgcaggagtccggcccaggactggtgaagccttcggagaccctgtccctcacctgcgttgtctctggtggctccatcagcagtagtaactggtggagctgggtccgccagcccccagggaaggggctggagtggattggggaaatctatcatagtgggagccccaactacaacccatccctcaagagtcgagtcaccatatcagtagacaagtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcatgactactcatactttcggttacgatgcttggggtcaaggtactctggt

gaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 825]
Amino Acid Sequence
QSVLTQPPSVSVSPGQTATIACSGHKLGDKYASWYQQKSGQSPVLIIYQDNKRPSGIPERFSGSNSGNTATLTISGTQALDEADYYCQAWDSSTYVAFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQESGPGLVKPSETLSLTCVVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSPNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARMTTHTFGYDAWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 826]

Table 194

ET200-045
DNA Sequence
cagcctgtgctgactcagccaccctcagtgtcagtggccccaggaaagacggccacgattacttgtgggggaaacaacattggaagtgaaagtgtgcactggtaccaccagaagccaggccaggcccctgtgttggtcatctatgatgatgccggccggccctcagggatccctgagcgattcactggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggacagaaatagtgctcagtttgtcttcggacctgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgcggtgttcatctggattggtggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 827]
Amino Acid Sequence
QPVLTQPPSVSVAPGKTATITCGGNNIGSESVHWYHQKPGQAPVLVIYDDAGRPSGIPERFTGSNSGNTATLTISRVEAGDEADYYCQVWDRNSAQFVFGPGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGVHLDWWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 828]

Table 195

ET200-069
DNA Sequence
cagtctgtcgtgacgcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtggttatgtcttcggaactgggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgcgcctgtacgaaggtggttaccatggttggggttcttggctgtcttctgattcttggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 829]
Amino Acid Sequence
QSVVTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYVFGTGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLYEGGYHGWGSWLSSDSWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 830]

Table 196

ET200-078
DNA Sequence
cagtctgtgttgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttattgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaa

gcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgcgcgaaggggcatttgatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 831]
Amino Acid Sequence
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGAFDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 832]

Table 197

ET200-079
DNA Sequence
tcctatgagctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaattatgtatactggtaccagcagctcccaggaacggcccccaaactcttcatctataggaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtggttatctcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaatggcgactccaactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 833]
Amino Acid Sequence
SYELTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLFIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYLFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCANGDSNYYYGMDVWGQGTTVTVSSTSGQAGQ

HHHHHHGAYPYDVPDYAS [SEQ ID NO: 834]

Table 198

ET200-081
DNA Sequence
cagtctgccctgactcagcctgcctccgtgtccgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacattggtggttataactatgtctcctggtaccaacaacacccaggcaaagcccccaaactcatgatttatgatgtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcatctcatatacacgcacctggaacccctatgtcttcgggagtgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctgggggaggcgtggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccgtcaagctccagggaagggtctggagtgggtctctcttattagtggggatggtggtagcacatactatgcagactctgtgaagggccgattcaccatctccagagacaacagcaaaaactccctgtatctgcaaatgaacagtctgagaactgaggacaccgccttgtattactgtgcaaaagatcgggcagcagctggctactactactacggtatggacgtctgggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 835]
Amino Acid Sequence
QSALTQPASVSGSPGQSITISCTGTSSDIGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCISYTRTWNPYVFGSGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGGGVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLISGDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRTEDTALYYCAKDRAAAGYYYYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 836]

Table 199

ET200-097
DNA Sequence
ctgcctgtgctgactcagccaccctcagtgtccgtgtccccaggacagacagccatcatcacctgctctggagataaattgggggaaaaatatgtttcctggtatcagcagaagccaggccagtcccctgtactggtcatcgatcaagataccaggaggccctcagggatccctgagcgattctctggctccaactctgggaccacagccactctgaccatcagcgggacccaggctatggatgaggctgactattactgtcaggcgtgggacaggggtgtggtattcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtct

gggggagacttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttaatgattatgccatgca ctgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggagtggtaataacataggctatgcgg actctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctg aggacacggccttgtattactgtgcaaaagatagtatacggtatggcatcacctggggaggttttgactactggggccaggg aaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacg ttccggactacgcttct [SEQ ID NO: 837]
<u>Amino Acid Sequence</u>
LPVLTQPPSVSVSPGQTAIITCSGDKLGEKYVSWYQQKPGQSPVLVIDQDTRR PSGIPERFSGSNSGTTATLTISGTQAMDEADYYCQAWDRGVVFGGGTKLTVL GSRGGGGSGGGGSGGGGSLEMAEVQLVESGGDLVQPGRSLRLSCAASGFTF NDYAMHWVRQAPGKGLEWVSGISWSGNNIGYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTALYYCAKDSIRYGITWGGFDYWGQGTLVTVSSTSGQAGQH HHHHHGAYPYDVPDYAS [SEQ ID NO: 838]

Table 200

ET200-098
<u>DNA Sequence</u>
cagcctgtgctgactcagccaccctcggtgtccaagggcttgagacagaccgccacactcacctgcactgggaacagca acaatgttggcaacctaggagtagcttggctgcagcagcaccagggccaccctcccaaactcctatcctacaggaataaca accggccctcagggatctcagagagattatctgcatccaggtcaggaaacacagcctccctgaccattactggactccagc ctgaggacgaggctgactattactgctcagcatgggacagtagcctcagtgcttgggtgttcggcggagggaccaagctg accgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggt gcagctggtggagtctgggggagtcgtggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttt gatgattatgccatgcactgggtccgtcaagctccggggaagggtctggagtgggtctctcttattaattgggatggtggtag cacctactatgcagactctgtgaagggtcgattcaccatctccagagacaacagcaaaaactccctgtatctgcaaatgaac agtctgagagctgaggacaccgccttgtattactgtgcaaaagggatgggcctgagggcgtttgactactggggccaggg aaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacg ttccggactacgcttct [SEQ ID NO: 839]
<u>Amino Acid Sequence</u>
QPVLTQPPSVSKGLRQTATLTCTGNSNNVGNLGVAWLQQHQGHPPKLLSYR NNNRPSGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLSAWVFGGG TKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGVVVQPGGSLRLSCA

ASGFTFDDYAMHWVRQAPGKGLEWVSLINWDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGMGLRAFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 840]

Table 201

ET200-099
DNA Sequence
cagtctgtgttgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtccggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcttcatgggatgacagcctgaatggccgttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggggctgaggtgaggaagcctggggcctcagtgaaggtttcctgcaagacttctggatacaccttcagttggtatgctatacattgggtgcgccaggcccccggacaaaggcttgagtggatgggatggatcaacgctggcaatggaaacacaaaatattcacagaaatttcagggcagagtcagtcttaccagggacacatccgcgagcacagcctacatggagctgagcagcctgagatctgatgacacggctgtgtattactgtgcgagacccgataattatggttcgggtggggatgtttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 841]
Amino Acid Sequence
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCASWDDSLNGRYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVRKPGASVKVSCKTSGYTFSWYAIHWVRQAPGQRLEWMGWINAGNGNTKYSQKFQGRVSLTRDTSASTAYMELSSLRSDDTAVYYCARPDNYGSGGDVFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 842]

Table 202

ET200-100
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactttgtgcagtggtaccagcagcgcccgggcagtgcccccacccctatgatctatgaggataacaacagacccccctggggtccctgatcggttctctgcctccgtcgacagctcctccaactctgcctccctcaccatctctggactgaag

actgaggacgaggctgactactactgtcagtcttatgataccagcaatgtggtattcggcgggggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggagggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatgaaatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtggtagtaccatatactacgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggctgtttattactgtgcacgctgggactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 843]
<u>Amino Acid Sequence</u>
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNFVQWYQQRPGSAPTPMIYEDNNRPPGVPDRFSASVDSSSNSASLTISGLKTEDEADYYCQSYDTSNVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARWDYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 844]

Table 203

ET200-101
<u>DNA Sequence</u>
caggctgtgctgactcagccaccctcagcgtctgggcccccgggcagagggtcaccgtctcttgttctggaagcaactccaacatcggaagtaactacgttaactggtaccagcagttcccaggaacggcccccaaactcctcatgtatagtagtagtcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccactctgaggatgaggctgattattactgtgctacatgggatgacagcctgaatgcttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaggaagcctggggcctcagtgaaggtttcctgcaagacttctggatacaccttcacttggtatgctatacattgggtgcgccaggcccccggacaaaggcttgagtggatgggatggatcaacgctggcagtggaaacacaaaatattcacagaaatttcagggcagagtcacccttaccagggacacatccgcgagcacagcgtacatggagctgagcagcctgagatctgatgacacggctgtgtattactgtgcgagacccaataactatggttcgggtggggatgtttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 845]
<u>Amino Acid Sequence</u>
QAVLTQPPSASGAPGQRVTVSCSGSNSNIGSNYVNWYQQFPGTAPKLLMYSS

SQRPSGVPDRFSGSKSGTSASLAISGLHSEDEADYYCATWDDSLNAWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVRKPGASVKVSCKTSGYTFTWYAIHWVRQAPGQRLEWMGWINAGSGNTKYSQKFQGRVTLTRDTSASTAYMELSSLRSDDTAVYYCARPNNYGSGGDVFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 846]

Table 204

ET200-102
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcaccggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgagtgcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaagtttcctgcaaggcttctggatacaccttcacgaactatgctctgcattgggtgcgccaggcccccggacaagggcttgagtggatggcatggatcaacggtggcaatggtaacacaaaatattcacagaacttccagggcagagtcaccattaccagggacacatccgcgagcacagcctatatggagctgagcagcctgagatctgaagacacggctgtgtattactgtgcgaaaccggaggaaacagctggaacaatccactttgactactggggccagggaaccccggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 847]
Amino Acid Sequence
QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTNYALHWVRQAPGQGLEWMAWINGGNGNTKYSQNFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAKPEETAGTIHFDYWGQGTPVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 848]

Table 205

ET200-103
DNA Sequence
caggctgtgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtgg

cagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcaccatcacggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtccagctggtacagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgggggagggttactatgatagtagtggttattccaacggtgatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 849]
Amino Acid Sequence
QAVLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTITVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAGEGYYDSSGYSNGDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 850]

Table 206

ET200-104
DNA Sequence
aattttatgctgactcagccccactctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagcattgccagcaactatgtgcagtggtaccagcagcgcccgggcagtgcccccaccactgtgatctatgaggataaccaaagaccctctggggtccctgatcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgatagcagcaatgtggtattcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggagggtccctgagactctcctgtgcagcctctggattcaccttcagtagttatgaaatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtggtagtaccatatactacgcagactctgtgaagggccgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggctgtttattactgtgcacgctgggactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 851]

Amino Acid Sequence
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSNVVFGGGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARWDYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 852]

Table 207

ET200-105
DNA Sequence
tcctatgtgctgactcagccaccctcagtgtccgtgtccccaggacagacagccagcatcacctgctctggagatagattgacgaataaatatgtttcctggtatcaacagaagccaggccagtcccctgtgttggtcatctatgaggatgccaagcggccctcagggatccctgcgcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctatggatgagtctgaatattactgtcaggcgtgggacagcagtgtggtggtttttggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggatttacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagtataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagatgaggacacggccttgtattactgtgcaaaagaccgaggggggggagttatcgttaaggatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 853]
Amino Acid Sequence
SYVLTQPPSVSVSPGQTASITCSGDRLTNKYVSWYQQKPGQSPVLVIYEDAKRPSGIPARFSGSNSGNTATLTISGTQAMDESEYYCQAWDSSVVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTALYYCAKDRGGGVIVKDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 854]

Table 208

ET200-106

DNA Sequence
tcctatgagctgactcagccacccgcagcgtctgggacccccggacagagagtcaccatctcttgttctgggggcgtctccaacatcgggagtggtgctctaaattggtaccagcaactcccaggaacggcccccaaactcctcatctatagttacaatcagcggccctcaggggtctctgaccgattctctggctccaggtctgccacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcaacctgggatgatagtgtgaatggttgggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctggagctgaggtgaagaagcctggggattcagtgaaggtctcctgcaagccttctggttacaattttctcaactatggtatcaactgggtgcgacaggcccctggacaagggcttgagtggatgggatggattagcacttacaccggtaacacaaactatgcacagaagctgcagggcagagtcaccttcaccacagacacatccacgagcacagcctacatggagatgaggagcctgagatctgacgacacggccgtgtattactgtgcgcgccagcagggtggtggttggtacgatgtttggggtcaaggtactctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 855]
Amino Acid Sequence
SYELTQPPAASGTPGQRVTISCSGGVSNIGSGALNWYQQLPGTAPKLLIYSYNQRPSGVSDRFSGSRSATSASLAISGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGAEVKKPGDSVKVSCKPSGYNFLNYGINWVRQAPGQGLEWMGWISTYTGNTNYAQKLQGRVTFTTDTSTSTAYMEMRSLRSDDTAVYYCARQQGGGWYDVWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 856]

Table 209

ET200-107
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggagagaaggtcaccatctcctgctctggaagcaacttcaatgttggaaataatgatgtatcctggtatcagcaactcccaggtgcagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctggacatcaccgggctccacagtgacgacgaggccgattattactgcggaacatgggatagcagcctgaatactgggggggtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatactatcagctgggtacgacaggcccctggacaagggcttgagtggatgggatggatcagcacttacaatggtctcacaaactatgcacagaacctccagggcagagtcaccatgactacagacacattcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattactgtgtgagagaggggtcccccgactacggtgacttcgcgtccttt

gactactggggccagggaaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 857]
Amino Acid Sequence
QSVVTQPPSVSAAPGEKVTISCSGSNFNVGNNDVSWYQQLPGAAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLDITGLHSDDEADYYCGTWDSSLNTGGVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYTISWVRQAPGQGLEWMGWISTYNGLTNYAQNLQGRVTMTTDTFTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFASFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 858]

Table 210

ET200-108
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctgcgcccccgggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagttcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggatttctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcgccggactccagactggggacgaggccgattattactgcggaacatgggataccagcctgagtggtttttatgtcttcggaagtgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatactatcagctgggtacgacaggcccctggacaagggcttgagtggatgggatggatcagcacttacaatggtctcacaaactatgcacagaacctccagggcagagtcaccatgactacagacacattcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattactgtgtgagagaggggtcccccgactacggtgacttcgcgtcctttgactactggggccagggaaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 859]
Amino Acid Sequence
QSVLTQPPSVSAPPGQKVTISCSGSSSNIGNNYVSWYQQFPGTAPKLLIYDNNKRPSGISDRFSGSKSGTSATLGIAGLQTGDEADYYCGTWDTSLSGFYVFGSGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYTISWVRQAPGQGLEWMGWISTYNGLTNYAQNLQGRVTMTTDTFTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFASFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 860]

Table 211

ET200-109
DNA Sequence
ctgcctgtgctgactcagccaccctcagcgtctgcgacccccgggcagagggtcaccatctcttgttctggaaccacctccaacatcggaagtaatactgtacactggtaccagcagctcccagggacggcccccaaactcctcatctataataataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctacatattcctgtgcaacatgggatgacagcctgagtggtgtggtcttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagatcccgcctacggtgactacgagtatgatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 861]
Amino Acid Sequence
LPVLTQPPSASATPGQRVTISCSGTTSNIGSNTVHWYQQLPGTAPKLLIYNNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEATYSCATWDDSLSGVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPAYGDYEYDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 862]

Table 212

ET200-110
DNA Sequence
cagtctgtgttgacgcagccgccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaactaatggtgtaaactggttccagcagttcccaggaacggcccccaaactcctcatctatactaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgcggatgaggctgattattactgtgcagtgtgggaccacagcctgaatggtccggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggta

cagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagaggggccggttttgatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 863]
Amino Acid Sequence
QSVLTQPPSASGTPGQRVTISCSGSSSNIGTNGVNWFQQFPGTAPKLLIYTNDQRPSGVPDRFSGSKSGTSASLAISGLQSADEADYYCAVWDHSLNGPVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGAGFDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 864]

Table 213

ET200-111
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgagactgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagaggggctagatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 865]
Amino Acid Sequence
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDETDYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLDAFDIWGQGTMVTVSSTSGQAGQHHHHHH

GAYPYDVPDYAS [SEQ ID NO: 866]

Table 214

ET200-112
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatgtatagtaatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattattgtgcagcatgggatgacagcctgaatggttatgtcttcgcagctgggacccagctcaccgttttaagttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagaggggctagatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 867]
Amino Acid Sequence
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLMYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFAAGTQLTVLSSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 868]

Table 215

ET200-113
DNA Sequence
cagtctgtcgtgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtaccagcagctcccaggaacagcccccaaactcctcatttatgacaataataagcgaccctcagggattcctgaccgattctctggctccaagtctggcacgtcagccaccctgggcatcactggactccagactggggacgaggccgattattactgcggaacatgggatagcagcctgagtgctgcttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtc

cagctggtacagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacagctttaccagctatactatcagctgggttcgacaggcccctggacaaggccttgagtggatgggatgggtcagcacttacaatggtctcagaaactatgcacagaacctccagggcagagtcaccatgactacagacacactcacgaccacagcctacatggagctgaggagcctcagatctgacgacacggccgtgtattattgtgtgagagaggggtcccccgactacggtgacttcgcggcctttgactactggggccagggcaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 869]
<u>Amino Acid Sequence</u>
QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAAYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYSFTSYTISWVRQAPGQGLEWMGWVSTYNGLRNYAQNLQGRVTMTTDTLTTTAYMELRSLRSDDTAVYYCVREGSPDYGDFAAFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 870]

Table 216

ET200-114
<u>DNA Sequence</u>
caggctgtgctgactcagccaccctcagcgtctgagacccccgggcagagggtcaccatctcttgttctggaagcaggtccaacatcggaactaatattgtacactggtaccagcagcgcccaggaatggcccccaaactcctcacttatggtagtcggcggccctcaggggtcccggaccgattctctggctccaagtttggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattattgtgcagcatgggatgacagtctgaatggtccggctttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctacagcagtggggcgcaggactgttgaagccttcggagaccctgtccctcacctgcgctgtctatggtgggtccttcagtggttactactggagctggatccgccagcccccagggaaggggctggagtggattggggaaatcaatcatagtggaagcaccaactacaacccgtccctcaagagtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcggacacggctgtgtattactgtgcgagagacggtgggggctactttgactactggggccagggaaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 871]
<u>Amino Acid Sequence</u>
QAVLTQPPSASETPGQRVTISCSGSRSNIGTNIVHWYQQRPGMAPKLLTYGSRRPSGVPDRFSGSKFGTSASLAISGLQSEDEADYYCAAWDDSLNGPAFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQWGAGLLKPSETLSLTCAVY

GGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGYFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 872]

Table 217

ET200-115
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccatctcctgcactgggagcagctccaatatcggggcacgttatgatgtacactggtaccagcaactcccaggaacagcccccgactcctcatctctgctaactacgatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcactgggctccaggctgaggatgaggctgattattactgccagtcctatgacagcagtgtgagtgcttgggtgttcggcggagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctggggctgaagtgaaggagcctggggcctcagtgaggatctcctgccaggcatctggatacaacttcatcagttattatatgcactgggtgcggcaggcccctgggcaaggtcttgagtggatgggcaccatcaacccaggcagtggtgagacagactactcacagaagttgcagggcagagtcaccatgaccagggacccgtccacgggtacattcgacatggggctgagcagcctgacatctggggacacggccgtctattattgtgcgacaggtctcatcagaggagctagcgatgcttttaatatctggggccgggggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 873]
Amino Acid Sequence
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGARYDVHWYQQLPGTAPRLLISANYDRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSVSAWVFGGGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKEPGASVRISCQASGYNFISYYMHWVRQAPGQGLEWMGTINPGSGETDYSQKLQGRVTMTRDPSTGTFDMGLSSLTSGDTAVYYCATGLIRGASDAFNIWGRGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 874]

Table 218

ET200-116
DNA Sequence
cagcctgtgctgactcagccaccctcagtgtccgtgtccccaggacagacggccgccatcccctgttctggagataagttgggggataaatttgcttcctggtatcagcagaagccaggccagtcccctgtgctggtcatctatcaagatactaagcggccctcagggatccctgagcgattctctggctccaactctgggaacacagccactctgaccatcagcgggacccaggctatggat

gaggctgactattactgtcagacgtgggccagcggcattgtggtgttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtacagctgcagcagtcaggtccaggactggtgaagccctcgcagaccctctcactcacctgtgccatctccggggacagtgtctctagcaacagtgctgcttggaactggatcaggcagtccccatcgagaggccttgagtggctgggaaggacatactacaggtccaagtggtataatgattatgcagtatctgtgaaaagtcgaataaccatcaacccagacacatccaagaaccagttctccctgcagctgaactctgtgactcccgaggacacggctgtgtattactgtgcaagagagcgcagtggctggaagggatttgactactggggccagggaaccctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 875]
Amino Acid Sequence
QPVLTQPPSVSVSPGQTAAIPCSGDKLGDKFASWYQQKPGQSPVLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQTWASGIVVFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARERSGWKGFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 876]

Table 219

ET200-117
DNA Sequence
gatgttgtgatgactcagtctccaccctccctgtccgtcacccctggagagccggcctccatcacctgcaggtctagtcagagcctcctggaaagaaatgcatacaactacttggattggtacctgcagaggccaggacagtctccacagctcctgatctacttgggttctaatcgggccgccggggtccctgacaggttcagtggcagtggatcaggcagagattttacactgaaaatcagcagagtggagcctgaggatgttggggtttattactgcatgcaagctctacaagctccgttcactttcggcggagggaccaaggtggagatcaaacgttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcagctattagtggtagtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacacggccgtatattactgtgcgaaatggggcccgtttcaggatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 877]
Amino Acid Sequence
DVVMTQSPPSLSVTPGEPASITCRSSQSLLERNAYNYLDWYLQRPGQSPQLLI

YLGSNRAAGVPDRFSGSGSGRDFTLKISRVEPEDVGVYYCMQALQAPFTFGGGTKVEIKRSRGGGGSGGGGSGGGGSLEMAEVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKWGPFQDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 878]

Table 220

ET200-118
DNA Sequence
caggctgtgctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacagcacccgggcaaagcccccaaactcatgatttatgaggtcagtaatcggccctcaggggtttctaatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccaggctgaggacgaggctgattattactgcagctcatatacaagcagcagcacccccttatgtcttcggagcagggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttgtattactgtgcaaaagccaggtggacagcagtggcatcagaccaccactttgactactggggccagggaacgctggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 879]
Amino Acid Sequence
QAVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTPYVFGAGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKARWTAVASDHHFDYWGQGTLVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 880]

Table 221

ET200-119
DNA Sequence
caggctgtgcttactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctcc

aacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtgcagtctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaaggcttctggaggcaccttcagcagctatgctatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggagggatcatccctatctttggtacagcaaactacgcacagaagttccagggcagagtcacgattaccgcggacgaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcgagagattgggactacatggacgtctggggcaaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO:881]
<u>Amino Acid Sequence</u>
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDWDYMDVWGKGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 882]

Table 222

ET200-120
<u>DNA Sequence</u>
tcctatgagctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtgcagctggtggagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagacctatctcggggagctaacccgcattactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 883]

Amino Acid Sequence
SYELTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLSRGANPHYYYYYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 884]

Table 223

ET200-121
DNA Sequence
cagtctgtgttgacgcagccgccctcagtgtctggggccccagggcagagggtcaccgtctcctgcactgggagcagatccaacatcggggcaggatatgatgtacactggtaccagcaacttccaggaacagcccccaaactcctcatctatggaaatagtaatcggcctccaggggtccctgaccgattctctgggtctaagtctggcacctcagcctccctggtcatcactgggctccaggctgaggatgccgctgattattactgccagtcctatgacaacactgtgcgtgaatcaccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggtttccggatacaccctcactgaattatccatgcactgggtgcgacaggctcctggaaaagggcttgagtggatgggaggttttgatcctgaagatggtgaaacaatctacgcacagaagttccagggcagagtcaccatgaccgaggacacatctacagacacagcctacatggagctgagcagcctgagatctgaggacacggccgtgtattactgtgcaacagagagtaatttagtgtcccggcactactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 885]
Amino Acid Sequence
QSVLTQPPSVSGAPGQRVTVSCTGSRSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPPGVPDRFSGSKSGTSASLVITGLQAEDAADYYCQSYDNTVRESPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATESNLVSRHYYYYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 886]

Table 224

ET200-122

DNA Sequence
ctgcctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaaccagctccaacatcggaagtaattctgtagactggtaccagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgaatctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaagtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaaccctaacagtggtggcacaaactatgcacagaagtttcagggcagggtcaccatgaccagggacacgtccatcagcacagcctacatggagctgagcaggctgagatctgacgacacggccgtgtattactgtgcgagagattacggatactatggttcggggagttattcgagcggccccctttactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 887]
Amino Acid Sequence
LPVLTQPPSASGTPGQRVTISCSGTSSNIGSNSVDWYQQLPGTAPKLLIYSNNQRPSGVPDRISGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDYGYYGSGSYSSGPLYYYYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 888]

Table 225

ET200-123
DNA Sequence
caggctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaacatcggaagtaatactgtaaactggtaccagcagctcccaggaacggcccccaaactcctcatgtataataatgatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccagtctgaggatgaggctgattattactgtgcagcatgggatgacagcctcaatggttatgtcttcggacctgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtggagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagacctatctcggggagctaacccgcattactactact

actacggtatggacgtctggggccaagggaccacggtcaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 889]
Amino Acid Sequence
QAVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLMYNNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGPGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLSRGANPHYYYYYGMDVWGQGTTVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 890]

Table 226

ET200-125
DNA Sequence
aattttatgctgactcagccccacgctgtgtcggagtctccggggaagacggtaaccatctcctgcacccgcagcagtggcagtattgccagcaactatgtgcagtggtaccagcagcgcccgggcagttcccccgcactgtgatttatgaggataatcaaagaccctctggggtccctggtcggttctctggctccatcgacagctcctccaactctgcctccctcaccatctctggactgaagactgaggacgaggctgactactactgtcagtcttatgattccaccagtgtgcttttcggcggagggaccaagctgaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggccgaggtccagctggtgcagtctggggctgaggtgaagaagccagggtcctcggtgaaggtctcctgcaaggcctcgggaggcaccttcagcagcaattctctcagctgggtgcgacaggcccctggacaagggcttgagtggatgggaaggatcttccctatcctgggtataacaaactatgcacagaagttccagggcagagtcacgattaccgcggacaaatccacgagcacagcctacatggagctgagcagcctgagatctgaggacacggccgtctattactgtgcgagaggaaactaccaatggtatgatgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 891]
Amino Acid Sequence
NFMLTQPHAVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPRTVIYEDNQRPSGVPGRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSTSVLFGGGTKLTVLGSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSNSLSWVRQAPGQGLEWMGRIFPILGITNYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGNYQWYDAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 892]

Table 227

ET200-005
DNA Sequence
cagcctgtgctgactcagccaccctcagtgtcagtggtcccaggaaagacggccaggattacctgtgggggaaaaacattggaagtaaaagtgtgcactggtaccagcagaagccaggccaggcccctgtggtggtcatccattatgatagtgaccggccctcagggatccctgagcgattctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaggtgtgggatagtagtagtgatcatccttatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccaactatggtatcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttacaatggtaacacaaactatgcacataagctccagggcagagtcaccatgaccacagacacatccacgagcacagccaacatggagctgaggagcctgagacctgacgacactgccgtgtattactgtgcgcgctcttacttcggttctcatgattactggggtcaaggtactctggtgaccgtctcctcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 893]
Amino Acid Sequence
QPVLTQPPSVSVVPGKTARITCGGKNIGSKSVHWYQQKPGQAPVVVIHYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHPYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQAPGQGLEWMGWISAYNGNTNYAHKLQGRVTMTTDTSTSTANMELRSLRPDDTAVYYCARSYFGSHDYWGQGTLVTVSSTSGQAGQHHHHHGAYPYDVPDYAS [SEQ ID NO: 894]

Table 228

ET200-124
DNA Sequence
tcctatgtgctgactcagccaccctcggtgtcagtggccccaggaaagacggccaggatttcctgtgggggaaacgacattggaagtaaaagtgttttctggtatcagcagaggccaggccaggcccctgtgttggtcgtctatgatgatagcgaccggccctcagggctccctgagcgattctctggcttcaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggatgaggccgactattactgtcaagtgtgggatagtagtagtgatcattatgtcttcggaactgggaccaaggtcaccgtcctaggttctagaggtggtggtggtagcggcggcggcggctctggtggtggtggatccctcgagatggcccaggtgcagctggtggagtctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgcagcctctggattcacctttgatgattatgccatgcactgggtccggcaagctccagggaagggcctggagtgggtctcaggtattagttggaatagtggtagcataggctatgcggactctgtgaagggccgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctga

gagctgaggacacggccttgtattactgtgcaaaagatataacctatggttcggggagttatggtgcttttgatatctggggccaagggacaatggtcaccgtctcttcaactagtggccaggccggccagcaccatcaccatcaccatggcgcatacccgtacgacgttccggactacgcttct [SEQ ID NO: 895]
<u>Amino Acid Sequence</u>
SYVLTQPPSVSVAPGKTARISCGGNDIGSKSVFWYQQRPGQAPVLVVYDDSDRPSGLPERFSGFNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLGSRGGGGSGGGGSGGGGSLEMAQVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDITYGSGSYGAFDIWGQGTMVTVSSTSGQAGQHHHHHHGAYPYDVPDYAS [SEQ ID NO: 896]

XIII. *CDR sequences of exemplary extracellular antigen-binding domains (e.g., scFvs)*

Table 229

Antibody	V_HCDR1	V_HCDR2	V_HCDR3	V_LCDR1	V_LCDR2	V_LCDR3
ET200-001	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	AREGPYDGFDS [SEQ ID NO: 311]	SSNIGSNT [SEQ ID NO: 312]	SNN [SEQ ID NO: 313]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-002	GYPFNKYD [SEQ ID NO: 315]	IIPIFRTT [SEQ ID NO: 316]	AREWFYWDI [SEQ ID NO: 317]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNSVV [SEQ ID NO: 320]
ET200-003	GFTFSSYG [SEQ ID NO: 321]	ISHDGSNK [SEQ ID NO: 322]	ARSNQWSGYFSFDY [SEQ ID NO: 323]	KLGTKY [SEQ ID NO: 324]	EDN [SEQ ID NO: 319]	QAWDSDTFVV [SEQ ID NO: 325]
ET200-005	GYTFTNYG [SEQ ID NO: 326]	ISAYNGNT [SEQ ID NO: 327]	ARSYFGSHDY [SEQ ID NO: 328]	NIGSKS [SEQ ID NO: 329]	YDS [SEQ ID NO: 330]	QVWDSSSDHPYV [SEQ ID NO: 331]
ET200-006	GYTFTTYG [SEQ ID NO: 332]	INTYNGHT [SEQ ID NO: 333]	ARVIYGSGDY [SEQ ID NO: 334]	NIGSKS [SEQ ID NO: 329]	YDS [SEQ ID NO: 330]	QVWDSSSDHPYV [SEQ ID NO: 331]
ET200-007	GYSISSGYF [SEQ ID NO: 335]	IYHSAST [SEQ ID NO: 336]	ARGYGYFDY [SEQ ID NO: 337]	NIGSKT [SEQ ID NO: 338]	YDS [SEQ ID NO: 330]	QVWDSSSDHRV [SEQ ID NO: 339]
ET200-008	GFTFGDYG [SEQ ID NO: 340]	INWNGGST [SEQ ID NO: 341]	ARSKYNFHVYYDY [SEQ ID NO: 342]	SSDVGGYNY [SEQ ID NO: 343]	DVS [SEQ ID NO: 344]	SSYTSSSTSKV [SEQ ID NO: 345]
ET200-009	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARSSGNMVSWFDM [SEQ ID NO: 347]	NSNIGSNY [SEQ ID NO: 348]	RNN [SEQ ID NO: 349]	AAWDDSLSAYV [SEQ ID NO: 350]
ET200-010	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARGAVAYHD [SEQ ID NO: 351]	SSDVGGYNS [SEQ ID NO: 352]	DVS [SEQ ID NO: 344]	SSYTSSSTPLV [SEQ ID NO: 353]
ET200-011	GGTLSSYA [SEQ ID NO: 354]	IIPMFGTA [SEQ ID NO: 355]	ARGVHYASFDH [SEQ ID NO: 356]	SSNISIYD [SEQ ID NO: 357]	SNN [SEQ ID NO: 358]	GTWDDSLSGGV [SEQ ID NO: 359]
ET200-012	GFPFNIFG [SEQ ID NO: 360]	ISGYNGNT [SEQ ID NO: 361]	ARGAYGGMDT [SEQ ID NO: 362]	DSNIGNNY [SEQ ID NO: 363]	DVK [SEQ ID NO: 364]	GTWDSRLDAYV [SEQ ID NO: 365]
ET200-013	GYMFTSYG [SEQ ID NO: 366]	ISANNGKT [SEQ ID NO: 367]	ARHIGGSYFDR [SEQ ID NO: 368]	TSNIGAGYD [SEQ ID NO: 369]	TNN [SEQ ID NO: 370]	GTWDSSLSAVV [SEQ ID NO: 371]
ET200-014	GFTFSSYA [SEQ ID NO: 372]	ISGSDGST [SEQ ID NO: 373]	ARSHEANLVGDW [SEQ ID NO: 374]	NIGSKS [SEQ ID NO: 329]	YDS [SEQ ID NO: 330]	QVWDSSSDHYV [SEQ ID NO: 375]
ET200-015	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARWGGFGAVDH [SEQ ID NO: 376]	NIGSKS [SEQ ID NO: 329]	YDS [SEQ ID NO: 330]	QVWDSSSDVV [SEQ ID NO: 377]
ET200-016	GFTFSSYS [SEQ ID NO: 378]	ISSSSSYI [SEQ ID NO: 379]	ARGQGYDY [SEQ ID NO: 380]	SLTSYH [SEQ ID NO: 381]	ATN [SEQ ID NO: 382]	NSRDSGTDEVL [SEQ ID NO: 383]
ET200-017	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	ARYYFGMDM [SEQ ID NO: 384]	NIGSKS [SEQ ID NO: 329]	DDS [SEQ ID NO: 385]	QVWDSSSDHTV [SEQ ID NO: 386]

Antibody	V_HCDR1	V_HCDR2	V_HCDR3	V_LCDR1	V_LCDR2	V_LCDR3
ET200-018	GYTLNELS [SEQ ID NO: 387]	FDPEDGET [SEQ ID NO: 388]	ARGGYGDS [SEQ ID NO: 389]	SSNIGRNG [SEQ ID NO: 390]	NDN [SEQ ID NO: 391]	AAWDDSLHGVV [SEQ ID NO: 392]
ET200-019	GGTFSSDA [SEQ ID NO: 393]	IIPMFGTA [SEQ ID NO: 355]	AREGYYYPSAYLGSVLNDIS SVYDE [SEQ ID NO: 394]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNSWV [SEQ ID NO: 395]
ET200-020	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARSMTSFDY [SEQ ID NO: 396]	TSNIGNND [SEQ ID NO: 397]	DNN [SEQ ID NO: 398]	GTWDSSVSAS [SEQ ID NO: 399]
ET200-021	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARSVYDLDT [SEQ ID NO: 400]	NSNIGNNY [SEQ ID NO: 401]	DNN [SEQ ID NO: 398]	GTWNTTVTPGYV [SEQ ID NO: 402]
ET200-022	GFTFDDYA [SEQ ID NO: 403]	ISWNSGSI [SEQ ID NO: 404]	ARYRQVGSAYDS [SEQ ID NO: 405]	SSNIGNNY [SEQ ID NO: 406]	DNN [SEQ ID NO: 398]	GTWDSSLGAPYV [SEQ ID NO: 407]
ET200-023	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARYWGFGVSDR [SEQ ID NO: 408]	NIGSKS [SEQ ID NO: 329]	ADS [SEQ ID NO: 409]	QVWDSSSYHNYV [SEQ ID NO: 410]
ET200-024	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARYNYYYYDS [SEQ ID NO: 413]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNLWV [SEQ ID NO: 414]
ET200-025	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARYWGYDSYDE [SEQ ID NO: 415]	QSISSY [SEQ ID NO: 416]	AAS [SEQ ID NO: 417]	QQSYSTPFT [SEQ ID NO: 418]
ET200-026	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARNNHYYNDY [SEQ ID NO: 349]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNWV [SEQ ID NO: 419]
ET200-027	GYTFTDYY [SEQ ID NO: 420]	VDPEDGET [SEQ ID NO: 421]	ARYWSYSFDYLYMPEGNDW [SEQ ID NO: 422]	SSNIGAGYD [SEQ ID NO: 423]	GNN [SEQ ID NO: 358]	QSYDSSLSDVV [SEQ ID NO: 424]
ET200-028	GYNFLNYG [SEQ ID NO: 425]	ISTYTGNT [SEQ ID NO: 426]	ARDLYYYEGVDY [SEQ ID NO: 427]	VSNIGSGA [SEQ ID NO: 428]	SYN [SEQ ID NO: 429]	ATWDDSVNG [SEQ ID NO: 430]
ET200-029	GFTFSSYA [SEQ ID NO: 372]	ISYDGSNK [SEQ ID NO: 431]	ARSYFTSGFYDY [SEQ ID NO: 432]	NIGSES [SEQ ID NO: 433]	YDT [SEQ ID NO: 434]	QVWDSSRDHVV [SEQ ID NO: 435]
ET200-030	GYTLTELS [SEQ ID NO: 436]	FDPEDGET [SEQ ID NO: 388]	ARMSSMYYD [SEQ ID NO: 437]	SSNIGAGYD [SEQ ID NO: 423]	GNS [SEQ ID NO: 438]	QSYDSSLSGSYV [SEQ ID NO: 439]
ET200-031	GFTVSDYY [SEQ ID NO: 440]	ISGSGNSI [SEQ ID NO: 441]	ARSTKFDY [SEQ ID NO: 442]	NIGSKS [SEQ ID NO: 329]	YDS [SEQ ID NO: 330]	QVWDSSSDYV [SEQ ID NO: 443]
ET200-032	GYSFTNYW [SEQ ID NO: 444]	IYPGDSDT [SEQ ID NO: 445]	ARSTGSSHMSDE [SEQ ID NO: 446]	SSNVGSYT [SEQ ID NO: 447]	NNN [SEQ ID NO: 448]	AAWDDRLGGYV [SEQ ID NO: 449]
ET200-033	GGSFSGYY [SEQ ID NO: 309]	ITHSGRS [SEQ ID NO: 450]	ARSSIMSDY [SEQ ID NO: 451]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNHWV [SEQ ID NO: 452]

Antibody	V_HCDR1	V_HCDR2	V_HCDR3	V_LCDR1	V_LCDR2	V_LCDR3
ET200-034	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARGSALDHYDR [SEQ ID NO: 453]	TSNIGAGYD [SEQ ID NO: 369]	NNR [SEQ ID NO: 454]	GTWDGSLTGAV [SEQ ID NO: 455]
ET200-035	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARYNYYFNDY [SEQ ID NO: 456]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSTNWV [SEQ ID NO: 457]
ET200-037	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARSMFGAHDS [SEQ ID NO: 458]	NIGSKS [SEQ ID NO: 329]	YDS [SEQ ID NO: 330]	QVWDSSSDHPYV [SEQ ID NO: 331]
ET200-038	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARGASFDRHDN [SEQ ID NO: 459]	SSNIGAGFD [SEQ ID NO: 460]	ANS [SEQ ID NO: 461]	QSYDSSLSGVV [SEQ ID NO: 462]
ET200-039	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARSNYYYNDY [SEQ ID NO: 463]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNWV [SEQ ID NO: 419]
ET200-040	GYTLTELS [SEQ ID NO: 436]	FDPEDGET [SEQ ID NO: 388]	ARYSGVYYD [SEQ ID NO: 464]	SSNIGAGYD [SEQ ID NO: 423]	GNS [SEQ ID NO: 430]	QSYDSSLSGYV [SEQ ID NO: 465]
ET200-041	GGTFSSYA [SEQ ID NO: 411]	MNPNSGNT [SEQ ID NO: 466]	ARYYSYGYD [SEQ ID NO: 467]	SGSIADNF [SEQ ID NO: 468]	NDD [SEQ ID NO: 469]	QSYDNNNRGV [SEQ ID NO: 470]
ET200-042	GDSVSTNSVA [SEQ ID NO: 471]	TYYRSKWSN [SEQ ID NO: 472]	ARSSSWYQIFDY [SEQ ID NO: 473]	SSNIGTGYF [SEQ ID NO: 474]	GNN [SEQ ID NO: 358]	QSYDSSLSGYV [SEQ ID NO: 465]
ET200-043	GFTFSSYA [SEQ ID NO: 372]	ISGSGGST [SEQ ID NO: 475]	ARSGAYWDYSVYDE [SEQ ID NO: 476]	SDSIANNY [SEQ ID NO: 477]	EDV [SEQ ID NO: 478]	QSYHSDNRWV [SEQ ID NO: 479]
ET200-044	GGSISSSNW [SEQ ID NO: 480]	IYHSGSP [SEQ ID NO: 481]	ARMTTHTFGYDA [SEQ ID NO: 482]	KLGDKY [SEQ ID NO: 483]	QDN [SEQ ID NO: 484]	QAWDSSTYVA [SEQ ID NO: 485]
ET200-045	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARGVHLDW [SEQ ID NO: 486]	NIGSES [SEQ ID NO: 433]	DDA [SEQ ID NO: 487]	QVWDRNSAQFV [SEQ ID NO: 488]
ET200-069	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	ARLYEGGYHGWGSWLSSDG [SEQ ID NO: 489]	SSNIGSNY [SEQ ID NO: 490]	SNN [SEQ ID NO: 313]	AAWDDSLSGYV [SEQ ID NO: 491]
ET200-078	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	AREGAFDAFDI [SEQ ID NO: 492]	SSNIGSNT [SEQ ID NO: 312]	SNN [SEQ ID NO: 313]	AAWDDSLNGY [SEQ ID NO: 493]
ET200-079	GFTFDDYA [SEQ ID NO: 403]	ISWNSGSI [SEQ ID NO: 404]	ANGDSNYYYGMDV [SEQ ID NO: 494]	SSNIGSNY [SEQ ID NO: 490]	RNN [SEQ ID NO: 349]	AAWDDSLSGYL [SEQ ID NO: 495]
ET200-081	GFTFDDYA [SEQ ID NO: 403]	ISGDGGST [SEQ ID NO: 496]	AKDRAAAGYYYYGMDV [SEQ ID NO: 497]	SSDIGGYNY [SEQ ID NO: 498]	DVS [SEQ ID NO: 344]	ISYTRTWNPYV [SEQ ID NO: 499]
ET200-097	GFTFNDYA [SEQ ID NO: 500]	ISWSGNNI [SEQ ID NO: 501]	AKDSIRYGITWGGFDY [SEQ ID NO: 502]	KLGEKY [SEQ ID NO: 503]	QDT [SEQ ID NO: 504]	QAWDRGVV [SEQ ID NO: 505]

Antibody	V_HCDR1	V_HCDR2	V_HCDR3	V_LCDR1	V_LCDR2	V_LCDR3
ET200-098	GFTFDDYA [SEQ ID NO: 403]	INWDGGST [SEQ ID NO: 506]	AKGMGLRAFDY [SEQ ID NO: 507]	SNNVGNLG [SEQ ID NO: 508]	RNN [SEQ ID NO: 349]	SAWDSSLSA [SEQ ID NO: 509]
ET200-099	GYTFSWYA [SEQ ID NO: 510]	INAGNGNT [SEQ ID NO: 511]	ARPDNYGSGGDVFDI [SEQ ID NO: 512]	SSNIGSNT [SEQ ID NO: 312]	SND [SEQ ID NO: 513]	ASWDDSLNGRYV [SEQ ID NO: 514]
ET200-100	GFTFSSYE [SEQ ID NO: 515]	ISSSGSTI [SEQ ID NO: 516]	ARWDYGMDV [SEQ ID NO: 517]	SGSIASNF [SEQ ID NO: 518]	EDN [SEQ ID NO: 319]	QSYDTSNVV [SEQ ID NO: 519]
ET200-101	GYTFTWYA [SEQ ID NO: 520]	INAGSGNT [SEQ ID NO: 521]	ARPNNYGSGGDVFDI [SEQ ID NO: 522]	NSNIGSNY [SEQ ID NO: 348]	SSS [SEQ ID NO: 523]	ATWDDSLNA [SEQ ID NO: 524]
ET200-102	GYTFTNYA [SEQ ID NO: 525]	INGGNGNT [SEQ ID NO: 526]	AKPEETAGTIHFDY [SEQ ID NO: 527]	SSNIGNNY [SEQ ID NO: 406]	DNN [SEQ ID NO: 398]	GTWDSSLSAYV [SEQ ID NO: 528]
ET200-103	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	AGEGYYDSSGYSNGDAFDI [SEQ ID NO: 529]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSTTTV [SEQ ID NO: 530]
ET200-104	GFTFSSYE [SEQ ID NO: 515]	ISSSGSTI [SEQ ID NO: 516]	ARWDYGMDV [SEQ ID NO: 517]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSSNVV [SEQ ID NO: 531]
ET200-105	GFTFDDYA [SEQ ID NO: 403]	ISWNSGSI [SEQ ID NO: 404]	AKDRGGGVIVKDAFDI [SEQ ID NO: 532]	RLTNKY [SEQ ID NO: 533]	EDA [SEQ ID NO: 534]	QAWDSSVVV [SEQ ID NO: 535]
ET200-106	GYNFLNYG [SEQ ID NO: 425]	ISTYTGNT [SEQ ID NO: 426]	ARQQGGGWYDV [SEQ ID NO: 536]	VSNIGSGA [SEQ ID NO: 428]	SYN [SEQ ID NO: 429]	ATWDDSVNG [SEQ ID NO: 430]
ET200-107	GYTFTSYT [SEQ ID NO: 537]	ISTYNGLT [SEQ ID NO: 538]	VREGSPDYGDFASFDY [SEQ ID NO: 539]	NFNVGNND [SEQ ID NO: 540]	DNN [SEQ ID NO: 398]	GTWDSSLNTGGV [SEQ ID NO: 541]
ET200-108	GYTFTSYT [SEQ ID NO: 537]	ISTYNGLT [SEQ ID NO: 538]	VREGSPDYGDFASFDY [SEQ ID NO: 539]	SSNIGNNY [SEQ ID NO: 406]	DNN [SEQ ID NO: 398]	GTWDTSLSGFYV [SEQ ID NO: 542]
ET200-109	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARDPAYGDYEYDAFDI [SEQ ID NO: 543]	TSNIGSNT [SEQ ID NO: 544]	NNN [SEQ ID NO: 448]	ATWDDSLSGVV [SEQ ID NO: 545]
ET200-110	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARGAGFDAFDI [SEQ ID NO: 546]	SSNIGTNG [SEQ ID NO: 547]	TND [SEQ ID NO: 548]	AVWDHSLNGPV [SEQ ID NO: 549]
ET200-111	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	AREGLDAFDI [SEQ ID NO: 550]	SSNIGSNT [SEQ ID NO: 312]	SNN [SEQ ID NO: 313]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-112	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	AREGLDAFDI [SEQ ID NO: 550]	SSNIGSNT [SEQ ID NO: 312]	SND [SEQ ID NO: 513]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-113	GYSFTSYT [SEQ ID NO: 551]	VSTYNGLR [SEQ ID NO: 552]	VREGSPDYGDFAAFDY [SEQ ID NO: 553]	SSNIGNNY [SEQ ID NO: 406]	DNN [SEQ ID NO: 398]	GTWDSSLSAAYV [SEQ ID NO: 554]

Antibody	V_HCDR1	V_HCDR2	V_HCDR3	V_LCDR1	V_LCDR2	V_LCDR3
ET200-114	GGSFSGYY [SEQ ID NO: 309]	INHSGST [SEQ ID NO: 310]	ARDGGGYFDY [SEQ ID NO: 555]	RSNIGTNI [SEQ ID NO: 556]	GS [SEQ ID NO: 557]	AAWDDSLNGPA [SEQ ID NO: 558]
ET200-115	GYNFISYY [SEQ ID NO: 559]	INPGSGET [SEQ ID NO: 560]	ATGLIRGASDAFNI [SEQ ID NO: 561]	SSNIGARYD [SEQ ID NO: 562]	ANY [SEQ ID NO: 563]	QSYDSSVSAWV [SEQ ID NO: 564]
ET200-116	GDSVSSNSAA [SEQ ID NO: 565]	TYYRSKWYN [SEQ ID NO: 566]	ARERSGWKGFDY [SEQ ID NO: 567]	KLGDKF [SEQ ID NO: 568]	QDT [SEQ ID NO: 504]	QTWASGIVV [SEQ ID NO: 569]
ET200-117	GFTFSSYA [SEQ ID NO: 372]	ISGSGGST [SEQ ID NO: 475]	AKWGPFQDAFDI [SEQ ID NO: 570]	QSLLERNAYNY [SEQ ID NO: 571]	LGS [SEQ ID NO: 572]	MQALQAPFT [SEQ ID NO: 573]
ET200-118	GFTFDDYA [SEQ ID NO: 403]	ISWNSGSI [SEQ ID NO: 404]	AKARWTAVASDHHFDY [SEQ ID NO: 574]	SSDVGGYNY [SEQ ID NO: 343]	EVS [SEQ ID NO: 575]	SSYTSSSTPYV [SEQ ID NO: 576]
ET200-119	GGTFSSYA [SEQ ID NO: 411]	IIPIFGTA [SEQ ID NO: 412]	ARDWDYMDV [SEQ ID NO: 577]	SSNIGSNT [SEQ ID NO: 312]	SNN [SEQ ID NO: 313]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-120	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARDLSRGANPHYYYYYGMDV [SEQ ID NO: 578]	SSNIGSNT [SEQ ID NO: 312]	SNN [SEQ ID NO: 313]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-121	GYTLTELS [SEQ ID NO: 436]	FDPEDGET [SEQ ID NO: 388]	ATESNLVSRHYYYYGMDV [SEQ ID NO: 579]	RSNIGAGYD [SEQ ID NO: 580]	GNS [SEQ ID NO: 438]	QSYDNTVRESPYV [SEQ ID NO: 581]
ET200-122	GYTFTGYY [SEQ ID NO: 582]	INPNSGGT [SEQ ID NO: 583]	ARDYGYYGSGSYSSGPLYYYYGMDV [SEQ ID NO: 584]	SSNIGSNS [SEQ ID NO: 585]	SNN [SEQ ID NO: 313]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-123	GYTFTSYG [SEQ ID NO: 346]	ISAYNGNT [SEQ ID NO: 327]	ARDLSRGANPHYYYYYGMDV [SEQ ID NO: 578]	SSNIGSNT [SEQ ID NO: 312]	NND [SEQ ID NO: 586]	AAWDDSLNGYV [SEQ ID NO: 314]
ET200-124	GFTFDDYA [SEQ ID NO: 403]	ISWNSGSI [SEQ ID NO: 404]	AKDITYGSGSYGAFDI [SEQ ID NO: 587]	DIGSKS [SEQ ID NO: 588]	DDS [SEQ ID NO: 385]	QVWDSSSDHYV [SEQ ID NO: 375]
ET200-125	GGTFSSNS [SEQ ID NO: 589]	IFPILGIT [SEQ ID NO: 590]	ARGNYQWYDAFDI [SEQ ID NO: 591]	SGSIASNY [SEQ ID NO: 318]	EDN [SEQ ID NO: 319]	QSYDSTSVL [SEQ ID NO: 592]

Table 230

CDR	CDR SEQUENCE	SEQ ID NO
V_HCDR1	IFGLH	SEQ ID NO:923
V_HCDR2	YISGDSNTIYYADTVKG	SEQ ID NO:924
V_HCDR3	NSYYALDY	SEQ ID NO:925
V_LCDR1	RASSSVSSSYLH	SEQ ID NO:926
V_LCDR2	STSNLAS	SEQ ID NO:927
V_LCDR3	QQYSGYPWT	SEQ ID NO:928
V_HCDR1	SFGMH	SEQ ID NO:929
V_HCDR2	YISSGSNNIYFADTVKG	SEQ ID NO:930
V_HCDR3	SEYYGSSHMDY	SEQ ID NO:931
V_LCDR1	KASQNVGTNVA	SEQ ID NO:932
V_LCDR2	SATYRNS	SEQ ID NO:933
V_LCDR3	QQYNRYPYT	SEQ ID NO:934

EXAMPLES

The practice of the present invention employs, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are well within the purview of the skilled artisan. Such techniques are explained fully in the literature, such as, “Molecular Cloning: A Laboratory Manual”, second edition (Sambrook, 1989); “Oligonucleotide Synthesis” (Gait, 1984); “Animal Cell Culture” (Freshney, 1987); “Methods in Enzymology” “Handbook of Experimental Immunology” (Weir, 1996); ”Gene Transfer Vectors for Mammalian Cells” (Miller and Calos, 1987); “Current Protocols in Molecular Biology” (Ausubel, 1987); “PCR: The Polymerase Chain Reaction”, (Mullis, 1994); “Current Protocols in Immunology” (Coligan, 1991). These techniques are applicable to the production of the polynucleotides and polypeptides of the invention, and, as such, may be considered in making and practicing the invention. Particularly useful techniques for particular embodiments will be discussed in the sections that follow.

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the assay, screening, and therapeutic methods of the invention, and are not intended to limit the scope of what the inventors regard as their invention.

Example 1 – FcRL5 Expression in various tissues

The expression of human FcRL5 was assessed and evaluated in various tissues. As shown in Figure 1, human FcRL5 was highly expressed in lymphoma and multiple myeloma, but not in other tissues. Top panel of Figure 1 shows differential expression of human FcRL5 in tumor cell lines from the Cancer Cell Line Encyclopedia (CCLE). The bottom panel of Figure 1 shows differential expression of human FcRL5 in normal tissue from BioGPS. As shown in Figure 1, human FcRL5 expression is limited to MM and lymphoma compared to other malignant cells. Normal expression appeared limited to B-cells and plasma cells. Potential FcRL5 targeted CAR T cell eradication of these normal cell types may not have significant adverse effects based on inventors' patient experience with CD19 targeted CAR T cells. Any lack of physiologic antibody production can be addressed with intravenous immunoglobulin treatment.

Example 2 – Selection of ScFv specific for FcRL5 using a fully human phage display library.

Phage display selection against FcRL5 was conducted using a cell panning strategy with 31 human scFv naïve and semi-synthetic phage sub-libraries. FcRL5 overexpressing 3T3 cells were used in positive panning, FcRL1, 2, 3, 4 and 6 overexpressing 3T3 cells (5 cell lines in total) were used in negative panning (Figure 2). Bound clones were then eluted and used to infect *E. Coli* XL1-Blue. The scFv phage clones expressed in the bacteria were purified as previously described (Yasmina, et al. Probing the binding mechanism and affinity of tanezumab, a recombinant humanized anti-NGF monoclonal antibody, using a repertoire of biosensors. Protein Science 2008, 17(8):1326-1335; Roberts, et al. Vaccination with CD20 peptides induces a biologically active, specific immune response in mice. Blood 2002, 99(10):3748-3755). Panning was performed for about 3 to about 4 cycles to enrich scFv phage clones that bind to FcRL5 specifically. Positive clones were determined by an ELISA method against His-tag FcRL5.

Positive clones were further tested for their binding to FcRL5 on live cell surfaces by flow cytometry, using FcRL5-overexpressing cell lines, 3T3 and Raji. The cells were then washed, and the staining was performed using the following steps: the cells can be first stained with purified scFv phage clones, and followed by staining with a mouse anti-M13 mAb, and finally the horse anti-mouse Ig's conjugate to PE. Each step of the staining was completed between 30-60 minutes on ice and the cells were washed twice between each step of the staining.

76 unique clones that were specific for FcRL5 were identifed and confirmed by screening (*see* Tables 1-229 and Figure 2).

Example 3 – Selection of ScFv specific for domain 9 of FcRL5.

FcRL5 contains 9 extracellular immunoglobulin-like domains (domains 1-9) and can be present within a cell in a soluble isoform, a glycosyl-phosphotidyl inositol (GPI)-anchor type isoform and a transmembrane-type isoform (Figure 3A). As shown in Figure 2A, the transmembrane-type isoform of FcRL5 has domain 9; whereas, the soluble isoform and the GPI-anchor type isoform do not.

To test if the scFvs were specific to domain 9 of FcRL5, the 76 clones were further screened on 3T3 cells overexpressing an vector encoding FcRL5 with a domain 9 deletion (FcRL5Δdom9) and further screened on Raji cells overexpressing full-length FcRL5 (Figure 4B-D). Some clones showed either reduced or diminished binding towards FcRL5-domain 9 deletion-overexpressing 3T3 cells compared to binding towards FcRL5-overexpressing 3T3 cells. Figure 4, 5, 6, 7 and 8 shows the specificity of ET200-39, ET200-104, ET200-105, ET200-109 and ET200-117 for domain 9 of FcRL5, respectively.

Example 4 – Construct of murine FcRL5-specific CARs

For generation of a scFv targeting human FcRL5, two commercially available mouse hybridomas binding different extracellular epitopes on human FcRL5 (Franco (2013); Ise *et al.* (2005); Ise *et al.* (2006)) were obtained. From these hybridomas, two scFvs targeting human FcRL5 were obtained. One scFv was generated by synthesizing the heavy and light chain variable region of murine anti-human FcRL5 antibody F56 as described in Ise *et al.* (2005) with a G4S linker having the amino acid sequence of SEQ ID NO:897. A second scFv was generated by synthesizing the heavy and light chain variable region of murine anti-human FcRL5 antibody F119 as described in Ise *et al.* (2005) with a G4S linker having the amino acid sequence of SEQ ID NO:897.

Two FcRL5 CARs were generated: F56 FcRL5-28z CAR and F119 FcRL5-

28z CAR. F56 FcRL5-28z CAR and F119 FcRL5-28z CAR have similar structure, *e.g.*, each has a transmembrance domain comprising a CD28 polypeptide, and an intracellular domain comprising a CD3ξ polypeptide and a co-stimulatory signaling region that comprises a CD28 polypeptide, as shown in Figure 9A. F56 FcRL5-28z CAR comprises an scFv derived from antibody F56, and F119 FcRL5-28z CAR comprises an scFv derived from antibody F119. Each of F56 FcRL5-28z CAR and F119 FcRL5-28z CAR were cloned into a retroviral vector 293galv9. Human T cells (unselected (CD4 and CD8) human T cells from a healthy donor) were transduced with each of F56 FcRL5-28z CAR and F119 FcRL5-28z CAR such that the T cells expressed F56 FcRL5-28z CAR or F119 FcRL5-28z CAR.

Example 5 – Construct of human FcRL5-specific CARs

This Example discloses the generation of CARs targeting human FcRL5 using the fully human scFvs described herein. ET200-31 scFv, ET200-39 scFv, ET200-69 scFv, ET200-104 scFv, ET200-105 scFv, ET200-109 scFv and ET200-117 scFvs were used to generate second generation FcRL5-targeted CARs designated as 31 FcRL5 BBz CAR, 39 FcRL5 BBz CAR, 69 FcRL5 BBz CAR, 104 FcRL5 BBz CAR, 105 FcRL5 BBz CAR, 109 FcRL5 BBz CAR and 117 FcRL5 BBz CAR with either a 4-1BB co-stimulatory domain and a CD3ξ polypeptide (*see* Figures 9B-16). The FcRL5-targeted 4-1BB containing CARs have a similar structure, *e.g.*, each has a CD8a polypeptide transmembrane domain, and an intracellular domain comprising co-stimulatory signaling region consisting of a CD3ξ polypeptide and a 4-1BB polypeptide, as shown in Figure 9B. Each of these FcRL5-targeted CARs were cloned into an SFG retroviral vector, as an example the 4-1BB containing CAR vectors are shown in Figures 10-16. These viral vectors are then transduced into HEK 293galv9 viral packaging cells in order to generate a stable packaging line for generation of CAR+ T cells.

Example 6 – Expression of human FcRL5-specific CARs in T cells

Human primary T cells were transduced using supernatant from retroviral galv9 HEK 293 packaging cells to express a FcRL5-targeted 4-1BBz CAR (generated using the anti-FcRL5 ET200-104 scFv). The cell surface expression of the FcRL5-targeted CAR was determined by binding to recombinant human FcRL5 which was modified to contain a His tag followed by the binding of a PE conjugated anti-HIS tag secondary antibody, as shown in Figure 17. Cell surface detection was validated by flow cytometry. As shown in Figure 17, the FcRL5-targeted CAR was expressed on the transduced T cells.

Example 7 – Cytotoxicity of human FcRL5-specific CARs

The cytotoxic effects of the FcRL5-targeted 4-1BB CAR T cells were analyzed using Raji (a Burkett's lymphoma cell line) cells transduced to express luciferase and FcRL5 antigen or the control GPRC5D (an irrelevant antigen). T cells expressing the 4-1BB CAR generated using the anti-FcRL5 ET200-69 scFv were used in these experiments (referred to herein as "αFcRL5-69 BBz"). The number of live cells is determined after 36h co-culture by bioluminescent imaging (BLI). As shown in Figure 18, FcRL5-targeted CAR T cells specifically lysed Raji cells transduced to express luciferase and FcRL5 antigen (Figure 18A) but not control GPRC5D expressing Raji cells which are lysed by GPRC5D-targeted CAR T cells (Figure 18B).

Example 8 – Cytokine secretion of human FcRL5-specific CARs

This Example describes the cytokine secretion of FcRL5-targeted CAR T cells. T cells expressing the 4-1BB CAR generated using the anti-FcRL5 ET200-69 scFv were used in these experiments. IL-2, INFγ, and TNFα secretion after 24h co-culture of FcRL5 targeted CAR T cells on a monolayer of 3T3 cells transduced with either FcRL5 or CD19 was assessed by Luminex multiplex analysis. As shown in Figure 19, signaling through the CAR of FcRL5-targeted CAR T cells induced cytokine secretion consistent with T cell activation.

Example 9 – Proliferation of human FcRL5-specific CARs

This Example describes the proliferation of FcRL5-targeted CAR T cells upon antigen stimulation. T cells expressing the 4-1BB CAR generated using the anti-FcRL5 ET200-69 scFv was used in these experiments. 500,000 FcRL5- or CD19-targeted CAR+ T cells/ml were placed on a monolayer of 3T3 cells that have been transduced with either FcRL5 or CD19 (3T3-FcRL; 3T3-CD19). After 4 days, CAR+ T cells were stained and counted by flow cytometry with the inclusion of a known concentration of counting microbeads. As shown in Figure 20, antigen stimulation of FcRL5-targeted CAR T cells induced proliferation. FcRL5-targeted CAR T cells co-cultured with 3T3-FcRL5 cells expanded to be 2.9 times greater then FcRL5-targeted CAR T cells co-cultured with 3T3-CD19 cells, while control CD19 targeted CAR T cells co-cultured with 3T3-CD19 cells similarly expanded to be 2.5 fold greater then CD19 targeted CAR T cells co-cultured with 3T3-FcRL5 cells (Figure 20).

Example 10 – Epitope mapping of human anti-FcRL5 antibodies

Two anti-FcRL5 bispecific antibodies, ET200-104 and ET200-117, were analyzed by Pepscan to determine epitope specificity. *See* Table 239. The target protein is human FcRL5 comprising amino acids 1-851 of SEQ ID NO: 899.

Table 239

Name	Origin	Concentration	Location
ET200-104 bispecific scFV	human	2.0 mg/ml	+4°C/22
ET200-117 bispecific scFV	human	1.6 mg/ml	+4°C/22

Methods

The principles of clips technology. CLIPS technology structurally fixes peptides into defined three-dimensional structures. This results in functional mimics of even the most complex binding sites. CLIPS technology is now routinely used to shape peptide libraries into single, double or triple looped structures as well as sheet- and helix-like folds (Figure 21).

Combinatorial clips library screening in detail. CLIPS library screening starts with the conversion of the target protein into a library of up to 10,000 overlapping peptide constructs, using a combinatorial matrix design. On a solid carrier, a matrix of linear peptides is synthesized, which are subsequently shaped into spatially defined CLIPS constructs (Figure 22). Constructs representing both parts of the discontinuous epitope in the correct conformation bind the antibody with high affinity, which is detected and quantified. Constructs presenting the incomplete epitope bind the antibody with lower affinity, whereas constructs not containing the epitope do not bind at all. Affinity information is used in iterative screens to define the sequence and conformation of epitopes in detail.

Heat map analysis. A heat map is a graphical representation of data where the values taken by a variable in a two-dimensional map are represented as colors. For double-looped CLIPS peptides, such a two-dimensional map can be derived from the independent sequences of the first and second loops. For example, the sequences of the 16 CLIPS peptides depicted in Figure 24 are effectively permutations of 4 unique sub-sequences in loop 1 (colored in blue in Figure 23) and 4 unique sub-sequences in loop 2 (colored in green in Figure 23). Thus, the observed ELISA data (colored in red in Figure 24A) can be plotted in a 4x4 matrix, where each X coordinate corresponds to the sequence of the first loop, and each Y coordinate corresponds to the sequence of the second loop. For instance, the ELISA value observed for CLIPS peptide CLSSERERVEDLFEYECELLTSEPIFHCRQEDC (indicated with an arrow in Figure 23A) can be found at the third row, third column of Figure 24B (indicated with an arrow and a red square). To further facilitate the visualization, ELISA values can be replaced with colors from a continuous gradient. In this case, extremely low values are colored in green, extremely high values are colored in red, and average values are colored in black (see Figure 24C). For the aforementioned example, the average value is 0.71. When this color map is applied to the data matrix depicted in Figure 24B, a color heat map is obtained (see Figure 24D, the original data is still indicated for extra clarity).

Synthesis of peptides. To reconstruct epitopes of the target molecule a library of peptides was synthesized. An amino functionalized polypropylene support was obtained by grafting with a proprietary hydrophilic polymer formulation, followed by reaction with t-butyloxycarbonyl-hexamethylenediamine (BocHMDA) using dicyclohexylcarbodiimide (DCC) with Nhydroxybenzotriazole (HOBt) and subsequent cleavage of the Boc-groups using trifluoroacetic acid (TFA). Standard Fmoc-peptide synthesis was used to synthesize peptides on the amino-functionalized solid support by custom modified JANUS liquid handling stations (Perkin Elmer). Synthesis of structural mimics was done using Pepscan’s proprietary Chemically Linked Peptides on Scaffolds (CLIPS) technology. CLIPS technology allows to structure peptides into single loops, doubleloops, triple loops, sheet-like folds, helix-like folds and combinations thereof. CLIPS templates are coupled to cysteine residues. The side-chains of multiple cysteines in the peptides were coupled to one or two CLIPS templates. For example, a 0.5 mM solution of the P2 CLIPS (2,6-bis(bromomethyl)pyridine) was dissolved in ammonium bicarbonate (20 mM, pH

7.8)/acetonitrile (1:3(v/v)). This solution was added onto the peptide arrays. The CLIPS template bound to side-chains of two cysteines as present in the solid-phase bound peptides of the peptide-arrays (455 wells plate with 3 µl wells). The peptide arrays were gently shaken in the solution for 30 to 60 minutes while completely covered in solution. Finally, the peptide arrays were washed extensively with excess of H_2O and sonicated in disrupt-buffer containing 1 % SDS/0.1 % beta-mercaptoethanol in PBS (pH 7.2) at 70°C for 30 minutes, followed by sonication in H_2O for another 45 minutes. The T3 CLIPS carrying peptides were made in a similar way but now with three cysteines.

ELISA Screening. The binding of antibody to each of the synthesized peptides was tested in a PEPSCAN-based ELISA. The peptide arrays were incubated with primary antibody solution (overnight at 4°C). After washing, the peptide arrays were incubated with a 1/1000 dilution of an appropriate antibody peroxidase conjugate (SBA) for one hour at 25°C. After washing, the peroxidase substrate 2,2'-azino-di-3-ethylbenzthiazoline sulfonate (ABTS) and 2 µl/ml of 3 percent H_2O_2 were added. After one hour, the color development was measured. The color development was quantified with a charge coupled device (CCD) - camera and an image processing system.

Data processing. The values obtained from the CCD camera ranged from 0 to 3000 mAU, similar to a standard 96-well plate ELISA-reader. The results were quantified and stored into the Peplab database. Occasionally a well contained an air-bubble resulting in a false-positive value, the cards were manually inspected and any values caused by an air-bubble were scored as 0.

Synthesis quality control. To verify the quality of the synthesized peptides, a separate set of positive and negative control peptides was synthesized in parallel. These were screened with antibody 57.9 (ref. Posthumus et al., J. Virology, 1990, 64:3304-3309).

Results

Screening. Antibody binding depends on a combination of factors, including concentration of the antibody and the amounts and nature of competing proteins in the ELISA buffer. Also, the pre-coat conditions (the specific treatment of the peptide arrays prior to incubation with the experimental sample) affected binding. These details are summed up in Table 240. For the Pepscan Buffer and Preconditioning

(SQ), the numbers indicate the relative amount of competing protein (a combination of horse serum and ovalbumin).

Table 240. Screening conditions

Label	Dilution	Sample Buffer	Pre-conditioning
ET200-104	8 µg/ml	PBS-Tween	PBS-Tween
ET200-117	3 µg/ml	PBS-Tween	0.1% SQ

Antibodies ET200-104 and ET200-117 were coated at 1 µg/ml on a Nunc Maxisorp plate for ELISA and detected with Goat Anti-Human Ig-HRP (Southern Biotech; #2010/05), the same conjugate that is used in minicard screenings. For ET200-104 and ET200-117 signal >1 OD was obtained for some dilutions of the secondary Ab, indicating that the secondary antibody is well suited for detection of these mAbs.

Herceptin was used as an internal negative control at high concentration in the absence of blocking buffer. Herceptin bound peptides with common sequences LRGSPLILYRF, LRGSSPILYWF and APRGSPPILYW (Figure 25). Peptides containing aforementioned sequences were excluded from epitope candidates for test samples.

When tested under low stringency conditions and at a high concentration antibody ET200-104 binds multiple peptide motifs in all sets (Figure 26). The majority of peptides bound were suspected to be the result of non-specific hydrophic interactions based on the results obtained for Herceptin (internal negative control). However, binding of peptides containing motif $_{657}$SRPILTFRAPR$_{667}$ was proposed to be specific, and was uniquely attributed to sample ET200-104.

When tested under low stringency conditions antibody ET200-117 resulted in weak binding of multiple peptide motifs on all sets. Cumulative data analysis of data obtained for all sets suggests that the antibody uniquely recognizes a region containing peptide stretch $_{829}$RSETVTLYITGL$_{840}$ in domain 9 of Fc receptor-like protein 5 distinct from the Herceptin internal negative control and ET200-104. Again the majority of other peptides bound were suspected to be the result of unspecific hydrophic interactions that shared as the same binding pattern was recorded under low stringency conditions for antibody ET200-104.

Conclusions

Cumulative data analysis of results collected for ET200-104, and ET200-117 vs. Herceptin suggest that antibody ET200-104 targets residues $_{657}$SRPILTFRAPR$_{667}$ within domain 8 of Fc receptor-like protein 5 and antibody ET200-117 targets residues $_{829}$RSETVTLYITGL$_{840}$ within domain 9. Additionally, for both samples multiple signals were recorded with peptides non-specifically bound by Herceptin. The epitope candidate identified for ET200-104 was visualized using a publically available 3D model of Fc receptor-like protein 5 (Figure 27). The epitope candidate for ET200-117 lies within the non-modeled part of the target and therefore cannot be visualized.

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From the foregoing description, it will be apparent that variations and modifications may be made to the invention described herein to adopt it to various usages and conditions. Such embodiments are also within the scope of the following claims.

All patents and publications and sequences referred to by accession or reference number mentioned in this specification are herein incorporated by reference to the same extent as if each independent patent and publication and sequence was specifically and individually indicated to be incorporated by reference.

The term “comprise” and variants of the term such as “comprises” or “comprising” are used herein to denote the inclusion of a stated integer or stated integers but not to exclude any other integer or any other integers, unless in the context or usage an exclusive interpretation of the term is required.

Any reference to publications cited in this specification is not an admission that the disclosures constitute common general knowledge in Australia.

CLAIMS

1. A chimeric antigen receptor (CAR), comprising an extracellular antigen-binding domain that binds to Fc Receptor-like 5 (FcRL5), a transmembrane domain, and an intracellular domain, wherein the extracellular antigen-binding domain comprises:

(aa) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:311;

(ab) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:320; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 315, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:316, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:317;

(ac) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 324, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:325; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 321, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:322, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:323;

(ad) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:331; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 326, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:328;

(ae) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:331; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set

forth in SEQ ID NO: 332, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:333, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:334;

(af) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 338, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:339; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 335, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:336, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:337;

(ag) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 343, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:344, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:345; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 340, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:341, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:342;

(ah) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 348, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:349, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:350; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:347;

(ai) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 352, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:344, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:353; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:351;

(aj) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 357, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:358, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:359; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 354, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:355, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:356;

(ak) a light chain variable region comprising a CDR1 comprising the amino acid

sequence set forth in SEQ ID NO: 363, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:364, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:365; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 360, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:361, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:362;

(al) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 369, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:370, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:371; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 366, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:367, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:368;

(am) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:375; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:373, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:374;

(an) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:377; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:376;

(ao) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 381, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:382, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:383; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 378, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:379, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:380;

(ap) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:385, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:386; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set

forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:384;

(aq) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 390, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:391, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:392; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 387, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:389;

(ar) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:395; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 393, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:355, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:394;

(as) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 397, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:399; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:396;

(at) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 401, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:402; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:400;

(au) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:407; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:405;

(av) a light chain variable region comprising a CDR1 comprising the amino acid

sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:409, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:410; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:408;

(aw) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:414; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:413;

(ax) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 416, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:417, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:418; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:415;

(ay) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:419; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:349;

(az) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 423, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:358, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:424; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 420, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:421, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:422;

(ba) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 428, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:429, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:430; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set

forth in SEQ ID NO: 425, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:426, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:427;

(bb) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 433, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:434, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:435; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:431, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:432;

(bc) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 423, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:438, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:439; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 436, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:437;

(bd) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:443; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 440, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:441, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:442;

(be) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 447, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:448, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:449; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 444, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:445, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:446;

(bf) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:452; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:450, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:451;

(bg) a light chain variable region comprising a CDR1 comprising the amino acid

sequence set forth in SEQ ID NO: 369, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:454, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:455; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:453;

(bh) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:457; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:456;

(bi) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:331; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:458;

(bj) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 460, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:461, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:462; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:459;

(bk) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:419; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:463;

(bl) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 423, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:438, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:465; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in

SEQ ID NO: 436, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:464;

(bm) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 468, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:469, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:470; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:466, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:467;

(bn) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 474, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:358, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:465; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 471, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:472, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:473;

(bo) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 477, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:478, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:479; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:475, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:476;

(bp) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 483, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:484, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:485; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 480, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:481, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:482;

(bq) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 433, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:487, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:488; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:486;

(br) a light chain variable region comprising a CDR1 comprising the amino acid

sequence set forth in SEQ ID NO: 490, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:491; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:489;

(bs) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:493; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:492;

(bt) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 490, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:349, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:495; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:494;

(bu) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 498, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:344, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:499; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:496, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:497;

(bv) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 503, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:504, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:505; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 500, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:501, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:502;

(bw) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 508, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:349, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:509; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set

forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:506, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:507;

(bx) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:513, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:514; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 510, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:511, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:512;

(by) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 518, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:519; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 515, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:516, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:517;

(bz) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 348, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:523, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:524; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 520, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:521, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:522;

(ca) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:528; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 525, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:526, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:527;

(cb) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:530; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:529;

(cc) a light chain variable region comprising a CDR1 comprising the amino acid

sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:531; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 515, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:516, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:517;

(cd) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 533, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:534, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:535; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:532;

(ce) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 428, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:429, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:430; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 425, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:426, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:536;

(cf) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 540, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:541; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 537, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:538, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:539;

(cg) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:542; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 537, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:538, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:539;

(ch) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 544, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:448, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:545; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set

forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:543;

(ci) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 547, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:548, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:549; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:546;

(cj) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:550;

(ck) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:513, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:550;

(cl) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 406, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:398, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:554; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 551, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:552, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:553;

(cm) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 556, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:557, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:558; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:555;

(cn) a light chain variable region comprising a CDR1 comprising the amino acid

sequence set forth in SEQ ID NO: 562, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:563, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:564; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 559, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:560, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:561;

(co) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 568, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:504, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:569; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 565, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:566, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:567;

(cp) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 571, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:572, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:573; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:475, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:570;

(cq) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 343, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:575, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:576; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:574;

(cr) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:577;

(cs) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set

forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:578;

(ct) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 580, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:438, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:581; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 436, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:388, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:579;

(cu) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 585, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 582, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:583, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:584;

(cv) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 312, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:586, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:314; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 346, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:327, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:578;

(cw) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 588, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:385, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:375; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:587;

(cx) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:592; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 589, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:590, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:591;

(cy) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 926, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:927, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:928; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 923, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:924, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:925; or

(cz) a light chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 932, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:933, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:934; and a heavy chain variable region comprising a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 929, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:930, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:931.

2. A chimeric antigen receptor (CAR), comprising an extracellular antigen-binding domain that binds to Fc Receptor-like 5 (FcRL5), a transmembrane domain, and an intracellular domain, wherein the extracellular antigen-binding domain comprises:

(aa) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:3, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:4;

(ab) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:7, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:8;

(ac) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:11, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:12;

(ad) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:299, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:300;

(ae) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:15, and a heavy chain variable region

comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:16;

(af) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:19, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:20;

(ag) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:23, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:24;

(ah) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:27, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:28;

(ai) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:31, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:32;

(aj) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:35, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:36;

(ak) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:39, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:40;

(al) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:43, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:44;

(am) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:47, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth

in SEQ ID NO:48;

(an) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:51, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:52;

(ao) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:55, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:56;

(ap) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:59, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:60;

(aq) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:63, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:64;

(ar) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:67, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:68;

(as) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:71, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:72;

(at) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:75, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:76;

(au) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:79, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:80;

(av) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:83, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:84;

(aw) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:87, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:88;

(ax) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:91, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:92;

(ay) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:95, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:96;

(az) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:99, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:100;

(ba) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:103, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:104;

(bb) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:107, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:108;

(bc) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:111, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:112;

(bd) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light

chain variable region sequence set forth in SEQ ID NO:115, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:116;

(be) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:119, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:120;

(bf) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:123, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:124;

(bg) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:127, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:128;

(bh) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:131, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:132;

(bi) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:135, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:136;

(bj) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:139, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:140;

(bk) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:143, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:144;

(bl) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:147, and a heavy chain variable region

comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:148;

(bm) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:151, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:152;

(bn) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:155, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:156;

(bo) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:159, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:160;

(bp) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:163, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:164;

(bq) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:167, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:168;

(br) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:171, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:172;

(bs) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:175, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:176;

(bt) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:179, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth

in SEQ ID NO:180;

(bu) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:183, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:184;

(bv) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:187, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:188;

(bw) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:191, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:192;

(bx) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:195, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:196;

(by) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:199, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:200;

(bz) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:203, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:204;

(ca) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:207, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:208;

(cb) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:211, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:212;

(cc) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:215, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:216;

(cd) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:219, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:220;

(ce) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:223, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:224;

(cf) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:227, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:228;

(cg) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:231, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:232;

(ch) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:235, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:236;

(ci) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:239, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:240;

(cj) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:243, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:244;

(ck) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light

chain variable region sequence set forth in SEQ ID NO:247, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:248;

(cl) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:251, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:252;

(cm) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:255, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:256;

(cn) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:259, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:260;

(co) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:263, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:264;

(cp) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:267, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:268;

(cq) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:271, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:272;

(cr) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:275, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:276;

(cs) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:279, and a heavy chain variable region

comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:280;

(ct) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:283, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:284;

(cu) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:287, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:288;

(cv) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:291, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:292;

(cw) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:303, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:304;

(cx) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:295, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:296;

(cy) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:915, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:917; or

(cz) a light chain variable region comprising a CDR1, a CDR2, and a CDR3 of the light chain variable region sequence set forth in SEQ ID NO:919, and a heavy chain variable region comprising a CDR1, a CDR2, and a CDR3 of the heavy chain variable region sequence set forth in SEQ ID NO:921.

3. The CAR of claim 1 or 2, wherein:

(aa) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:3, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:4;

(ab) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:7, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:8;

(ac) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:11, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:12;

(ad) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:299, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:300;

(ae) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:15, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:16;

(af) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:19, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:20;

(ag) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:23, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:24;

(ah) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:27, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:28;

(ai) the light chain variable region comprises an amino acid sequence that has at least

about 90% sequence identity to the sequence set forth in SEQ ID NO:31, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:32;

(aj) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:35, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:36;

(ak) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:39, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:40;

(al) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:43, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:44;

(am) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:47, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:48;

(an) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:51, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:52;

(ao) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:55, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:56;

(ap) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:59, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:60;

(aq) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:63, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:64;

(ar) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:67, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:68;

(as) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:71, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:72;

(at) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:75, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:76;

(au) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:79, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:80;

(av) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:83, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:84;

(aw) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:87, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:88;

(ax) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:91, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:92;

(ay) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:95, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:96;

(az) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:99, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:100;

(ba) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:103, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:104;

(bb) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:107, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:108;

(bc) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:111, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:112;

(bd) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:115, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:116;

(be) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:119, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:120;

(bf) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:123, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:124;

(bg) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:127, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:128;

(bh) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:131, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:132;

(bi) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:135, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:136;

(bj) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:139, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:140;

(bk) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:143, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:144;

(bl) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:147, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:148;

(bm) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:151, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:152;

(bn) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:155, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:156;

(bo) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:159, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:160;

(bp) the light chain variable region comprises an amino acid sequence that has at least

about 90% sequence identity to the sequence set forth in SEQ ID NO:163, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:164;

(bq) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:167, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:168;

(br) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:171, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:172;

(bs) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:175, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:176;

(bt) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:179, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:180;

(bu) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:183, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:184;

(bv) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:187, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:188;

(bw) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:191, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:192;

(bx) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:195, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:196;

(by) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:199, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:200;

(bz) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:203, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:204;

(ca) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:207, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:208;

(cb) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:211, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:212;

(cc) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:215, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:216;

(cd) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:219, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:220;

(ce) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:223, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:224;

(cf) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:227, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:228;

(cg) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:231, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:232;

(ch) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:235, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:236;

(ci) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:239, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:240;

(cj) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:243, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:244;

(ck) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:247, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:248;

(cl) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:251, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:252;

(cm) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:255, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:256;

(cn) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:259, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:260;

(co) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:263, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:264;

(cp) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:267, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:268;

(cq) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:271, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:272;

(cr) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:275, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:276;

(cs) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:279, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:280;

(ct) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:283, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:284;

(cu) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:287, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:288;

(cv) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:291, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:292;

(cw) the light chain variable region comprises an amino acid sequence that has at least

about 90% sequence identity to the sequence set forth in SEQ ID NO:303, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:304;

(cx) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:295, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:296 ;

(cy) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:915, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:917; or

(cz) the light chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:919, and the heavy chain variable region comprises an amino acid sequence that has at least about 90% sequence identity to the sequence set forth in SEQ ID NO:921.

4. The CAR of any one of claims 1-3, wherein:

(aa) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:3, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:4;

(ab) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:7, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:8;

(ac) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:11, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:12;

(ad) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:299, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:300;

(ae) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:15, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:16;

(af) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:19, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:20;

(ag) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:23, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:24;

(ah) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:27, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:28;

(ai) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:31, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:32;

(aj) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:35, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:36;

(ak) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:39, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:40;

(al) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:43, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:44;

(am) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:47, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:48;

(an) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:51, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:52;

(ao) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:55, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:56;

(ap) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:59, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:60;

(aq) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:63, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:64;

(ar) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:67, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:68;

(as) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:71, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:72;

(at) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:75, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:76;

(au) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:79, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:80;

(av) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:83, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:84;

(aw) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:87, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:88;

(ax) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:91, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:92;

(ay) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:95, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:96;

(az) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:99, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:100;

(ba) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:103, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:104;

(bb) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:107, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:108;

(bc) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:111, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:112;

(bd) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:115, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:116;

(be) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:119, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:120;

(bf) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:123, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:124;

(bg) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:127, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:128;

(bh) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:131, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:132;

(bi) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:135, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:136;

(bj) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:139, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:140;

(bk) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:143, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:144;

(bl) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:147, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:148;

(bm) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:151, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:152;

(bn) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:155, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:156;

(bo) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:159, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:160;

(bp) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:163, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:164;

(bq) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:167, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:168;

(br) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:171, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:172;

(bs) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:175, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:176;

(bt) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:179, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:180;

(bu) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:183, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:184;

(bv) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:187, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:188;

(bw) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:191, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:192;

(bx) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:195, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:196;

(by) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:199, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:200;

(bz) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:203, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:204;

(ca) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:207, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:208;

(cb) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:211, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:212;

(cc) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:215, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:216;

(cd) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:219, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:220;

(ce) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:223, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:224;

(cf) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:227, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:228;

(cg) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:231, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:232;

(ch) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:235, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:236;

(ci) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:239, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:240;

(cj) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:243, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:244;

(ck) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:247, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:248;

(cl) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:251, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:252;

(cm) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:255, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:256;

(cn) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:259, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:260;

(co) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:263, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:264;

(cp) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:267, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:268;

(cq) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:271, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:272;

(cr) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:275, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:276;

(cs) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:279, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:280;

(ct) the light chain variable region comprises the amino acid sequence set forth in SEQ

ID NO:283, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:284;

(cu) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:287, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:288;

(cv) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:291, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:292;

(cw) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:303, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:304;

(cx) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:295, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:296;

(cy) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:915, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:917; or

(cz) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:919, and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:921.

5. The CAR of any one of claims 1-3, wherein:

(a) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:419; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:463;

(b) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 318, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:319, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:531; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 515, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:516, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:517;

(c) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 533, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:534, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:535; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 403, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:404, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:532;

(d) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 544, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:448, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:545; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 411, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:412, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:543;

(e) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 571, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:572, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:573; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 372, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:475, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:570;

(f) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 329, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:330, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:443; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 440, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:441, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:442; or

(g) the light chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 490, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:313, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:491; and the heavy chain variable region comprises a CDR1 comprising the amino acid sequence set forth in SEQ ID NO: 309, a CDR2 comprising the amino acid sequence set forth in SEQ ID NO:310, and a CDR3 comprising the amino acid sequence set forth in SEQ ID NO:489.

6. The CAR of any one of claims 1-5, wherein:

(a) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:143; and the heavy chain variable region comprises the amino acid sequence set forth in

SEQ ID NO:144;

(b) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:215; and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:216;

(c) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:219; and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:220;

(d) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:235; and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:236;

(e) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:267; and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:268;

(f) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:115; and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:116; or

(g) the light chain variable region comprises the amino acid sequence set forth in SEQ ID NO:171; and the heavy chain variable region comprises the amino acid sequence set forth in SEQ ID NO:172.

7. The CAR of any one of claims 1-6, wherein the extracellular antigen-binding domain is a single-chain variable fragment (scFv), a Fab, or a $F(ab)_2$.

8. The CAR of any one of claims 1-7, wherein the extracellular antigen-binding domain comprises the amino acid sequence set forth in SEQ ID NO: 594, SEQ ID NO: 596, SEQ ID NO: 598, SEQ ID NO: 600, SEQ ID NO: 602, SEQ ID NO: 604, SEQ ID NO: 606, SEQ ID NO: 608, SEQ ID NO: 610, SEQ ID NO: 612, SEQ ID NO: 614, SEQ ID NO: 616, SEQ ID NO: 618, SEQ ID NO: 620, SEQ ID NO: 622, SEQ ID NO: 624, SEQ ID NO: 626, SEQ ID NO: 628, SEQ ID NO: 630, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 636, SEQ ID NO: 638, SEQ ID NO: 640, SEQ ID NO: 642, SEQ ID NO: 644, SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 650, SEQ ID NO: 652, SEQ ID NO: 654, SEQ ID NO: 656, SEQ ID NO: 658, SEQ ID NO: 660, SEQ ID NO: 662, SEQ ID NO: 664, SEQ ID NO: 666, SEQ ID NO: 668, SEQ ID NO: 670, SEQ ID NO: 672, SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678, SEQ ID NO: 680, SEQ ID NO: 682, SEQ ID NO: 684, SEQ ID NO: 686, SEQ ID NO: 688, SEQ ID NO: 690, SEQ ID NO: 692,

SEQ ID NO: 694, SEQ ID NO: 696, SEQ ID NO: 698, SEQ ID NO: 700, SEQ ID NO: 702, SEQ ID NO: 704, SEQ ID NO: 706, SEQ ID NO: 708, SEQ ID NO: 710, SEQ ID NO: 712, SEQ ID NO: 714, SEQ ID NO: 716, SEQ ID NO: 718, SEQ ID NO: 720, SEQ ID NO: 722, SEQ ID NO: 724, SEQ ID NO: 726, SEQ ID NO: 728, SEQ ID NO: 730, SEQ ID NO: 732, SEQ ID NO: 734, SEQ ID NO: 736, SEQ ID NO: 738, SEQ ID NO: 740, SEQ ID NO: 742, or SEQ ID NO: 744.

9. The CAR of any one of claims 1-8, wherein the transmembrane domain comprises a CD8 polypeptide, a CD28 polypeptide, a CD3ζ polypeptide, a CD4 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a CTLA-4 polypeptide, a PD-1 polypeptide, a LAG-3 polypeptide, a 2B4 polypeptide, a BTLA polypeptide, a synthetic peptide, or a combination thereof.

10. The CAR of any one of claims 1-9, wherein the intracellular domain comprises a CD3ζ polypeptide.

11. The CAR of any one of claims 1-10, wherein the intracellular domain further comprises at least one signaling region.

12. The CAR of claim 11, wherein the at least one signaling region comprises a PD-1 polypeptide, a CTLA-4 polypeptide, a LAG-3 polypeptide, a 2B4 polypeptide, a BTLA polypeptide, a synthetic peptide, or a combination thereof.

13. The CAR of claim 11 or 12, wherein the signaling region comprises at least one co-stimulatory signaling region.

14. The CAR of claim 13, wherein the at least one co-stimulatory signaling region comprises a CD28 polypeptide, a 4-1BB polypeptide, an OX40 polypeptide, an ICOS polypeptide, a DAP-10 polypeptide, or a combination thereof.

15. The CAR of claim 13 or 14, wherein:

the transmembrane domain comprises a CD28 polypeptide, the intracellular domain comprises a CD3ζ polypeptide and the at least one co-stimulatory signaling domain comprises a CD28 polypeptide;

the transmembrane domain comprises a CD8 polypeptide, the intracellular domain comprises a CD3ζ polypeptide and the at least one co-stimulatory signaling domain comprises a 4-1BB polypeptide; or

the transmembrane domain comprises a CD28 polypeptide, the intracellular domain comprises a CD3ζ polypeptide and the at least one co-stimulatory signaling domain comprises a 4-1BB polypeptide.

16. A nucleic acid molecule encoding the chimeric antigen receptor (CAR) of any one of claims 1-15.

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

18. The vector of claim 17, wherein the vector is a γ-retroviral vector or a lentiviral vector.

19. An immunoresponsive cell comprising the CAR of any one of claims 1-15, the nucleic acid molecule of claim 16 or the vector of claim 17 or 18.

20. The immunoresponsive cell of claim 19, wherein the immunoresponsive cell is further transduced with a nucleic acid molecule encoding at least one co-stimulatory ligand such that the immunoresponsive cell expresses the at least one co-stimulatory ligand, wherein the at least one co-stimulatory ligand is selected from the group consisting of 4-1BBL, CD80, CD86, CD70, OX40L, CD48, TNFRSF14, and combinations thereof, and/or a nucleic acid molecule encoding at least one cytokine such that the immunoresponsive cell secretes the at least one cytokine, wherein the at least one cytokine is selected from the group consisting of IL-2, IL-3, IL-6, IL-7, IL-11, IL-12, IL-15, IL-17, IL-21, and combinations thereof.

21. The immunoresponsive cell of claim 19 or 20, wherein the immunoresponsive cell is selected from the group consisting of a T cell, a Natural Killer (NK) cell, a cytotoxic T lymphocyte (CTL), a regulatory T cell, a human embryonic stem cell, a lymphoid progenitor cell, a T cell-precursor cell, and a pluripotent stem cell from which lymphoid cells may be differentiated.

22. A T cell comprising the CAR of any one of claims 1-15, the nucleic acid molecule of claim 16 or the vector of claim 17 or 18.

23. A method of reducing tumor burden or increasing or lengthening survival of a subject having a tumor expressing FcRL5, comprising administering to the subject an effective amount of the immunoresponsive cell of any one of claims 19-21 or the T cell of claim 22.

24. The method of claim 23, wherein: the method reduces the number of tumor cells; the method reduces tumor size; or the method eradicates the tumor in the subject.

25. A method for producing an immunoresponsive cell that binds to Fc Receptor-like 5 (FcRL5), comprising introducing into the immunoresponsive cell a nucleic acid sequence that

encodes the chimeric antigen receptor (CAR) of any one of claims 1-15, the nucleic acid molecule of claim 16 or the vector of claim 17 or 18.

26. An immunoresponsive cell that binds to Fc Receptor-like 5 (FcRL5) produced by the method of claim 25.

27. A pharmaceutical composition comprising an effective amount of the immunoresponsive cell of any one of claims 19-21 or 26 or the T cell of claim 22 and a pharmaceutically acceptable excipient.

28. The pharmaceutical composition of claim 27, wherein the pharmaceutical composition is for treating a tumor expressing FcRL5.

29. A kit for treating a tumor expressing FcRL5, comprising the immunoresponsive cell of any one of claims 19-21 or the T cell of claim 22.

30. Use of an effective amount of the immunoresponsive cell of any one of claims 19-21 or the T cell of claim 22 in the manufacture of a medicament for treating a tumor expressing FcRL5 in a subject.

31. The method of claim 23 or 24, the pharmaceutical composition of claim 28 or the use of claim 30, wherein the tumor is selected from the group consisting of multiple myeloma, Non-Hodgkin Lymphoma, Mantle Cell Lymphoma, Hodgkin Lymphoma, Chronic Lymphocytic Leukemia (CLL), Acute lymphocytic leukemia (ALL), Hairy Cell Leukemia, Burkitt’s Lymphoma, and Waldenstrom’s Macroglobulinemia.

Memorial Sloan-Kettering Cancer Center
Eureka Therapeutics, Inc.
Patent Attorneys for the Applicant/Nominated Person
SPRUSON & FERGUSON

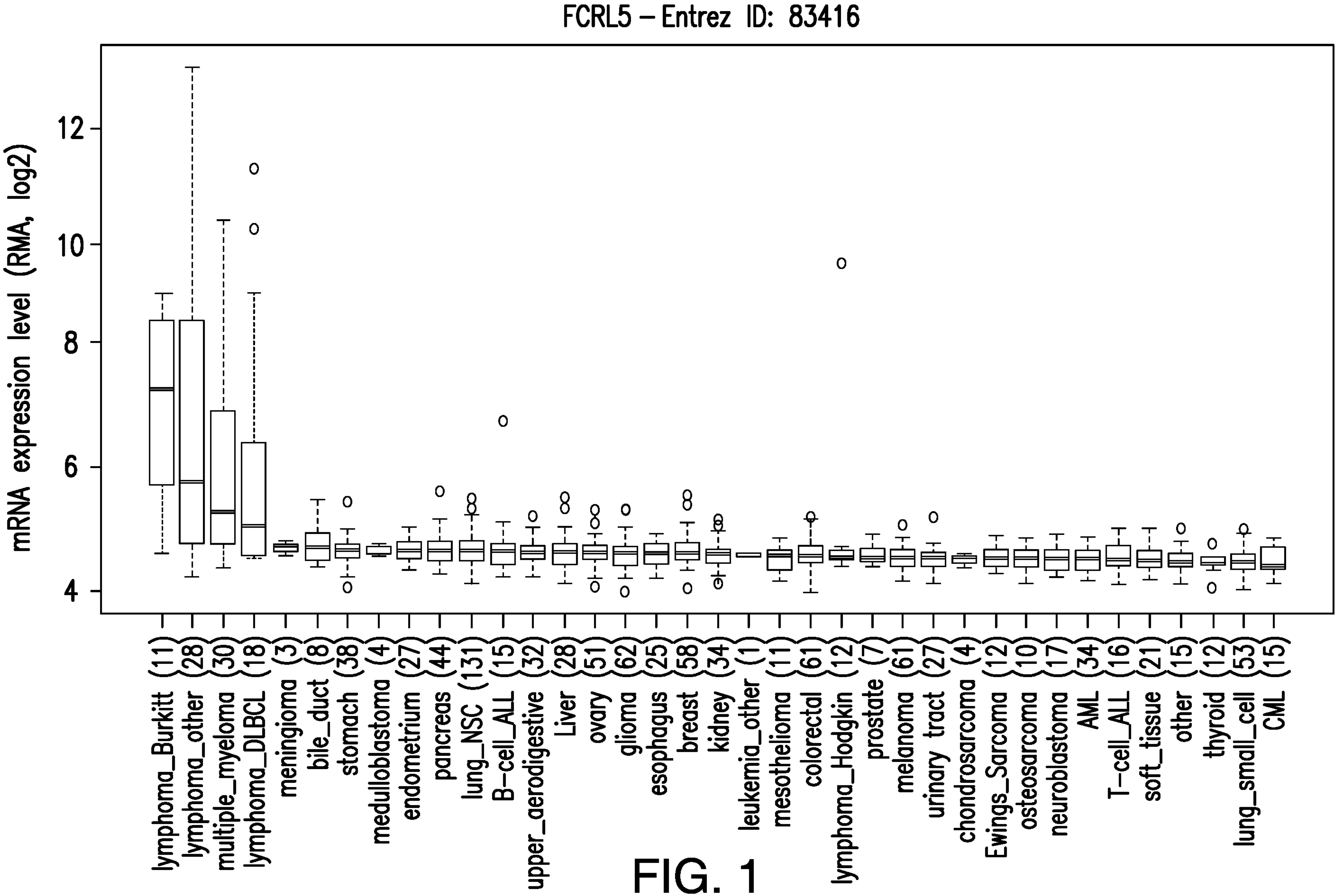

FCRL5 – Entrez ID: 83416
mRNA expression level (RMA, log2)
12
10
8
6
4
lymphoma_Burkitt (11)
lymphoma_other (28)
multiple_myeloma (30)
lymphoma_DLBCL (18)
meningioma (3)
bile_duct (8)
stomach (38)
medulloblastoma (4)
endometrium (27)
pancreas (44)
lung_NSC (131)
B–cell_ALL (15)
upper_aerodigestive (32)
Liver (28)
ovary (51)
glioma (62)
esophagus (25)
breast (58)
kidney (34)
leukemia_other (1)
mesothelioma (11)
colorectal (61)
lymphoma_Hodgkin (12)
prostate (7)
melanoma (61)
urinary tract (27)
chondrosarcoma (4)
Ewings_Sarcoma (12)
osteosarcoma (10)
neuroblastoma (17)
AML (34)
T–cell_ALL (16)
soft_tissue (21)
other (15)
thyroid (12)
lung_small_cell (53)
CML (15)

FIG. 1

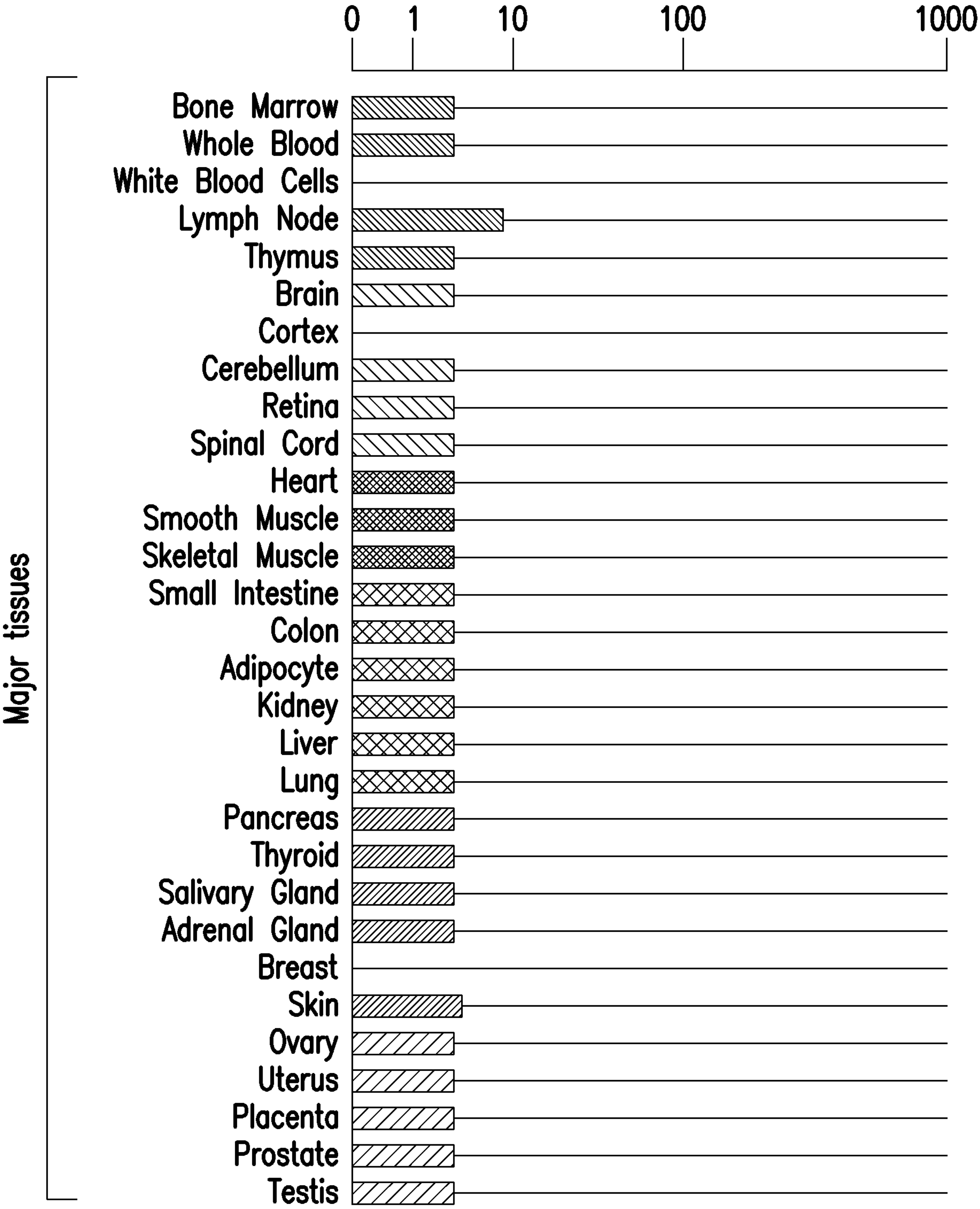


FIG. 1 (continued)

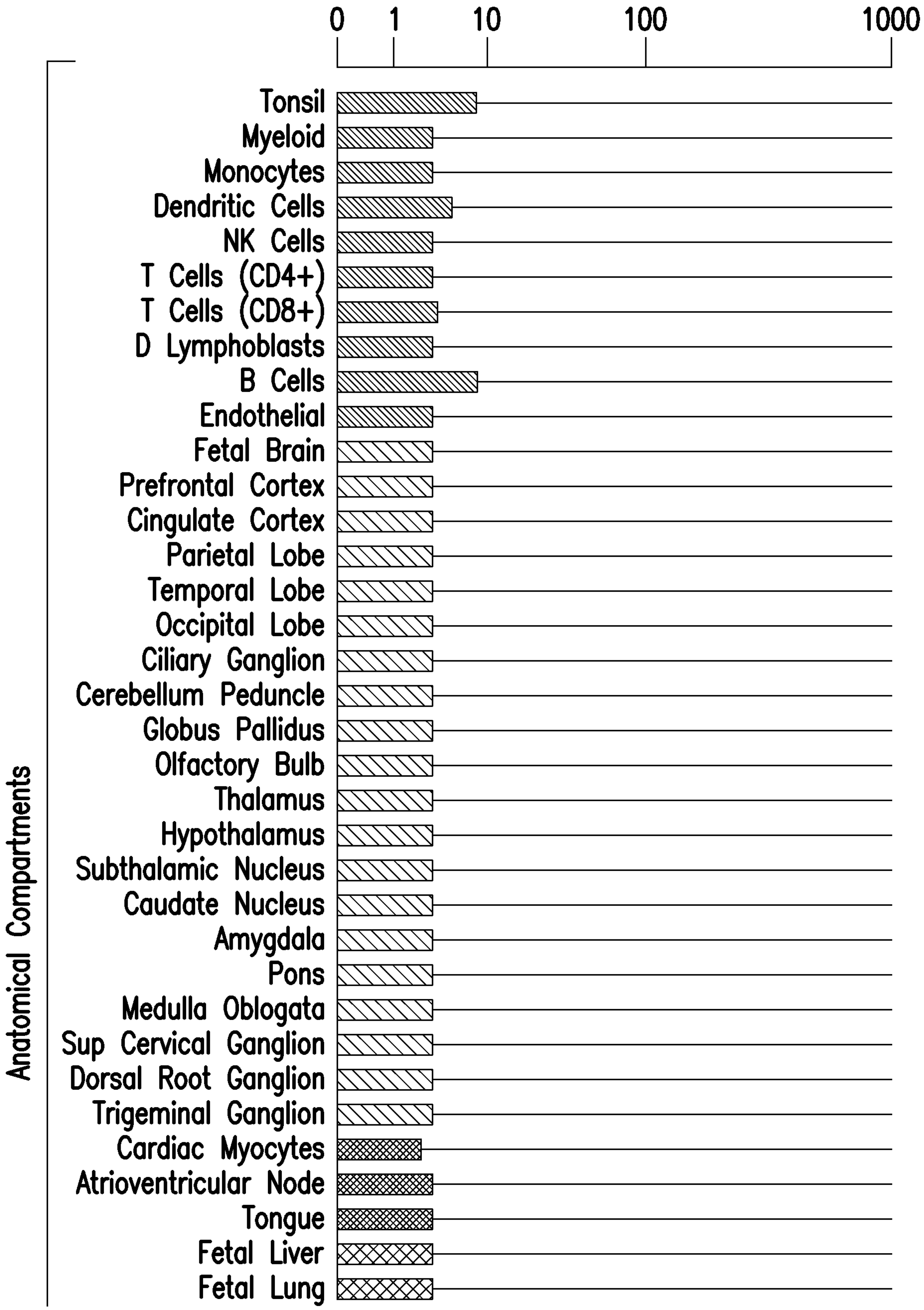


FIG. 1 (continued)

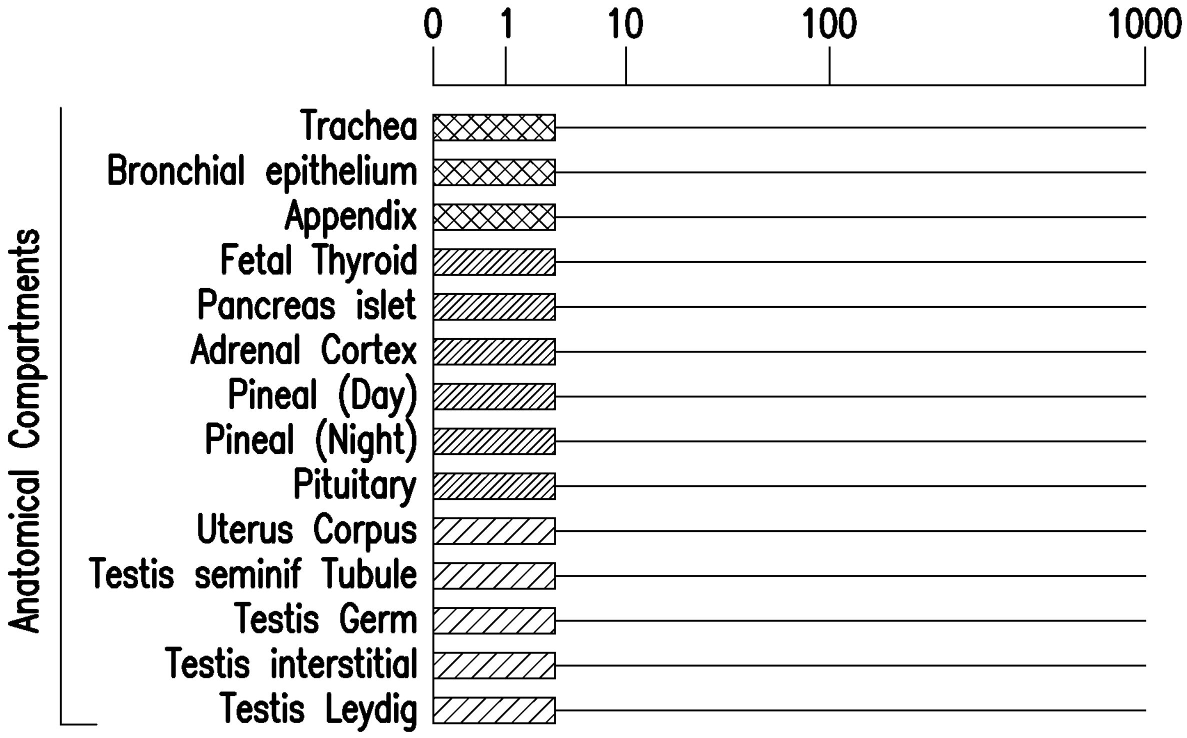
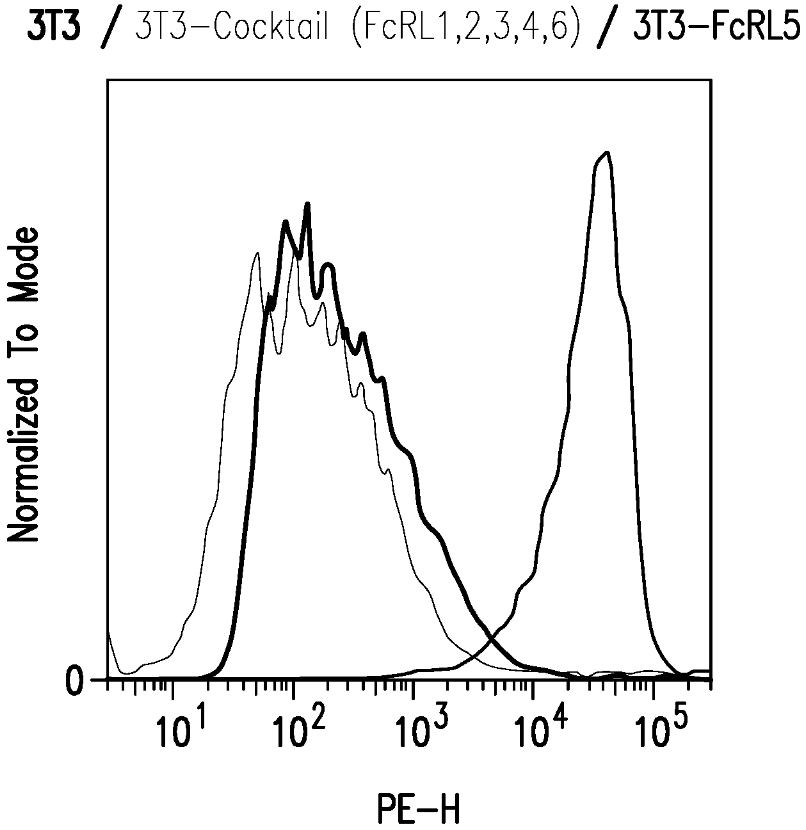
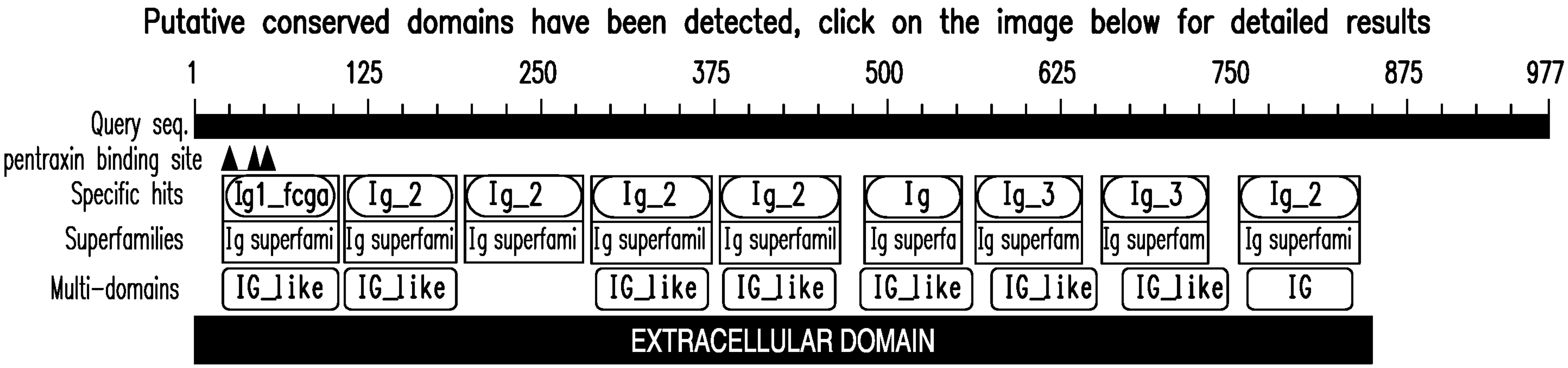


FIG. 1 (continued)



	Sample Name	Median, PE-H
─	Plate1 E12.fcs	124
—	Plate1 E11.fcs	3.15E4
━	Plate1 E10.fcs	216

FIG. 2



Epitope locations of anti-CD307(IRTA2/FcRH5/FCRL5) MAbs (Satoshi Nagata 070201)

IRTA2–structure

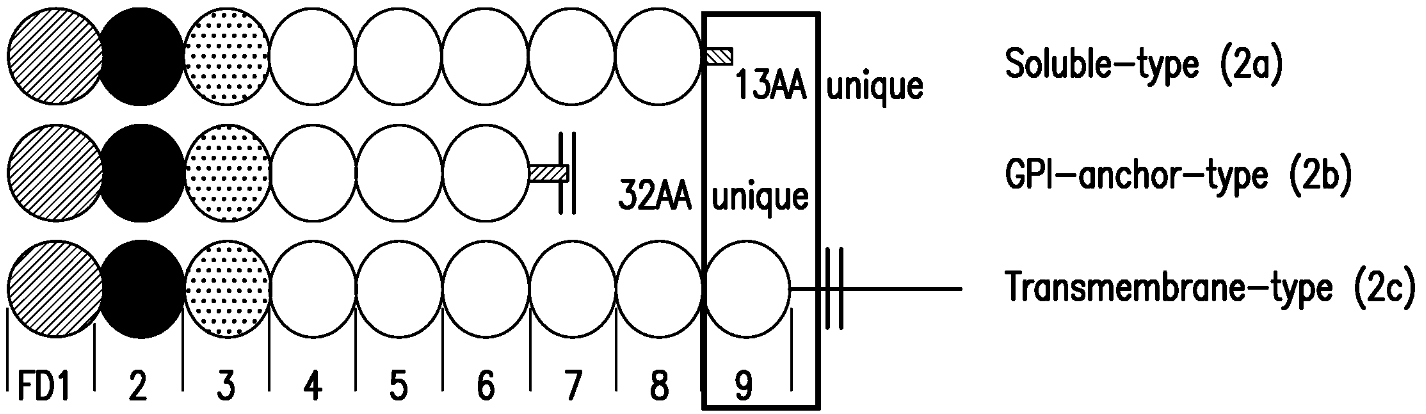


FIG. 3A

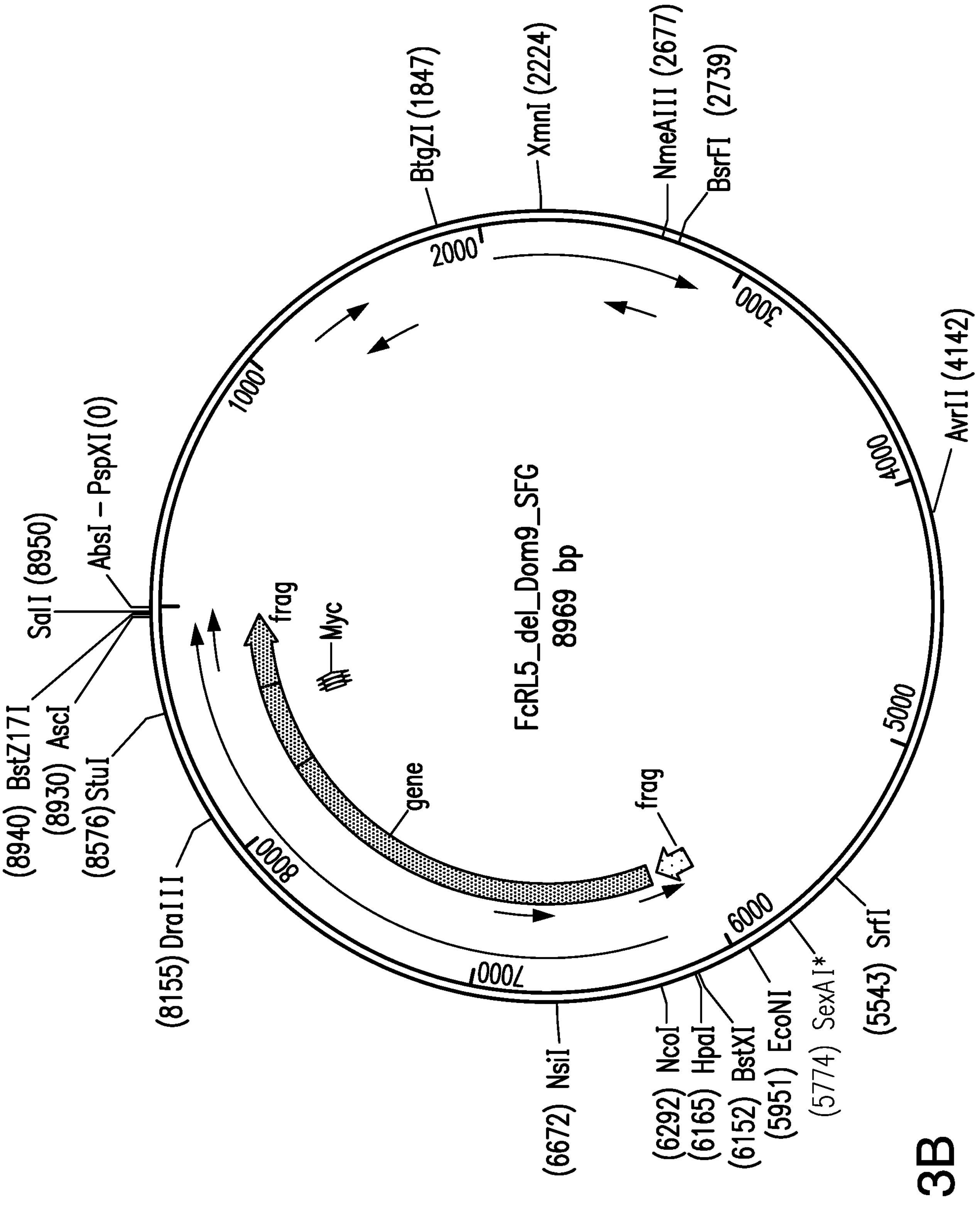

FcRL5_del_Dom9_SFG
8969 bp
AbsI - PspXI (0)
SalI (8950)
(8940) BstZ17I
(8930) AscI
(8576) StuI
(8155) DraIII
(6672) NsiI
(6292) NcoI
(6165) HpaI
(6152) BstXI
(5951) EcoNI
(5774) SexAI*
(5543) SrfI
AvrII (4142)
BsrFI (2739)
NmeAIII (2677)
XmnI (2224)
BtgZI (1847)
1000
2000
3000
4000
5000
6000
7000
8000
frag
Myc
gene
frag

FIG. 3B

Domain 1-8
Domain 9
TM
Myc3

>MSK_delDOM9_myc_mCD8

MLLWVILLVLAPVSGQFARTPR**PIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYLGKEILRET**
PDNILEVQESGEYRCQAQGSPLSSPVHLDFSSAS**LILQAPLSVFEGDSVVLRCRAKAEVTLNNTIYKNDN**
VLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSNTVKIQVQEPFT**RPVLRASSFQPISGNPVTLT**
CETQLSLERSDVPLRFRFFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRSWIQV
QIPASH**PVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENS**
GNYYCTADNGLGAKPSKAVSLSVTVPVSH**PVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA**
LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHP**VLTLSSAEALTFEGATV**
TLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYYCTADNGFGPQRSEVVSLFVT
VPVS**RPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGEASFNLSLTAEHSG**
NYSCEANNGLVAQHSDTISLSVIVPVS**RPILTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTL**
GKISAPSGGGASFNLSLTTEHSGIYSC**EADN**GLEAQRSEMVTLKVAAAAEQKLISEEDLEQKLISEEDLE
QKLISEEDLTGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPSDSDSQEPTYHNVPAWEELQP
VYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVASTPVSGSLFL
ASSAPHR*

>gi|14278719|gb|AAK50059.2|AF369794_1 B cell crosslinked IgM-activating sequence protein [Homo sapiens]

MLLWVILLVLAPVSGQFARTPR**PIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYLGKEILRET**
PDNILEVQESGEYRCQAQGSPLSSPVHLDFSSAS**LILQAPLSVFEGDSVVLRCRAKAEVTLNNTIYKNDN**
VLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSNTVKIQVQEPFT**RPVLRASSFQPISGNPVTLT**
CETQLSLERSDVPLRFRFFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRSWIQV
QIPASH**PVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENS**
GNYYCTADNGLGAKPSKAVSLSVTVPVSH**PVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA**
LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHP**VLTLSSAEALTFEGATV**
TLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYYCTADNGFGPQRSEVVSLFVT
VPVS**RPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGEASFNLSLTAEHSG**
NYSCEANNGLVAQHSDTISLSVIVPVS**RPILTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTL**
GKISAPSGGGASFNLSLTTEHSGIYSCEADNGPEAQRSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDLLE
LHCEALRGSPLILYRFFHEDVTLGNRSSPSGGASLNLSLTAEHSGNYSCEADNGLGAQRSETVTLYITGL
TANRSGPFATGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPPDSDSQEPTYHNVPAWEELQP
VYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVASTPVSGSLFLASSAPHR

FIG. 3C

MSK_delDOM9_myc3_mCD8	MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHR
gi|14278719|gb|AAK50059.2|AF3697	MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHR

MSK_delDOM9_myc3_mCD8	YLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVV
gi|14278719|gb|AAK50059.2|AF3697	YLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVV

MSK_delDOM9_myc3_mCD8	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSMT
gi|14278719|gb|AAK50059.2|AF3697	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSMT

MSK_delDOM9_myc3_mCD8	VKIQVQEPFTRPVLRASSFQPISGNPVTLTCETQLSLERSDVPLRFRFFRDDQTLGLGWS
gi|14278719|gb|AAK50059.2|AF3697	VKIQVQEPFTRPVLRASSFQPISGNPVTLTCETQLSLERSDVPLRFRFFRDDQTLGLGWS

MSK_delDOM9_myc3_mCD8	LSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRSWIQVQIPASHPVLTLSPEKALNFE
gi|14278719|gb|AAK50059.2|AF3697	LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE

MSK_delDOM9_myc3_mCD8	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSGNYYCTADNG
gi|14278719|gb|AAK50059.2|AF3697	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSGNYYCTADNG

MSK_delDOM9_myc3_mCD8	LGAKPSKAVSLSVTVPVSHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA
gi|14278719|gb|AAK50059.2|AF3697	LGAKPSKAVSLSVTVPVSHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA

MSK_delDOM9_myc3_mCD8	LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHPVLTLSSA
gi|14278719|gb|AAK50059.2|AF3697	LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHPVLTLSSA

FIG. 3D

MSK_delDOM9_myc3_mCD8	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYY
gi|14278719|gb|AAK50059.2|AF3697	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYY

MSK_delDOM9_myc3_mCD8	CTADNGFGPQRSEVVSLFVTVPVSRPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWF
gi|14278719|gb|AAK50059.2|AF3697	CTADNGFGPQRSEVVSLFVTVPVSRPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWF

MSK_delDOM9_myc3_mCD8	YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANNGLVAQHSDTISLSVIVPVSRPI
gi|14278719|gb|AAK50059.2|AF3697	YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANNGLVAQHSDTISLSVIVPVSRPI

MSK_delDOM9_myc3_mCD8	LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTTE
gi|14278719|gb|AAK50059.2|AF3697	LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTTE

MSK_delDOM9_myc3_mCD8	HSGIYSCEADNGlEAQRSEMVTLKVAaaaaQkLIS--------------------------
gi|14278719|gb|AAK50059.2|AF3697	HSGIYSCEADNGpEAQRSEMVTLKVAvpvsRpVLTlrapgthaavgdllelhcealrgsp

MSK_delDOM9_myc3_mCD8	---------------------eedLeqkLiSEedleqkliSEedL---------------
gi|14278719|gb|AAK50059.2|AF3697	lilyrffhedvtlgnrsspsggasLnlsLtAEhsgnysceADngLgaqrsetvtlyitgl

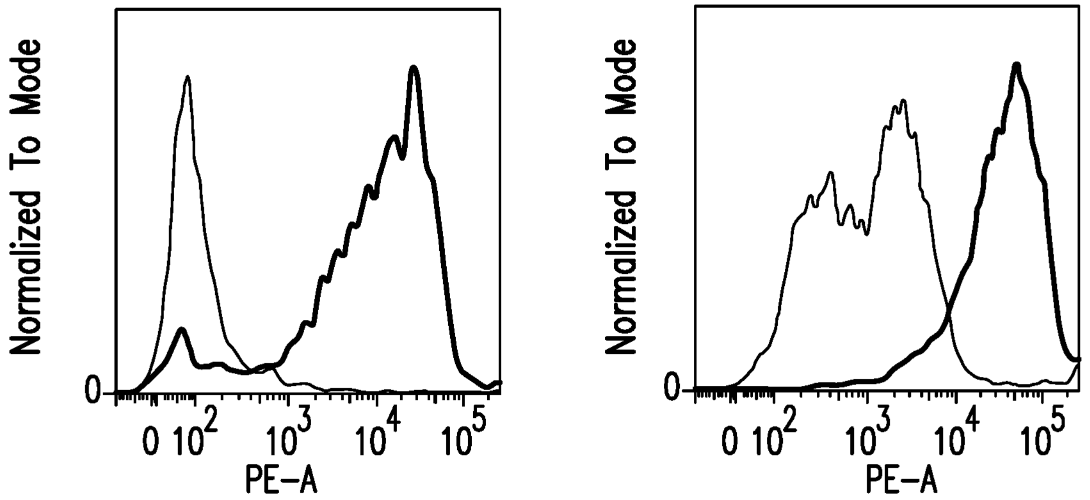
MSK_delDOM9_myc3_mCD8	---------TGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPsDSDSQEPTYH
gi|14278719|gb|AAK50059.2|AF3697	tanrsgpfaTGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPpDSDSQEPTYH

MSK_delDOM9_myc3_mCD8	NVPAWEELQPVYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA
gi|14278719|gb|AAK50059.2|AF3697	NVPAWEELQPVYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA

MSK_delDOM9_myc3_mCD8	STPVSGSLFLASSAPHR
gi|14278719|gb|AAK50059.2|AF3697	STPVSGSLFLASSAPHR

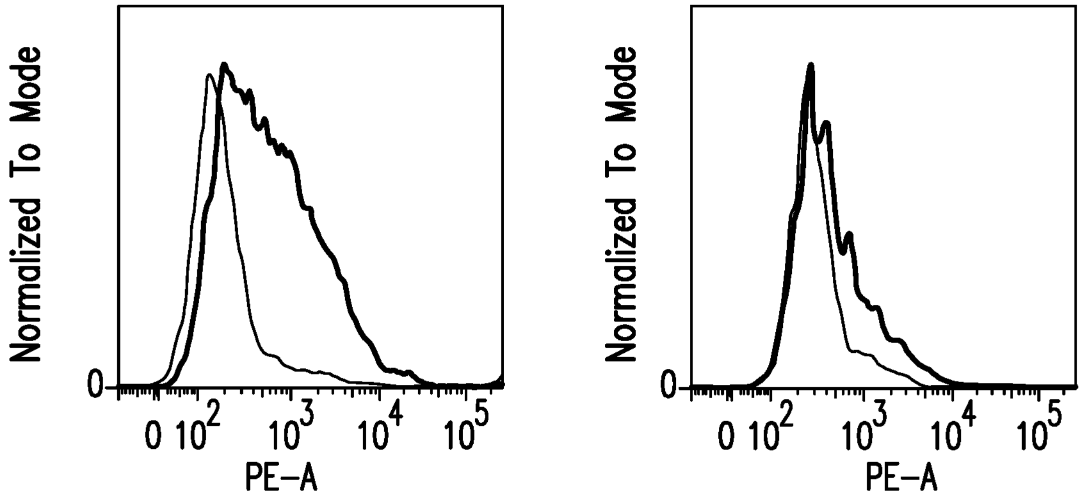
FIG. 3D (continued)

ET200-39



	Sample Name	Median, PE-A
━━	D05+Raji-FcRL5.fcs	1.11E4
──	A04+Raji-FcRL5.fcs	82.1

	Sample Name	Median, PE-A
━━	D05+3T3-FcRL5.fcs	3.76E4
──	A04+3T3-FcRL5.fcs	1137



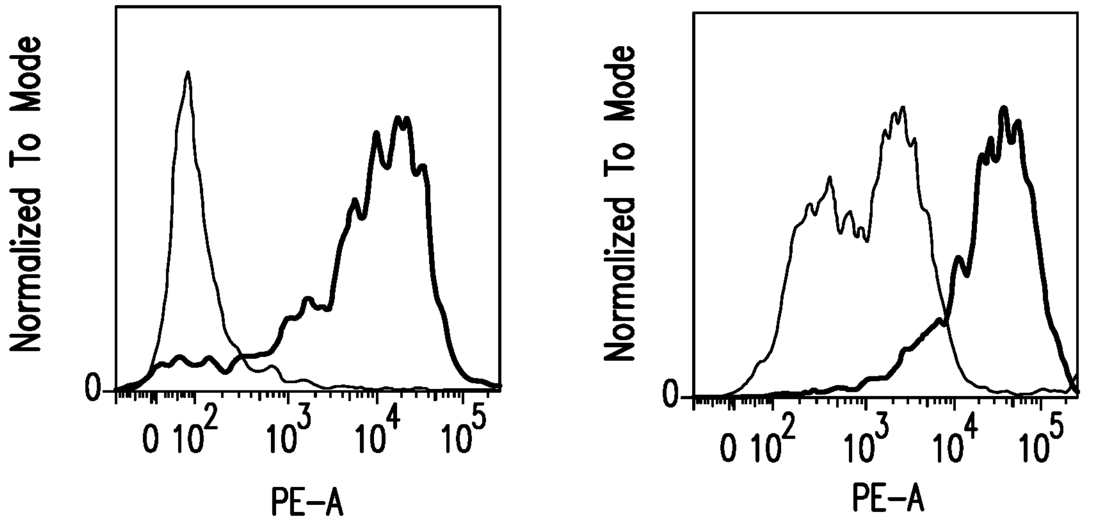
	Sample Name	Median, PE-A
━━	D05+3T3-FcRL5-Delta.fcs	496
──	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
━━	D05+NIH 3T3.fcs	379
──	A04+NIH 3t3.fcs	271

── Negative control phage
━━ ET200 phage

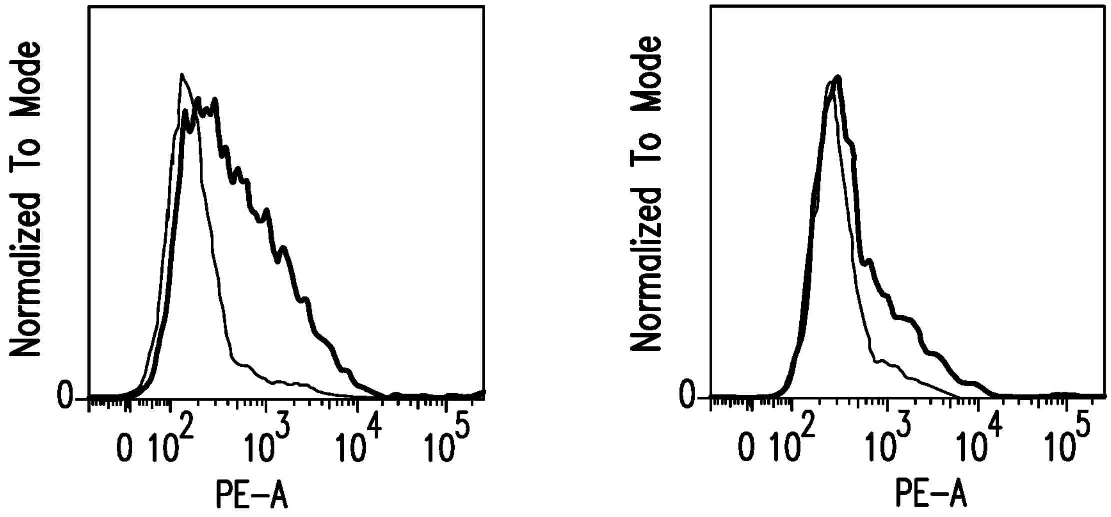
FIG.4

ET200-104



	Sample Name	Median, PE-A
━━	E11+Raji-FcRL5.fcs	9165
──	A04+Raji-FcRL5.fcs	82.1

	Sample Name	Median, PE-A
━━	E11+3T3-FcRL5.fcs	2.91E4
──	A04+Raji-FcRL5.fcs	1137



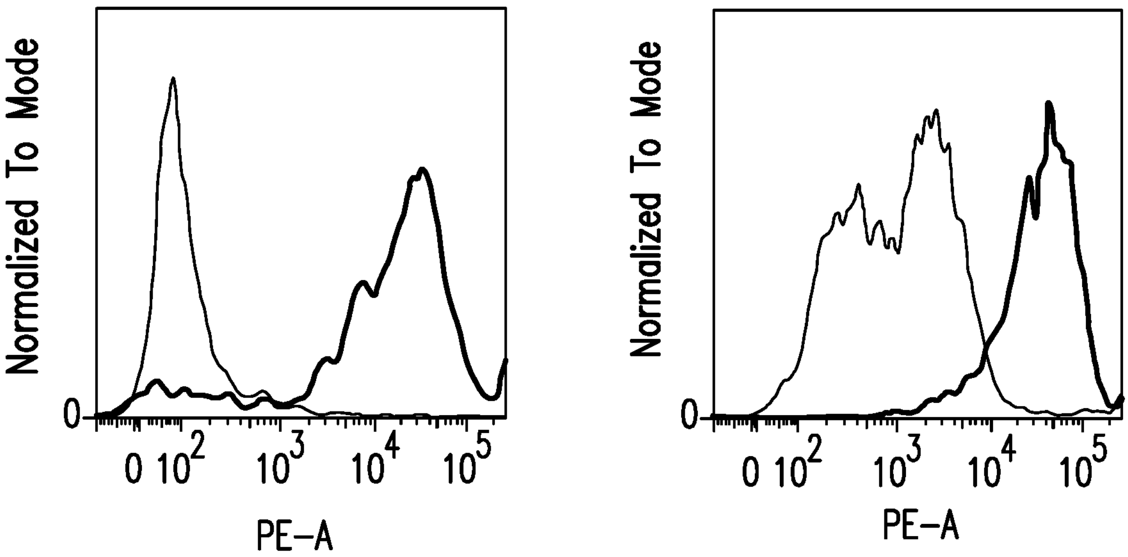
	Sample Name	Median, PE-A
━━	E11+3T3-FcRL5-Delta.fcs	387
──	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
━━	E11+NIH 3T3.fcs	360
──	A04+NIH 3T3.fcs	271

── Negative control phage
━━ ET200 phage

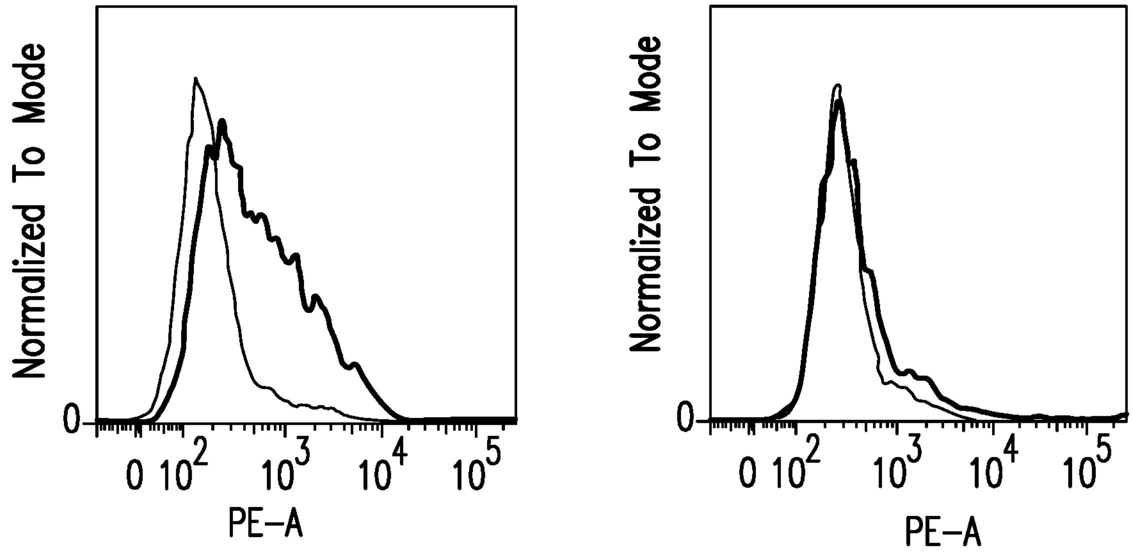
FIG. 5

ET200-105



	Sample Name	Median, PE-A
━	E12+Raji-FcRL5.fcs	1.80E4
─	A04+Raji-FcRL5.fcs	82.1

	Sample Name	Median, PE-A
━	E12+3T3-FcRL5.fcs	3.52E4
─	A04+3T3-FcRL5.fcs	1137

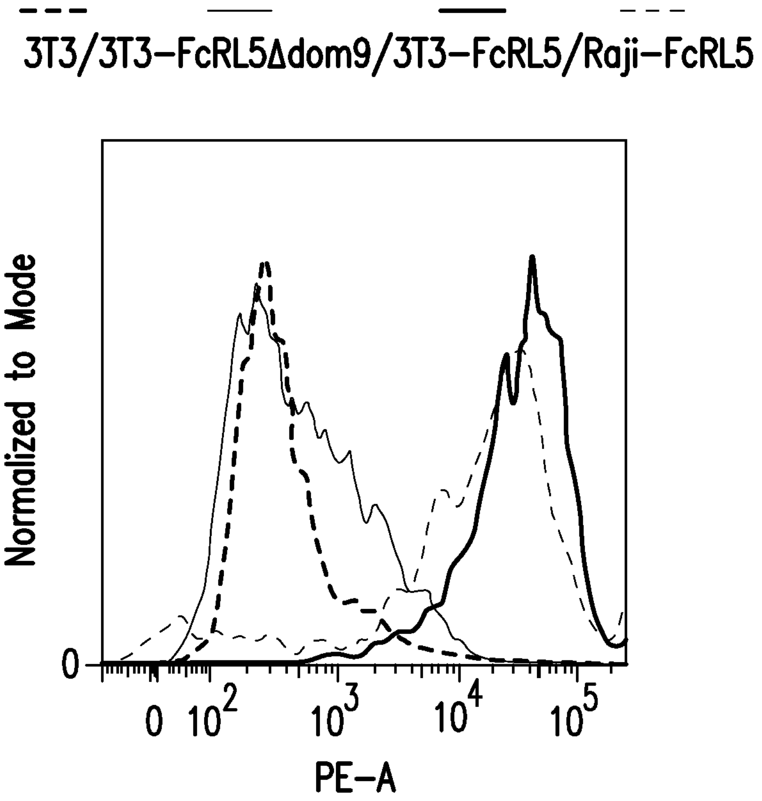


	Sample Name	Median, PE-A
━	E12+3T3-FcRL5-Delta.fcs	415
─	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
━	E12+NIH 3T3.fcs	309
─	A04+NIH 3T3.fcs	271

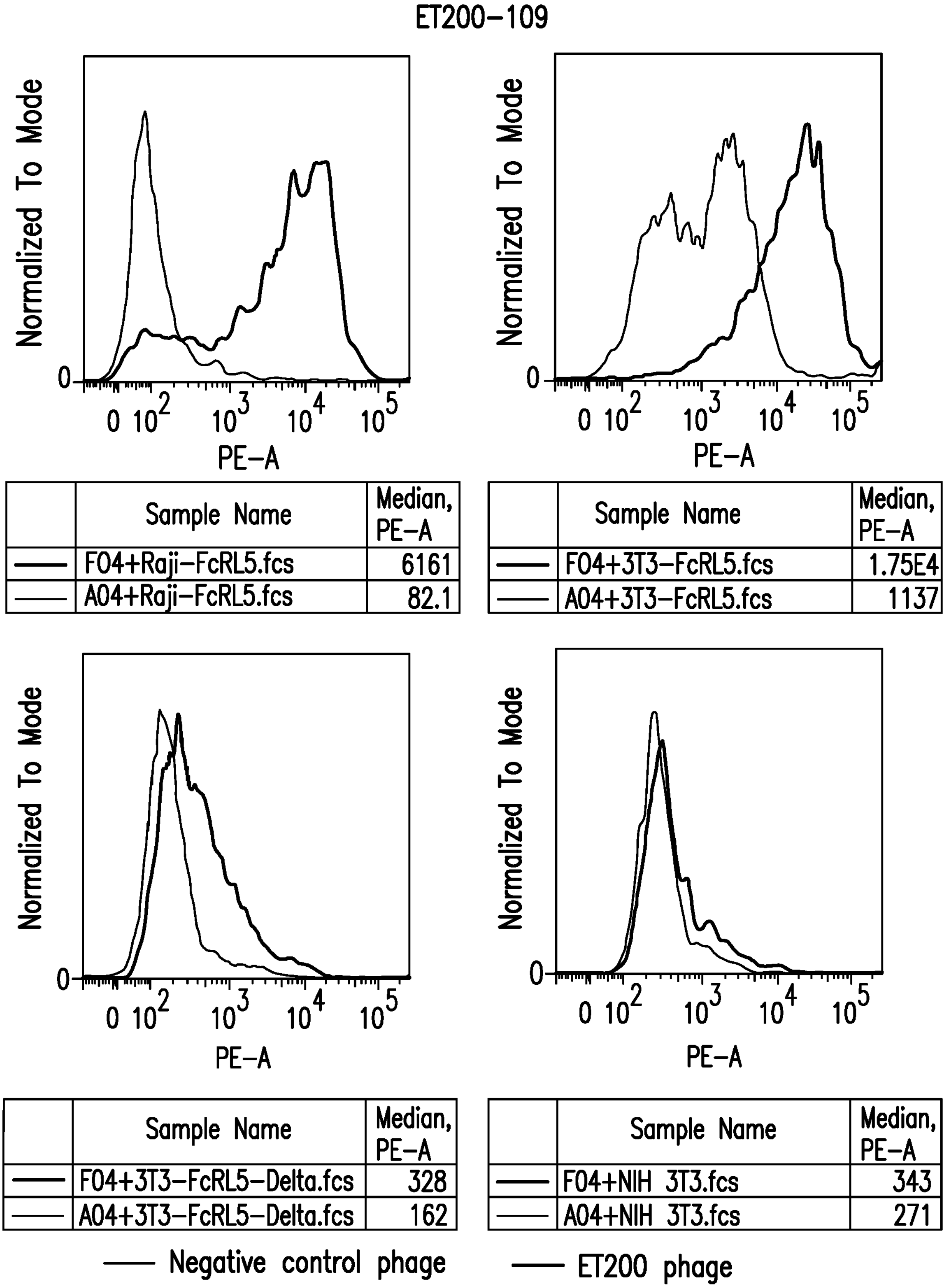
─ Negative control phage ━ ET200 phage

FIG. 6



	Sample Name	Median, PE-A
- - -	E12+Raji-FcRL5.fcs	1.80E4
– – –	E12+NIH 3T3.fcs	309
—	E12+3T3-FcRL5-Delta.fcs	415
━	E12+3T3-FcRL5.fcs	3.52E4

FIG. 6 (continued)



	Sample Name	Median, PE-A
━	F04+Raji-FcRL5.fcs	6161
─	A04+Raji-FcRL5.fcs	82.1

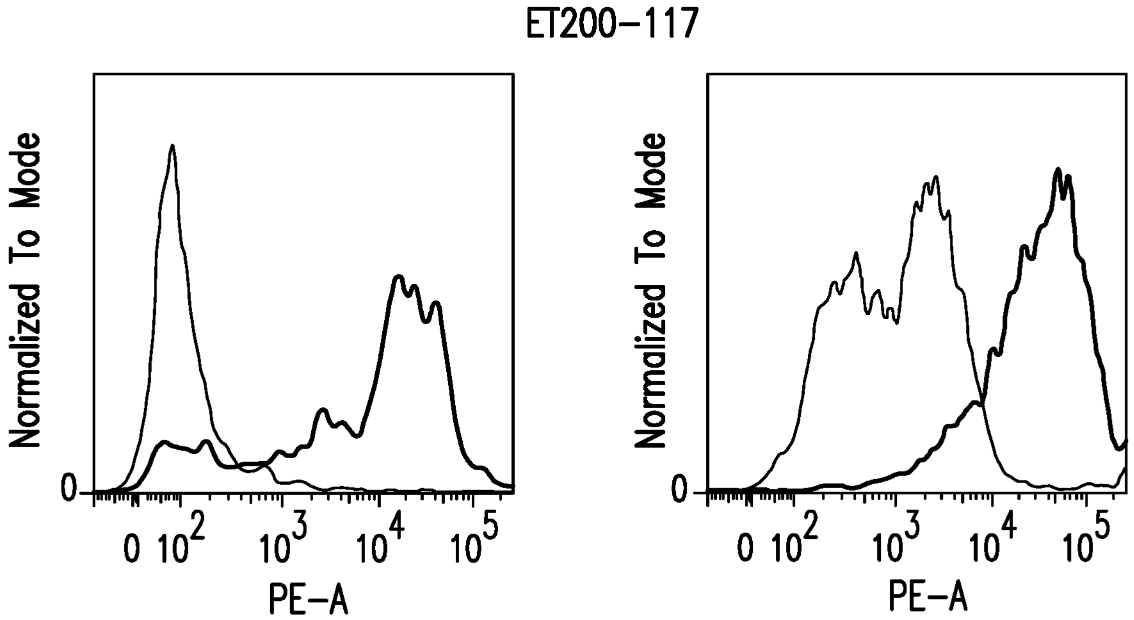
	Sample Name	Median, PE-A
━	F04+3T3-FcRL5.fcs	1.75E4
─	A04+3T3-FcRL5.fcs	1137

	Sample Name	Median, PE-A
━	F04+3T3-FcRL5-Delta.fcs	328
─	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
━	F04+NIH 3T3.fcs	343
─	A04+NIH 3T3.fcs	271

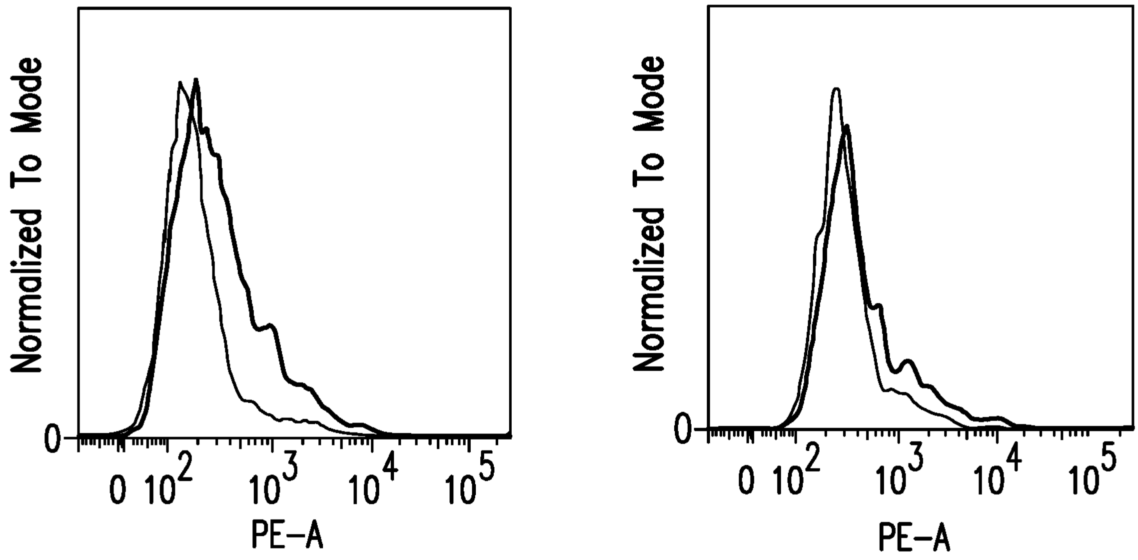
─ Negative control phage ━ ET200 phage

FIG. 7



	Sample Name	Median, PE-A
——	F12+Raji-FcRL5.fcs	1.27E4
——	A04+Raji-FcRL5.fcs	82.1

	Sample Name	Median, PE-A
——	F12+3T3-FcRL5.fcs	3.23E4
——	A04+3T3-FcRL5.fcs	1137



	Sample Name	Median, PE-A
——	F12+3T3-FcRL5-Delta.fcs	260
——	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
——	F12+NIH 3T3.fcs	317
——	A04+NIH 3T3.fcs	271

—— Negative control phage —— ET200 phage

FIG. 8

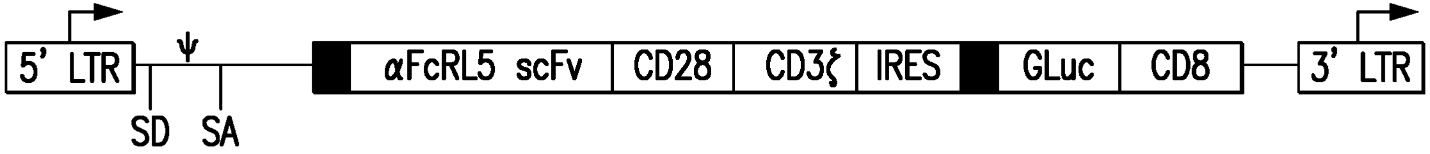

5' LTR
ψ
SD
SA
αFcRL5 scFv
CD28
CD3ζ
IRES
GLuc
CD8
3' LTR

FIG. 9A

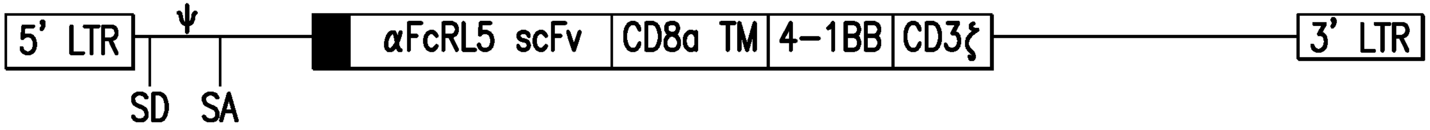

5' LTR
ψ
SD
SA
αFcRL5 scFv
CD8a TM
4-1BB
CD3ζ
3' LTR

FIG. 9B

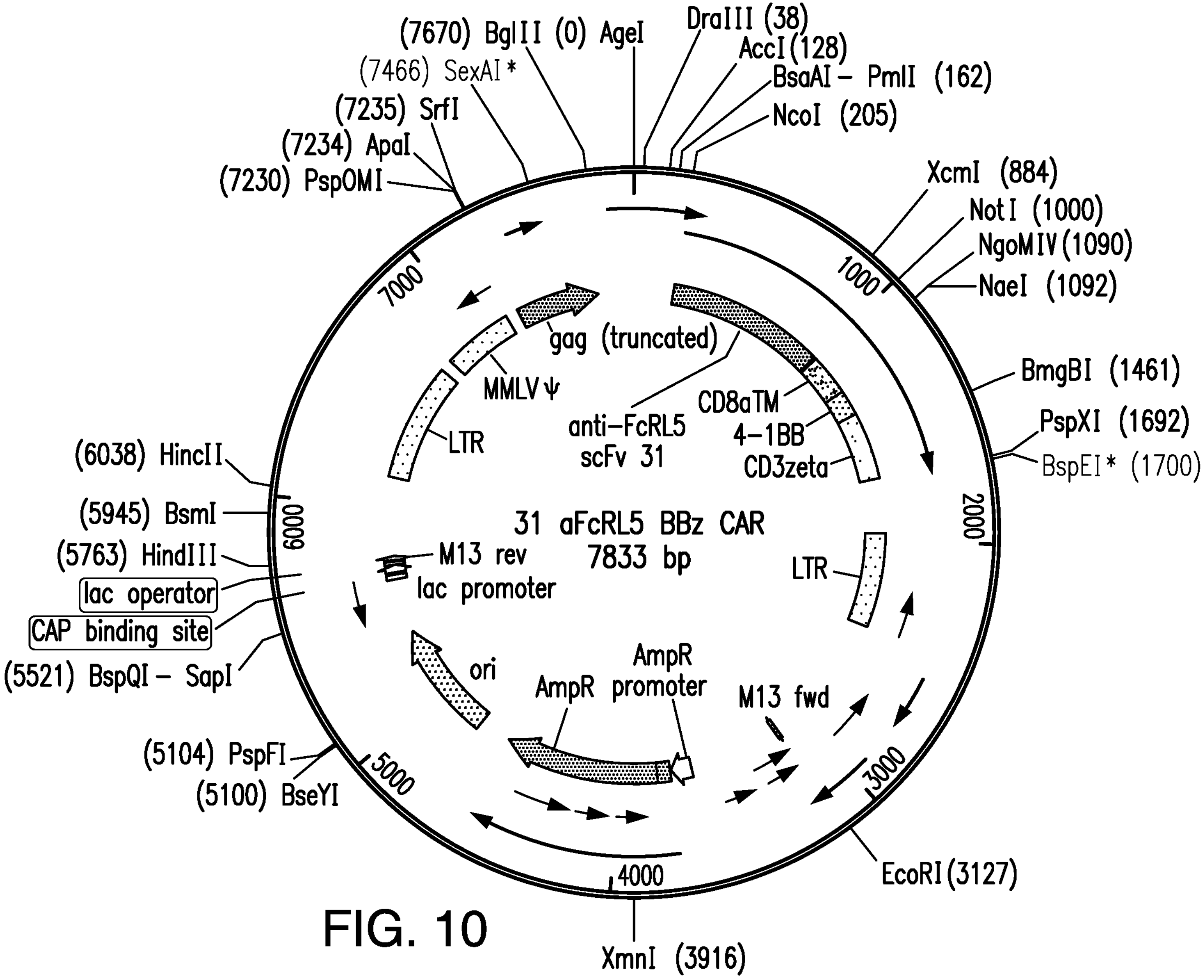

(7670) BglII (0) AgeI
DraIII (38)
AccI (128)
BsaAI – PmlI (162)
NcoI (205)
(7466) SexAI*
(7235) SrfI
(7234) ApaI
(7230) PspOMI
XcmI (884)
NotI (1000)
NgoMIV (1090)
NaeI (1092)
BmgBI (1461)
PspXI (1692)
BspEI* (1700)
EcoRI (3127)
XmnI (3916)
(5104) PspFI
(5100) BseYI
(5521) BspQI – SapI
CAP binding site
lac operator
(5763) HindIII
(5945) BsmI
(6038) HincII
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
MMLV Ψ
LTR
anti–FcRL5
scFv 31
CD8aTM
4–1BB
CD3zeta
31 aFcRL5 BBz CAR
7833 bp
M13 rev
lac promoter
LTR
ori
AmpR
AmpR
promoter
M13 fwd

FIG. 10

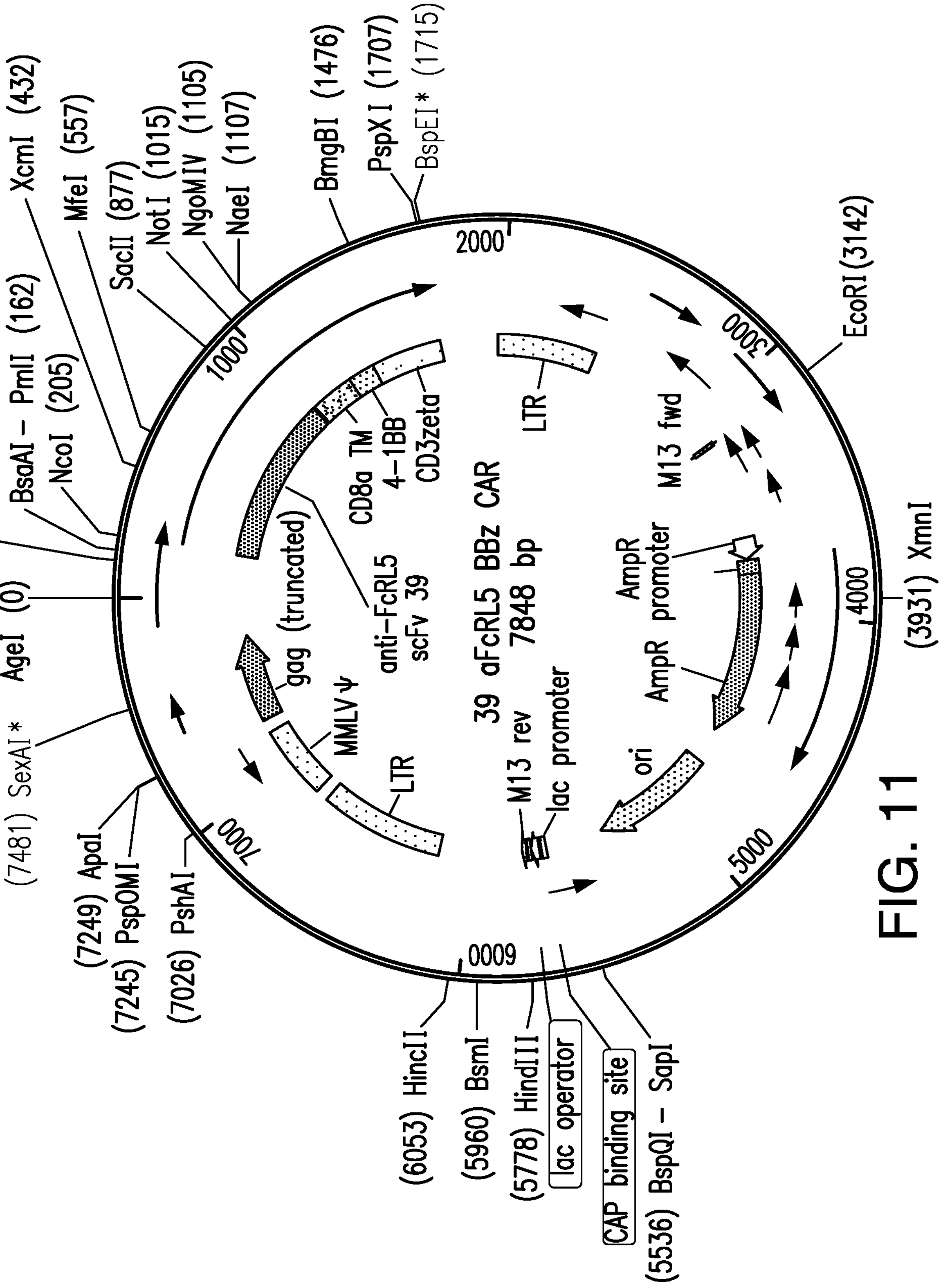

39 aFcRL5 BBz CAR
7848 bp
AgeI (0)
AccI (128)
BsaAI - PmlI (162)
NcoI (205)
XcmI (432)
MfeI (557)
SacII (877)
NotI (1015)
NgoMIV (1105)
NaeI (1107)
BmgBI (1476)
PspXI (1707)
BspEI* (1715)
EcoRI (3142)
(3931) XmnI
(5536) BspQI - SapI
CAP binding site
lac operator
(5778) HindIII
(5960) BsmI
(6053) HincII
(7026) PshAI
(7245) PspOMI
(7249) ApaI
(7481) SexAI*
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
anti-FcRL5 scFv 39
CD8a TM
4-1BB
CD3zeta
LTR
M13 fwd
AmpR promoter
AmpR promoter
AmpR
ori
M13 rev
lac promoter
MMLV Ψ
LTR

FIG. 11

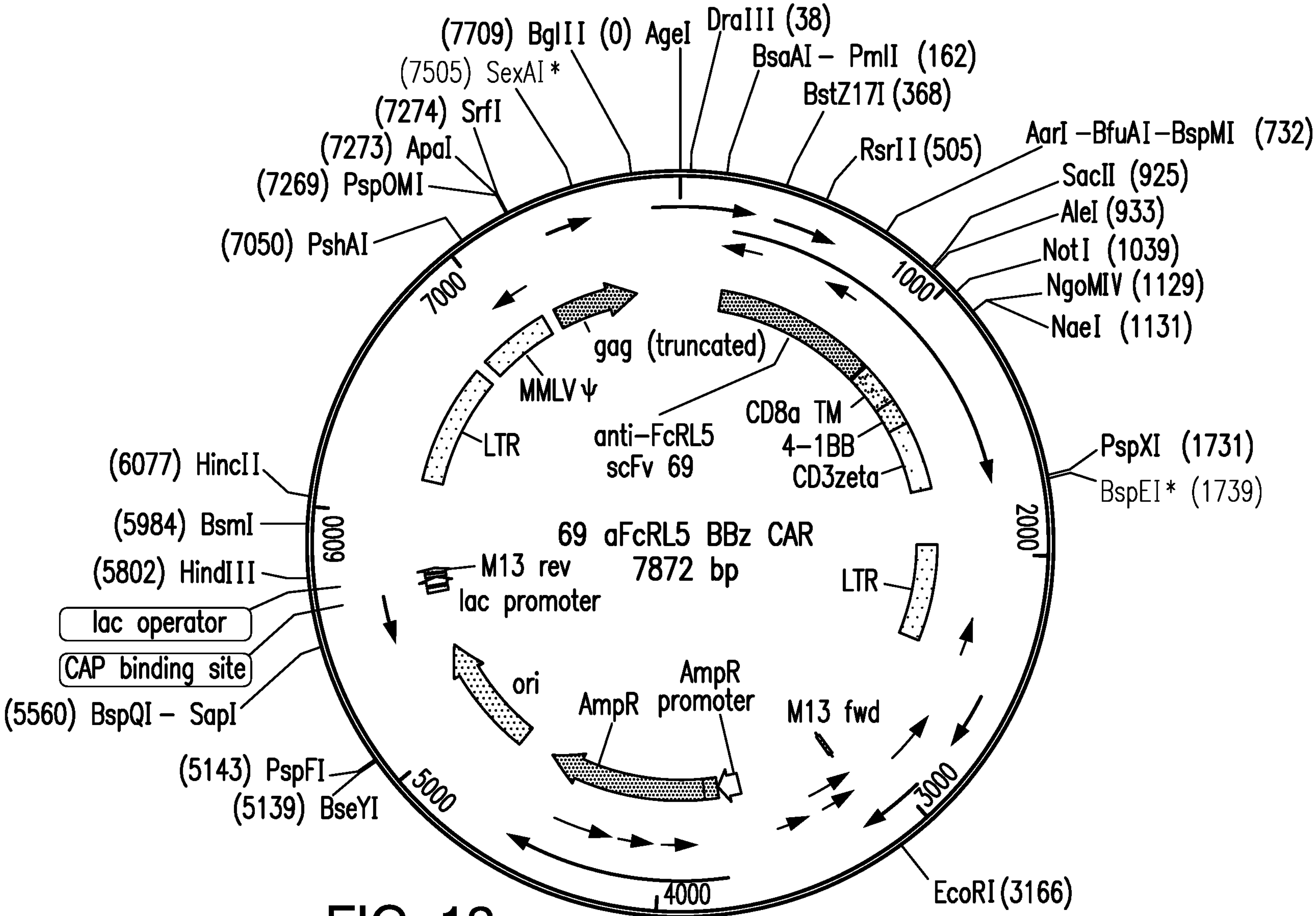

(7709) BglII (0) AgeI
DraIII (38)
BsaAI – PmlI (162)
BstZ17I (368)
RsrII (505)
AarI –BfuAI–BspMI (732)
SacII (925)
AleI (933)
NotI (1039)
NgoMIV (1129)
NaeI (1131)
PspXI (1731)
BspEI* (1739)
EcoRI (3166)
(5139) BseYI
(5143) PspFI
(5560) BspQI – SapI
CAP binding site
lac operator
(5802) HindIII
(5984) BsmI
(6077) HincII
(7050) PshAI
(7269) PspOMI
(7273) ApaI
(7274) SrfI
(7505) SexAI*
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
MMLV ψ
LTR
anti–FcRL5
scFv 69
CD8a TM
4–1BB
CD3zeta
69 aFcRL5 BBz CAR
7872 bp
M13 rev
lac promoter
LTR
ori
AmpR
AmpR
promoter
M13 fwd

FIG. 12

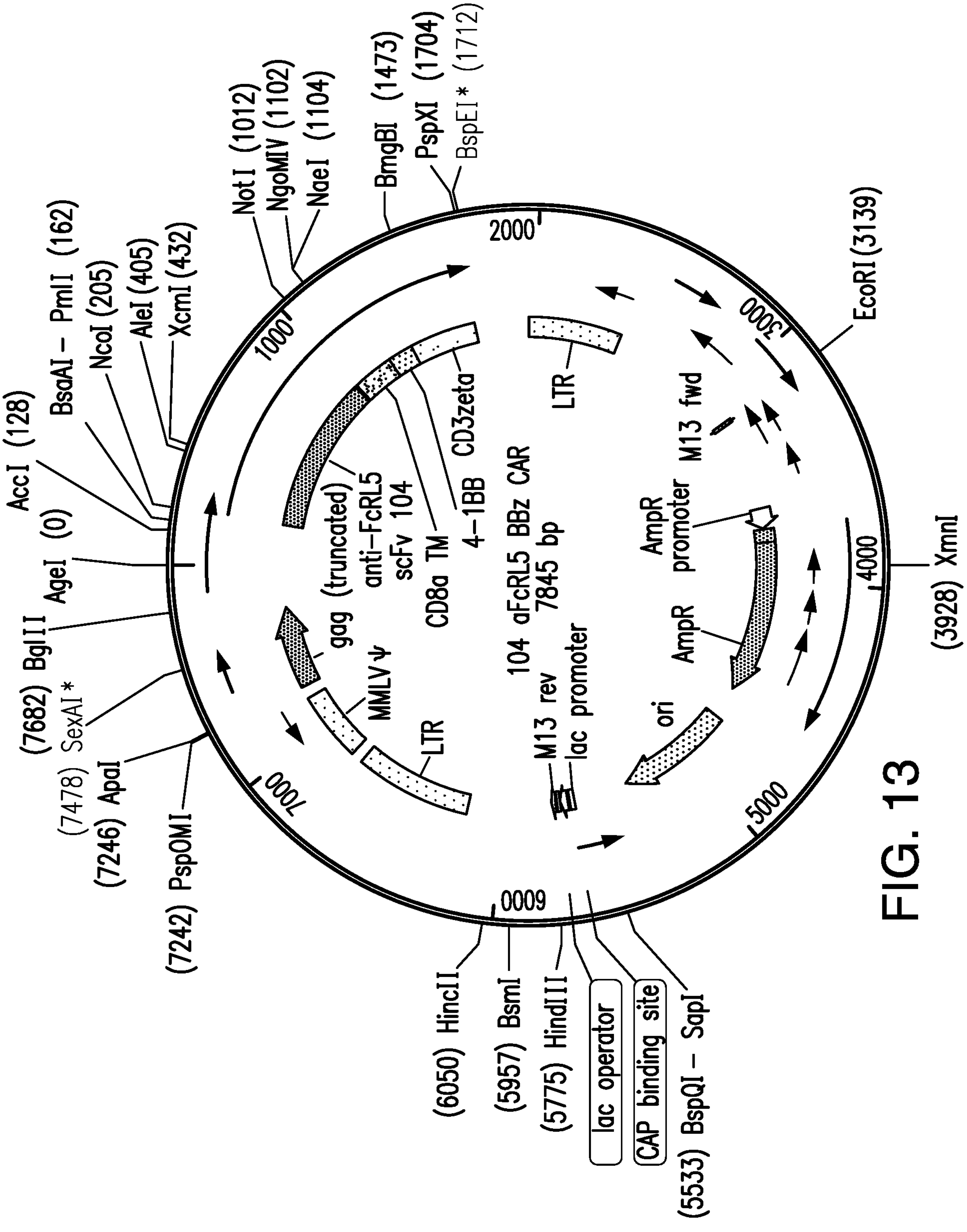

104 aFcRL5 BBz CAR
7845 bp
AgeI (0)
AccI (128)
BsaAI - PmlI (162)
NcoI (205)
AleI (405)
XcmI (432)
NotI (1012)
NgoMIV (1102)
NaeI (1104)
BmgBI (1473)
PspXI (1704)
BspEI* (1712)
EcoRI (3139)
(3928) XmnI
(5533) BspQI - SapI
CAP binding site
lac operator
(5775) HindIII
(5957) BsmI
(6050) HincII
(7242) PspOMI
(7246) ApaI
(7478) SexAI*
(7682) BglII
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
anti-FcRL5
scFv 104
CD8a TM
4-1BB
CD3zeta
LTR
M13 fwd
AmpR promoter
AmpR
ori
M13 rev
lac promoter
LTR
MMLV Ψ

FIG. 13

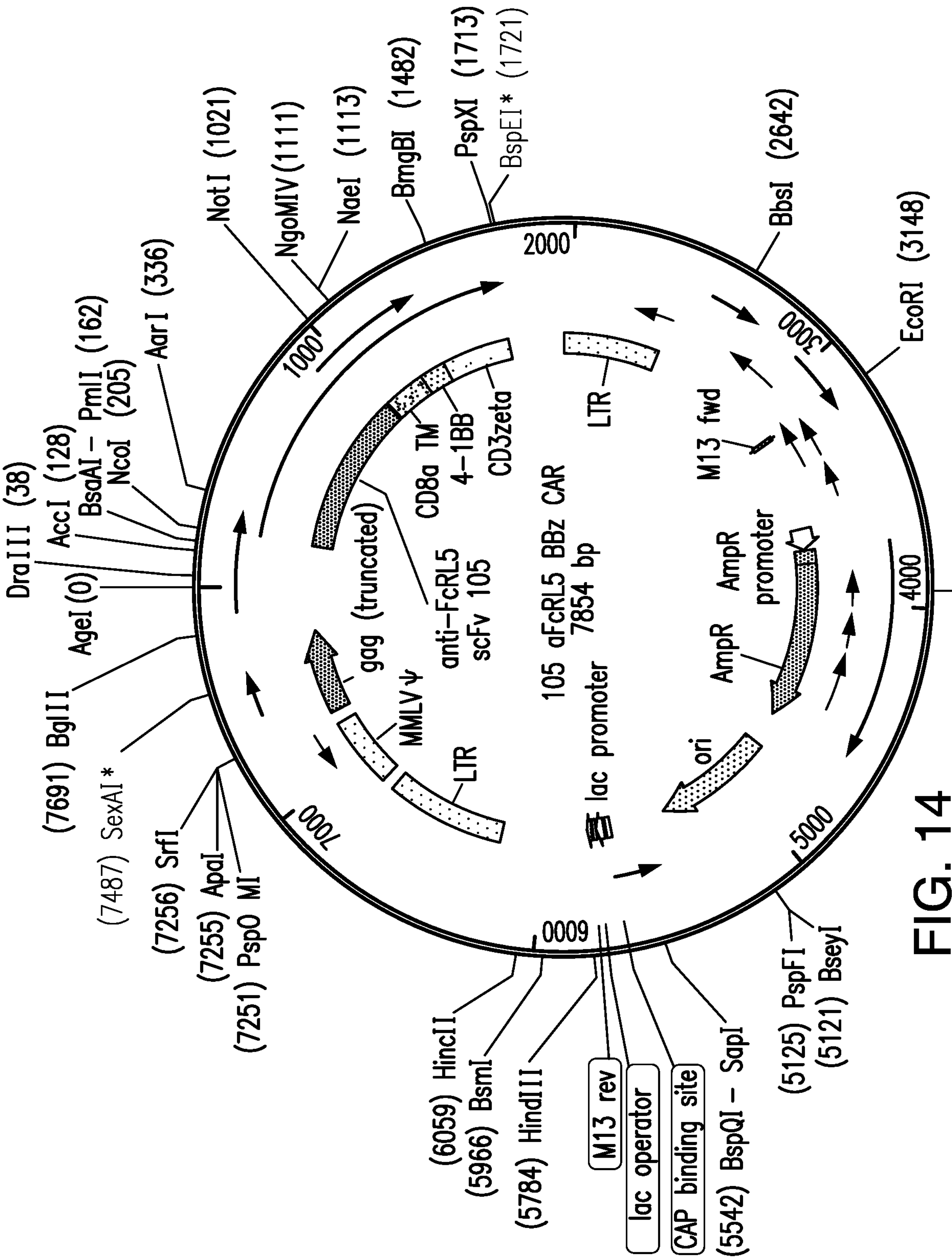

105 aFcRL5 BBz CAR
7854 bp
AgeI (0)
DraIII (38)
AccI (128)
BsaAI - PmlI (162)
NcoI (205)
AarI (336)
NotI (1021)
NgoMIV (1111)
NaeI (1113)
BmgBI (1482)
PspXI (1713)
BspEI* (1721)
BbsI (2642)
EcoRI (3148)
(3937) XmnI
(5121) BseyI
(5125) PspFI
(5542) BspQI - SapI
CAP binding site
lac operator
M13 rev
(5784) HindIII
(5966) BsmI
(6059) HincII
(7251) PspO MI
(7255) ApaI
(7256) SrfI
(7487) SexAI*
(7691) BglII
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
anti-FcRL5 scFv 105
CD8a TM
4-1BB
CD3zeta
LTR
M13 fwd
AmpR promoter
AmpR
ori
lac promoter
MMLV Ψ
LTR

FIG. 14

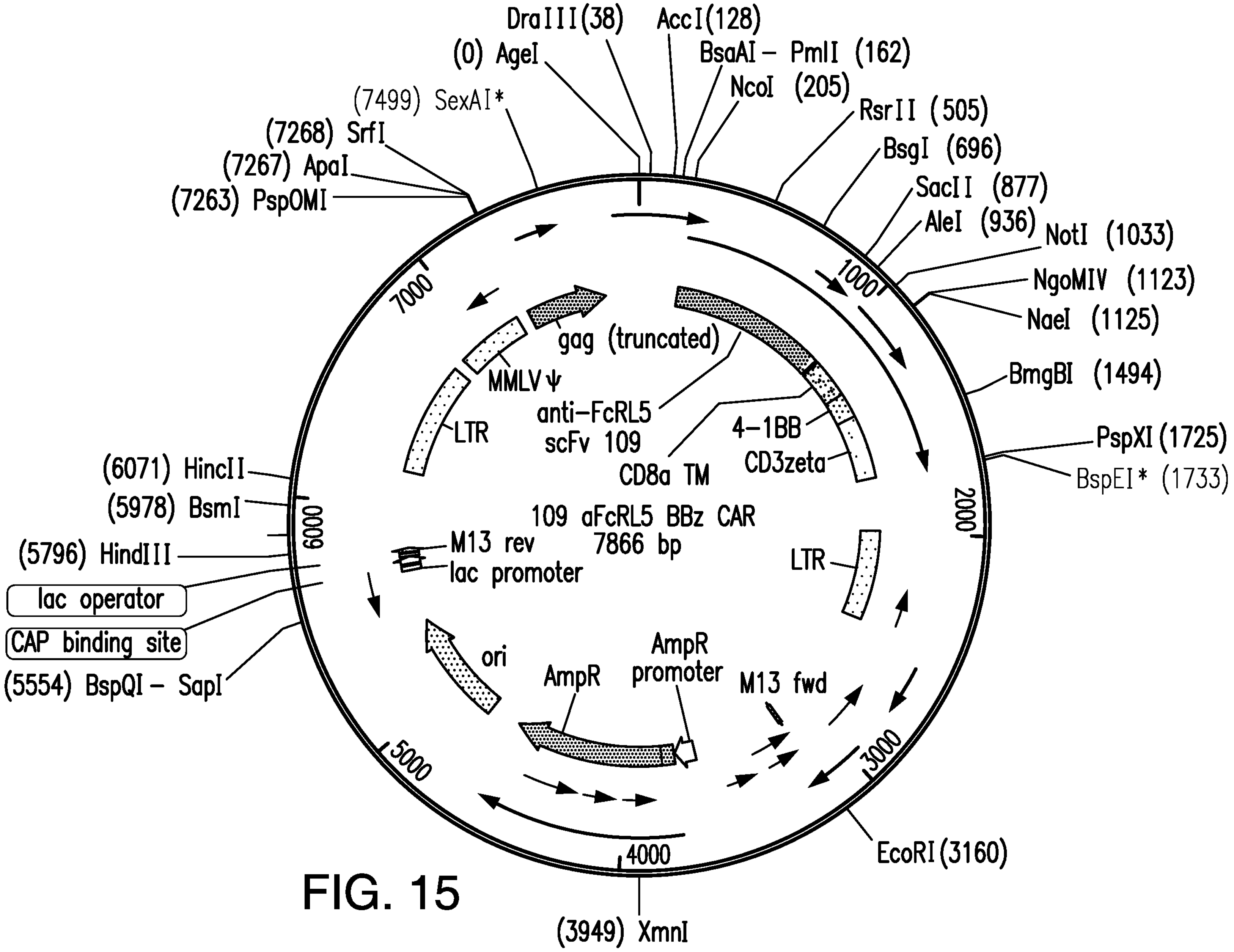

(0) AgeI
DraIII(38)
AccI(128)
BsaAI – PmlI (162)
NcoI (205)
RsrII (505)
BsgI (696)
SacII (877)
AleI (936)
NotI (1033)
NgoMIV (1123)
NaeI (1125)
BmgBI (1494)
PspXI (1725)
BspEI* (1733)
EcoRI (3160)
(3949) XmnI
(5554) BspQI – SapI
CAP binding site
lac operator
(5796) HindIII
(5978) BsmI
(6071) HincII
(7263) PspOMI
(7267) ApaI
(7268) SrfI
(7499) SexAI*
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
MMLV ψ
LTR
anti-FcRL5
scFv 109
CD8a TM
4-1BB
CD3zeta
109 aFcRL5 BBz CAR
7866 bp
M13 rev
lac promoter
LTR
ori
AmpR
AmpR
promoter
M13 fwd

FIG. 15

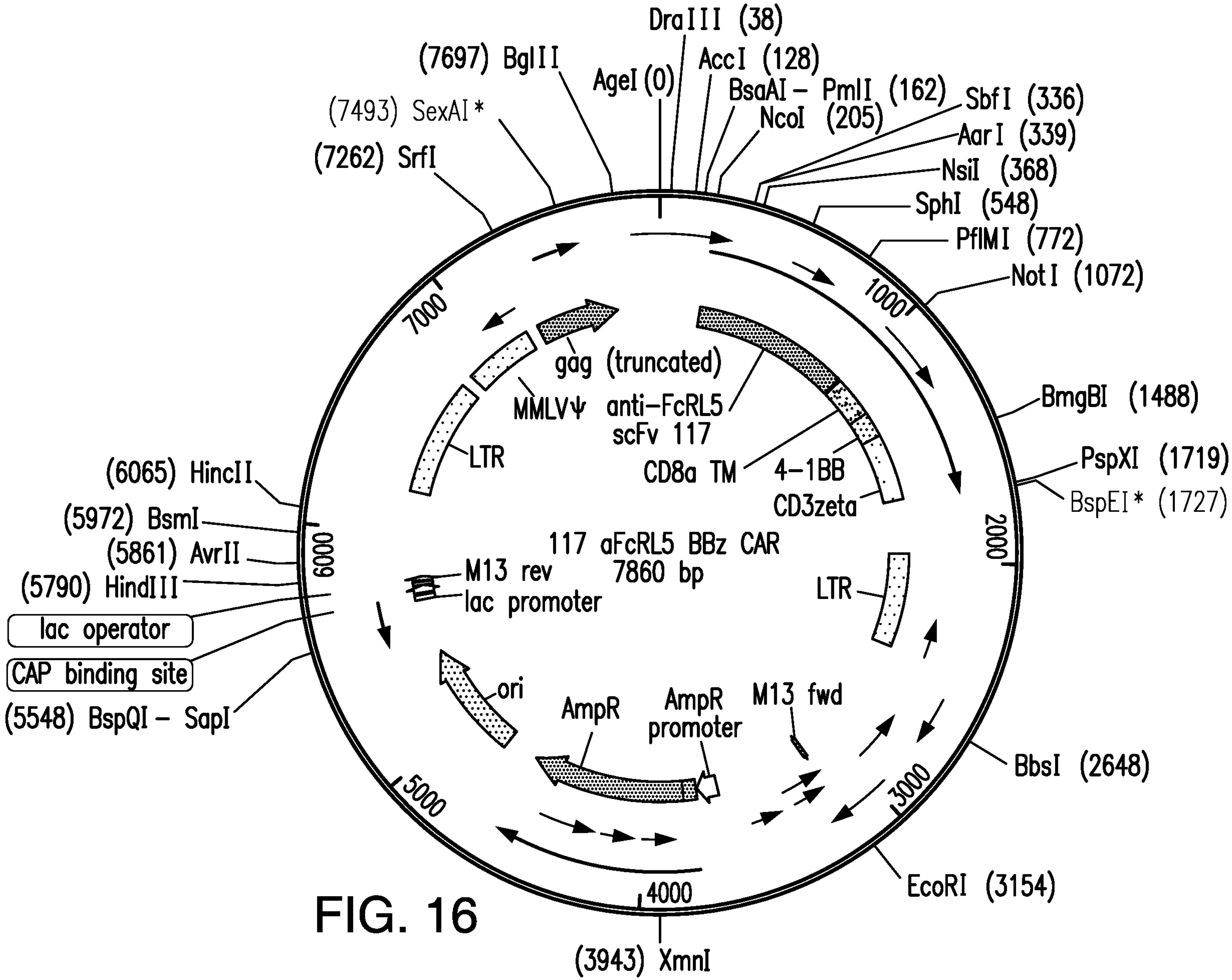

DraIII (38)
(7697) BglII
AgeI (0)
AccI (128)
BsaAI - PmlI (162)
NcoI (205)
(7493) SexAI*
SbfI (336)
AarI (339)
NsiI (368)
SphI (548)
PflMI (772)
(7262) SrfI
NotI (1072)
7000
1000
gag (truncated)
MMLVψ
anti-FcRL5
scFv 117
LTR
BmgBI (1488)
CD8a TM
4-1BB
CD3zeta
PspXI (1719)
BspEI* (1727)
(6065) HincII
(5972) BsmI
(5861) AvrII
(5790) HindIII
lac operator
CAP binding site
(5548) BspQI - SapI
6000
2000
117 aFcRL5 BBz CAR
7860 bp
M13 rev
lac promoter
LTR
ori
AmpR
AmpR
promoter
M13 fwd
BbsI (2648)
5000
3000
EcoRI (3154)
4000
(3943) XmnI

FIG. 16

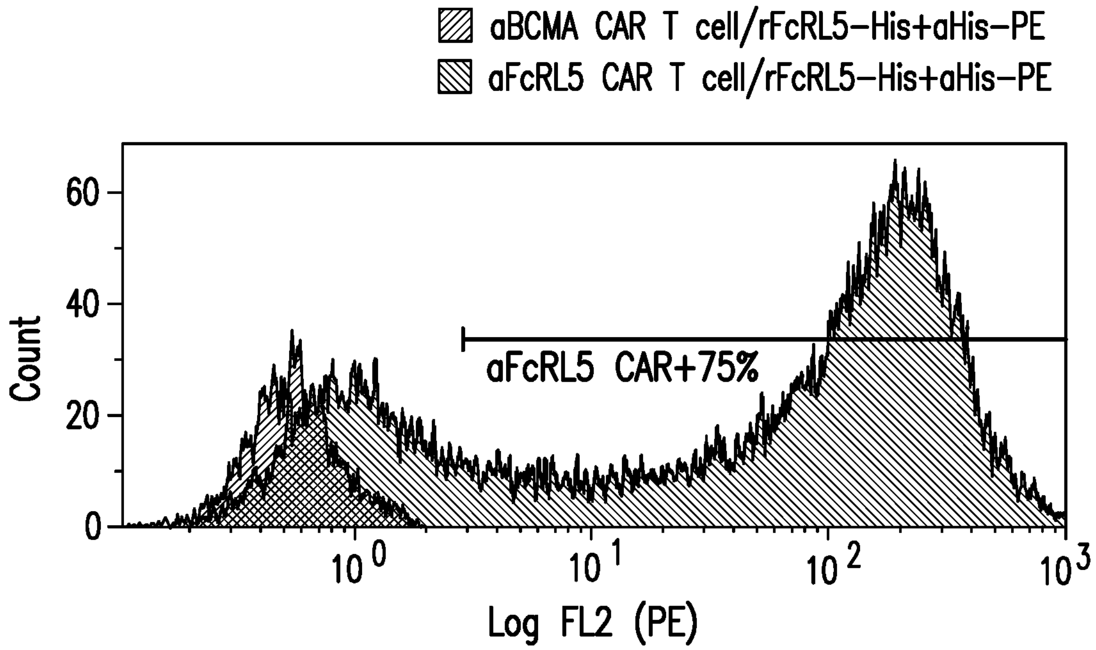

▨ aBCMA CAR T cell/rFcRL5-His+aHis-PE
▧ aFcRL5 CAR T cell/rFcRL5-His+aHis-PE
aFcRL5 CAR+75%
Count
0
20
40
60
10^0
10^1
10^2
10^3
Log FL2 (PE)

FIG. 17

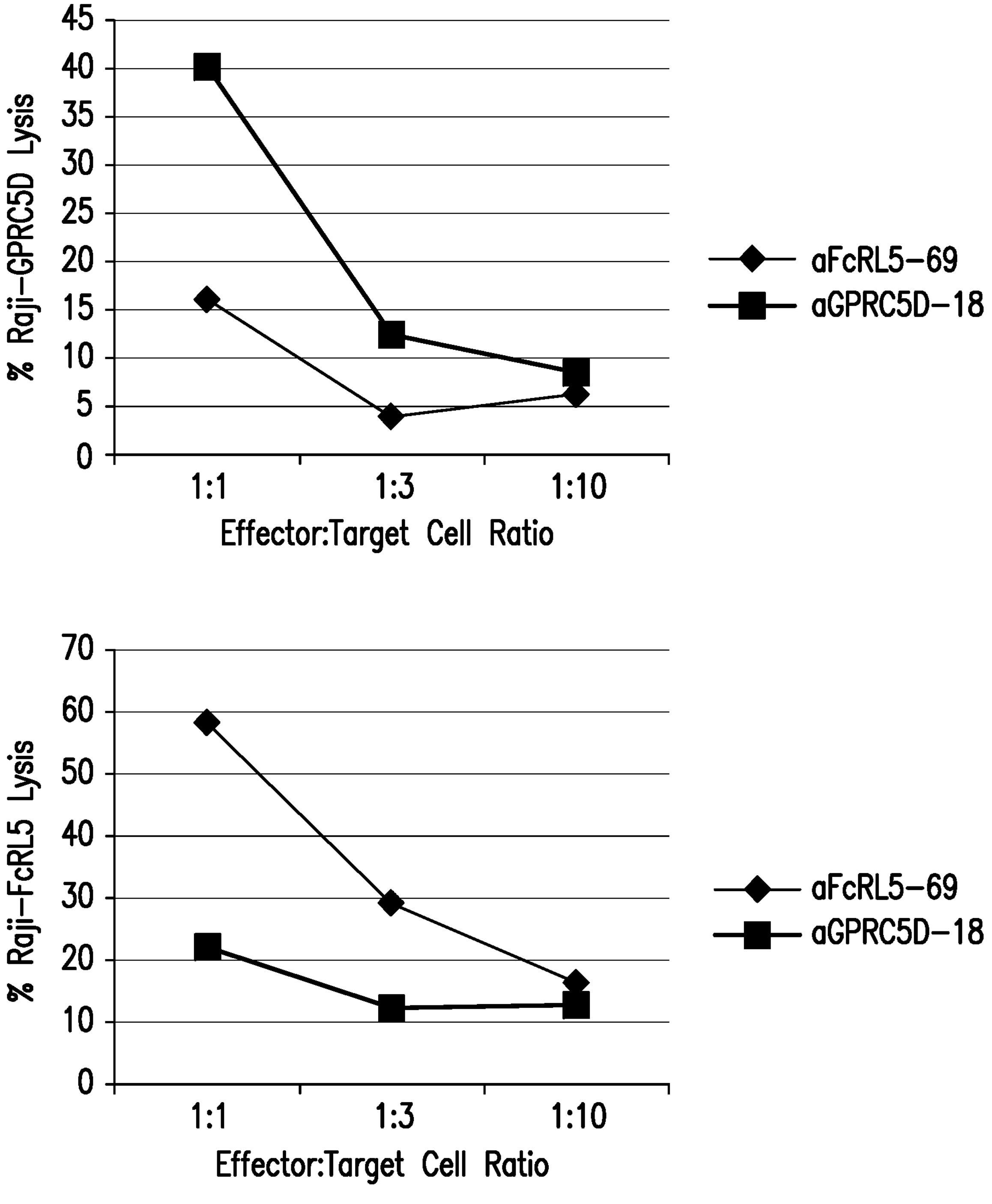

45
40
35
30
25
20
15
10
5
0
% Raji–GPRC5D Lysis
1:1
1:3
1:10
Effector:Target Cell Ratio
aFcRL5–69
aGPRC5D–18
70
60
50
40
30
20
10
0
% Raji–FcRL5 Lysis
1:1
1:3
1:10
Effector:Target Cell Ratio
aFcRL5–69
aGPRC5D–18

FIG. 18

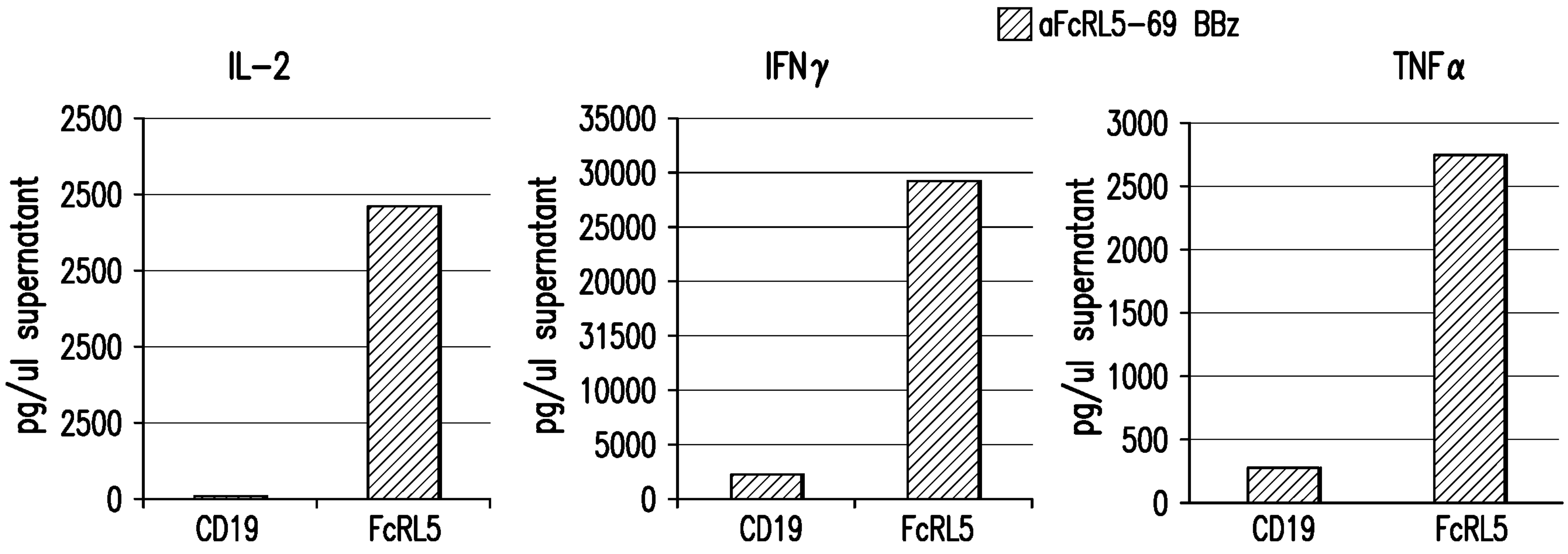

▨ aFcRL5-69 BBz
IL-2
pg/ul supernatant
2500
2500
2500
2500
2500
0
CD19
FcRL5
IFNγ
pg/ul supernatant
35000
30000
25000
20000
31500
10000
5000
0
CD19
FcRL5
TNFα
pg/ul supernatant
3000
2500
2000
1500
1000
500
0
CD19
FcRL5

FIG. 19

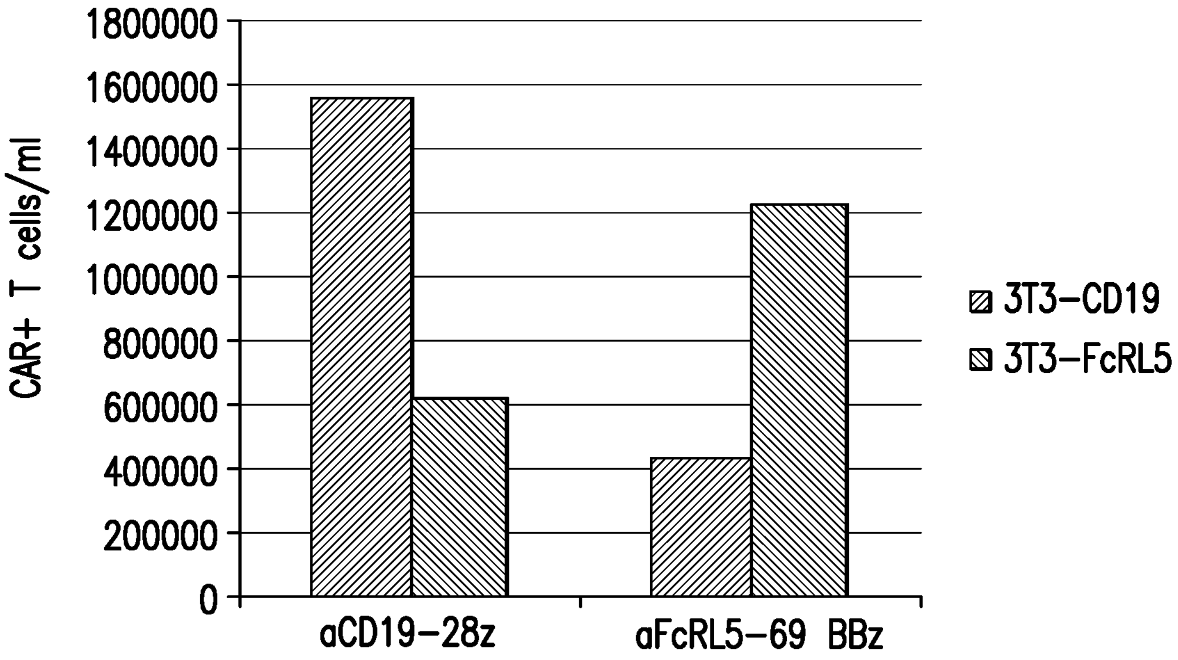

CAR+ T cells/ml
1800000
1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
aCD19-28z
aFcRL5-69 BBz
▨ 3T3-CD19
▧ 3T3-FcRL5

FIG. 20

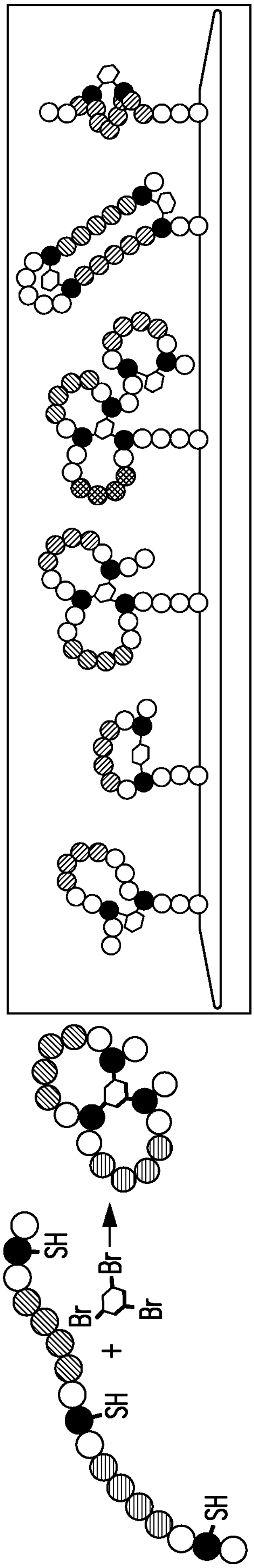


FIG. 21

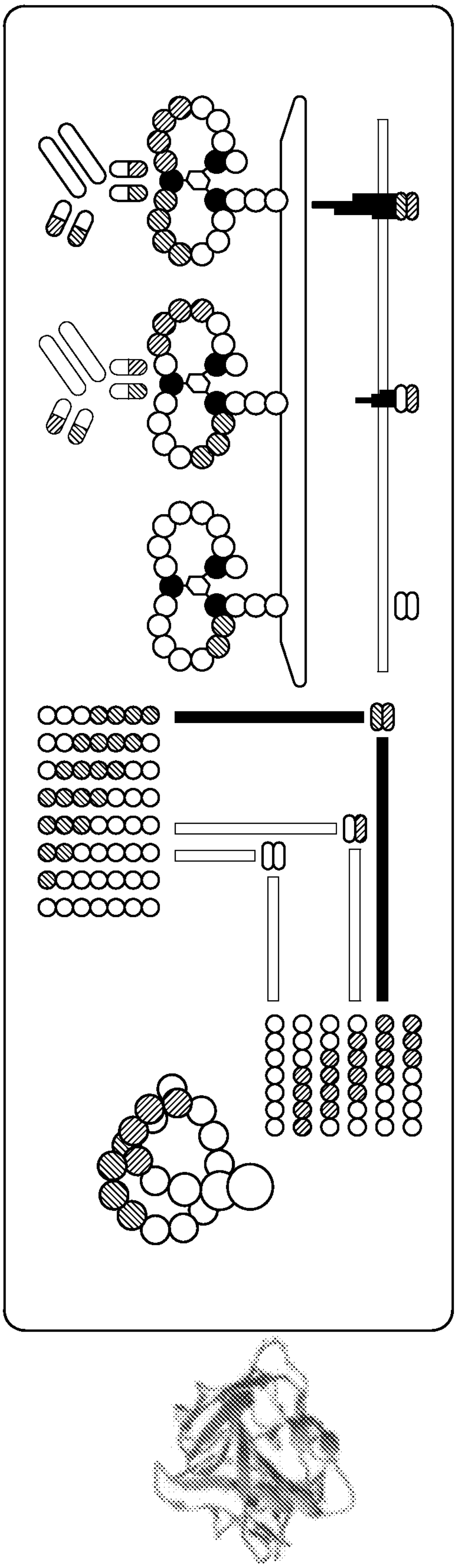


FIG. 22

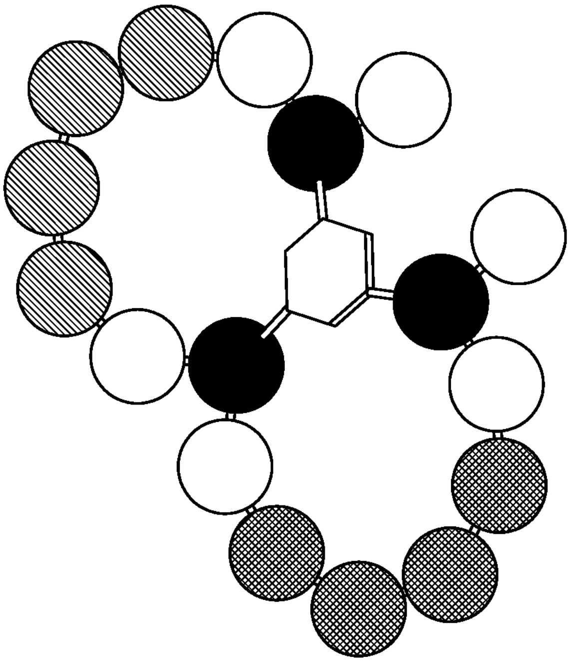


FIG. 23

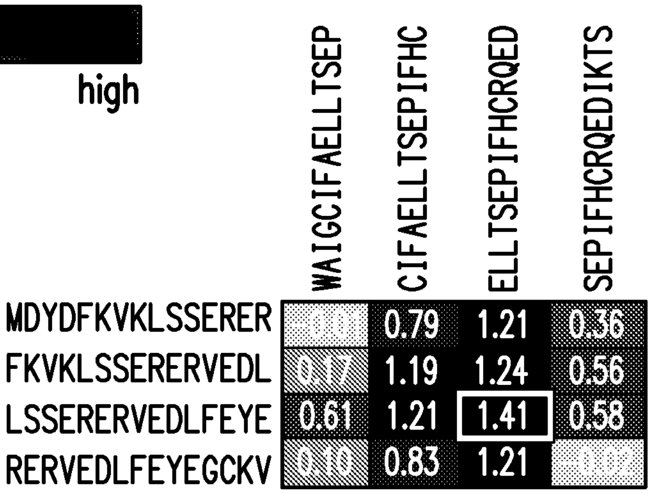
	Loop 1		Loop 2		ELISA
C	MDYDFKVKLSSERER	C	WAIGCIFAELLTSEP	C	−0.01
C	MDYDFKVKLSSERER	C	CIFAELLTSEPIFHC	C	0.79
C	MDYDFKVKLSSERER	C	ELLTSEPIFHCRQED	C	1.21
C	MDYDFKVKLSSERER	C	SEPIFHCRQEDIKTS	C	0.36
C	FKVKLSSERERVEDL	C	WAIGCIFAELLTSEP	C	0.17
C	FKVKLSSERERVEDL	C	CIFAELLTSEPIFHC	C	1.19
C	FKVKLSSERERVEDL	C	ELLTSEPIFHCRQED	C	1.24
C	FKVKLSSERERVEDL	C	SEPIFHCRQEDIKTS	C	0.56
C	LSSERERVEDLFEYE	C	WAIGCIFAELLTSEP	C	0.61
C	LSSERERVEDLFEYE	C	CIFAELLTSEPIFHC	C	1.21
C	LSSERERVEDLFEYE	C	ELLTSEPIFHCRQED	C	1.41 ←
C	LSSERERVEDLFEYE	C	SEPIFHCRQEDIKTS	C	0.58
C	RERVEDLFEYEGCKV	C	WAIGCIFAELLTSEP	C	0.10
C	RERVEDLFEYEGCKV	C	CIFAELLTSEPIFHC	C	0.83
C	RERVEDLFEYEGCKV	C	ELLTSEPIFHCRQED	C	1.21
C	RERVEDLFEYEGCKV	C	SEPIFHCRQEDIKTS	C	−0.02

FIG. 24A

Loop 1 \ Loop 2	WAIGCIFAELLTSEP	CIFAELLTSEPIFHC	ELLTSEPIFHCRQED	SEPIFHCRQEDIKTS
MDYDFKVKLSSERER	−0.01	0.79	1.21	0.36
FKVKLSSERERVEDL	0.17	1.19	1.24	0.56
LSSERERVEDLFEYE	0.61	1.21	1.41 ↑	0.58
RERVEDLFEYEGCKV	0.10	0.83	1.21	−0.02

FIG. 24B

FIG. 24C



	WAIGCIFAELLTSEP	CIFAELLTSEPIFHC	ELLTSEPIFHCRQED	SEPIFHCRQEDIKTS
MDYDFKVKLSSERER	−0.01	0.79	1.21	0.36
FKVKLSSERERVEDL	0.17	1.19	1.24	0.56
LSSERERVEDLFEYE	0.61	1.21	1.41	0.58
RERVEDLFEYEGCKV	0.10	0.83	1.21	−0.02

FIG. 24D

FIGURE 25

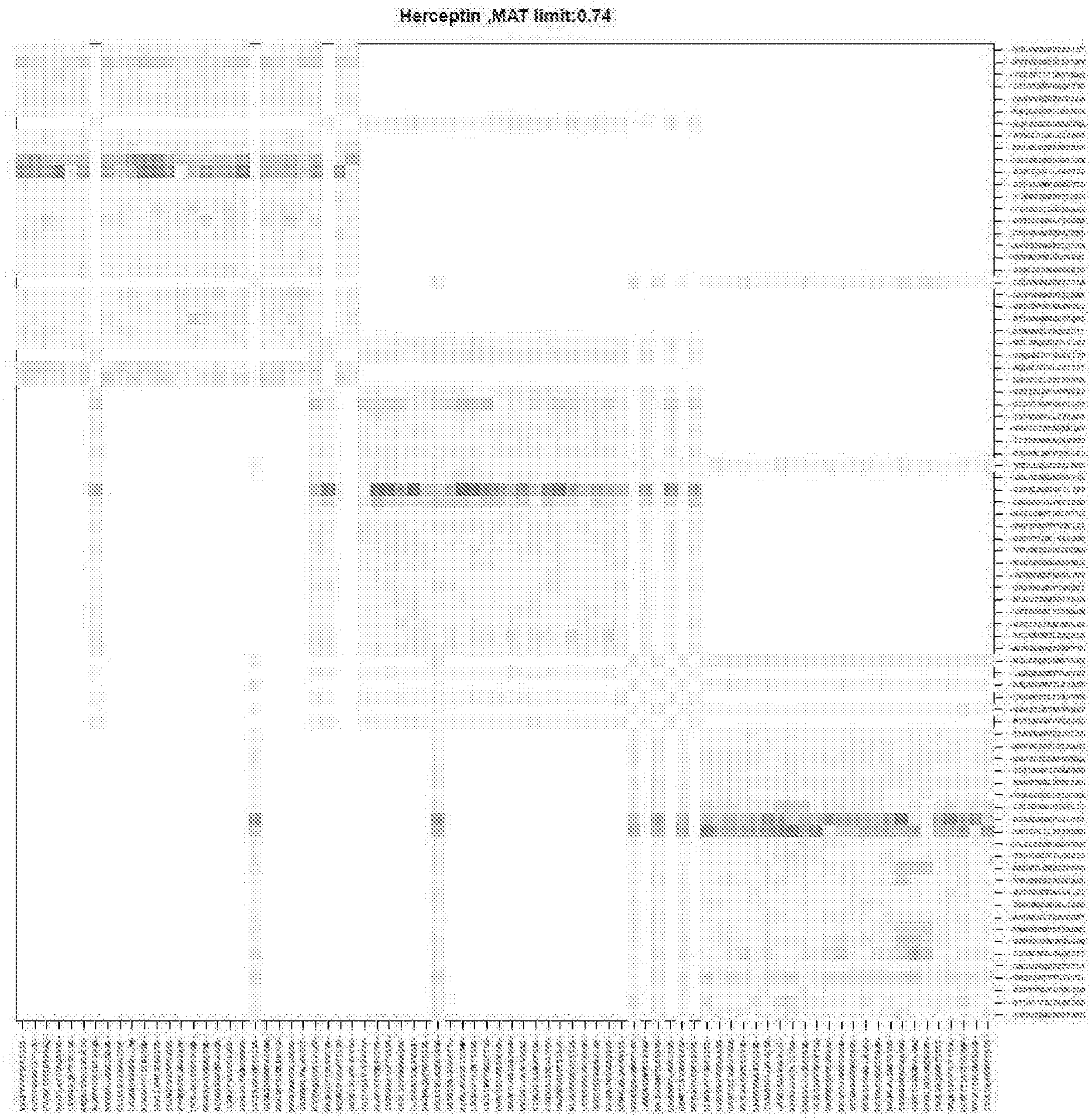


FIGURE 26

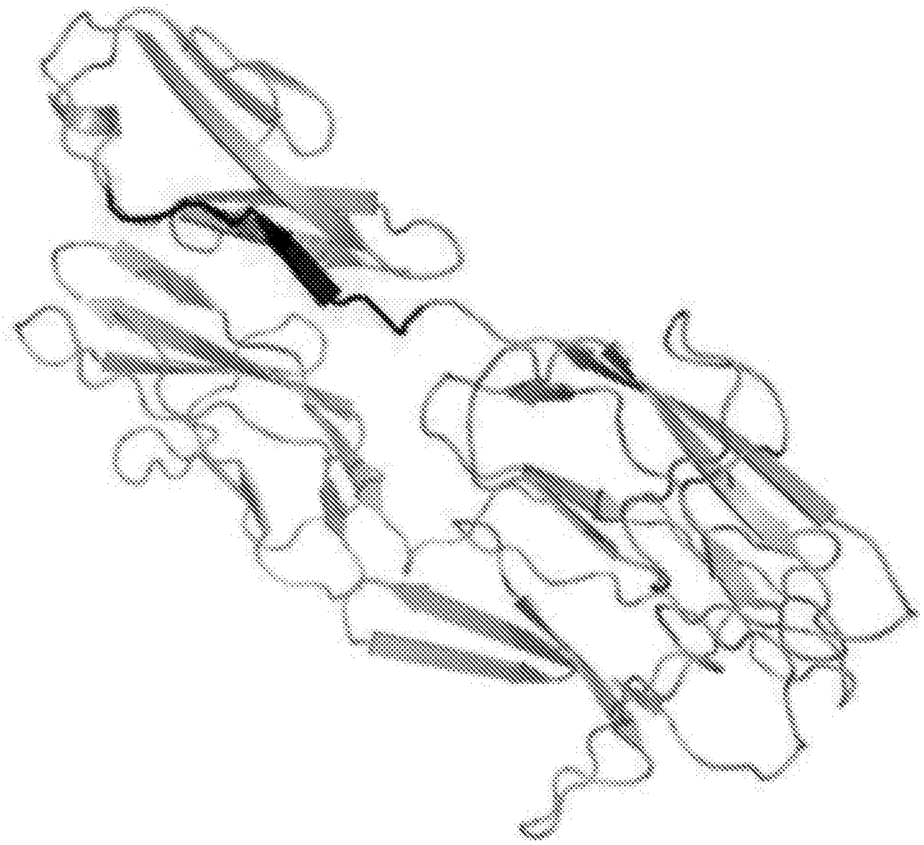


FIG. 27